```
Asp Leu Val Leu Gly Gly His Asp His Ile Tyr Thr Arg Ser His Leu
            100                 105                 110

Met Asn Gly Phe Thr Pro Val Asp Ala Gly Arg Glu Ala Val Val Gly
        115                 120                 125

Glu Thr Leu Asn Pro Lys Ala Gly Glu Val Val Tyr Leu Ala Thr Asn
    130                 135                 140

Ser Ser Ser Gly Ser Lys Phe Tyr Asp Phe Tyr Asp Phe Gln Leu Gly
145                 150                 155                 160

Gln Arg Tyr Asp Thr Gly Leu Asp Phe Gln Glu Thr Val Asp Gln Lys
                165                 170                 175

Lys Ile Arg Thr Tyr Thr Ala Val Trp Asn Gln Asp Gln Val Gln Asp
            180                 185                 190

Tyr Thr Asn Val Glu Leu Thr Pro Glu Gly Leu Thr Val Thr Thr Lys
        195                 200                 205

Asp Ala Val Ser Gly Glu Leu Val Asp Gln Phe Thr Leu Ser Lys Gln
    210                 215                 220

Asp Arg Asp Glu Glu Ser Glu Val Pro Val Glu Asp Asp Lys Asp Gly
225                 230                 235                 240

Asp Asn Ala Thr Gly Ser Ser Asn Leu Gly Leu Ala Ala Ile Leu Ala
                245                 250                 255

Pro Val Leu Ala Ile Phe Gly Phe Val Gly Gly Leu Phe Val Gly Gly
            260                 265                 270

Gly Ser Leu Ala Glu Phe Phe Ala Asn Leu Gly Val Lys Met Pro Phe
        275                 280                 285
```

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<210> 879
<211> 969
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(946)
<223> RXN01908

<400> 879
tccacgacat ctgacacaga aagaagattc accatgtcta agaacaacgc agctcacccg 60

cagtctgtct tccatatttc atatcccagc acataccact atg cac tct gac cgc 115
                                                Met His Ser Asp Arg
                                                  1   5

ttt gag cac cca gac aac ggc tat ggc tac acc att cgt cag gac act 163
Phe Glu His Pro Asp Asn Gly Tyr Gly Tyr Thr Ile Arg Gln Asp Thr
                10   15   20

```
gat gca gag aac ccg atg acc cat cac gat acg aaa gat gca gct ctc   211
Asp Ala Glu Asn Pro Met Thr His His Asp Thr Lys Asp Ala Ala Leu
            25                  30                  35

tgg gtt cac aac cga cca cga cgc gga gat acc gtc gcc gat aag cca   259
Trp Val His Asn Arg Pro Arg Arg Gly Asp Thr Val Ala Asp Lys Pro
        40                  45                  50

gaa ggc aat gag att ctc gac atc ttt gcc aag ttc atc tgc ggc cag   307
Glu Gly Asn Glu Ile Leu Asp Ile Phe Ala Lys Phe Ile Cys Gly Gln
    55                  60                  65

cac gat aat gat gac aac ccg ttc gaa gtc tgg tcc gac ggt gac tcg   355
His Asp Asn Asp Asp Asn Pro Phe Glu Val Trp Ser Asp Gly Asp Ser
70                  75                  80                  85

gat gca tca ctc atc cgc acc aag gcg tat gtt gcc gag cac cac ccc   403
Asp Ala Ser Leu Ile Arg Thr Lys Ala Tyr Val Ala Glu His His Pro
                90                  95                  100

gaa ctt ata ttc gac atc tct gcg aaa acc atc acg ggt tat tcc caa   451
Glu Leu Ile Phe Asp Ile Ser Ala Lys Thr Ile Thr Gly Tyr Ser Gln
            105                 110                 115

ggc gat tgg ctc gat gtg gtc tgt gtt act act gcc gcc act tgc gac   499
Gly Asp Trp Leu Asp Val Val Cys Val Thr Thr Ala Ala Thr Cys Asp
        120                 125                 130

gaa ctt atc cct gct gac agt ctt att gac atc tac cgc cag tgg gct   547
Glu Leu Ile Pro Ala Asp Ser Leu Ile Asp Ile Tyr Arg Gln Trp Ala
    135                 140                 145

ttt ggt gat gtg tgg aca gtg att cct gat tct cag cca ggt ctc gca   595
Phe Gly Asp Val Trp Thr Val Ile Pro Asp Ser Gln Pro Gly Leu Ala
150                 155                 160                 165

ggt att tat gct gac gat cca gct gac gcc ctt gcg tac tat caa gag   643
Gly Ile Tyr Ala Asp Asp Pro Ala Asp Ala Leu Ala Tyr Tyr Gln Glu
                170                 175                 180

aat ttc gaa gat gaa ccc atc tgg gat ctc tta agc cgc cac gac gct   691
Asn Phe Glu Asp Glu Pro Ile Trp Asp Leu Leu Ser Arg His Asp Ala
            185                 190                 195

gac aaa gac gcc gca gca ctg gca gct gcc tct gct gca gaa aac cac   739
Asp Lys Asp Ala Ala Ala Leu Ala Ala Ala Ser Ala Ala Glu Asn His
        200                 205                 210

gca cta gcg cga ggt act acc cca gtc gtt atc cgt acc caa gac atc   787
Ala Leu Ala Arg Gly Thr Thr Pro Val Val Ile Arg Thr Gln Asp Ile
    215                 220                 225

atc act aac gcg cga tac ctc atg tct gat agt gct gat gac aat cca   835
Ile Thr Asn Ala Arg Tyr Leu Met Ser Asp Ser Ala Asp Asp Asn Pro
230                 235                 240                 245

gaa tac gat cgc gcc ttg gtc gaa ctt agt gct tat ctc tta agt atc   883
Glu Tyr Asp Arg Ala Leu Val Glu Leu Ser Ala Tyr Leu Leu Ser Ile
                250                 255                 260
```

```
gac ctc gat gat cgc gtt gct gca gag atg acc att tta ggt cgc cct   931
Asp Leu Asp Asp Arg Val Ala Ala Glu Met Thr Ile Leu Gly Arg Pro
            265                 270                 275

gtg cct aaa gaa gga taaccaccac accagaaaag aag                    969
Val Pro Lys Glu Gly
        280


<210> 880
<211> 282
<212> PRT
<213> Corynebacterium glutamicum

<400> 880
Met His Ser Asp Arg Phe Glu His Pro Asp Asn Gly Tyr Gly Tyr Thr
  1               5                  10                  15

Ile Arg Gln Asp Thr Asp Ala Glu Asn Pro Met Thr His His Asp Thr
             20                  25                  30

Lys Asp Ala Ala Leu Trp Val His Asn Arg Pro Arg Arg Gly Asp Thr
         35                  40                  45

Val Ala Asp Lys Pro Glu Gly Asn Glu Ile Leu Asp Ile Phe Ala Lys
     50                  55                  60

Phe Ile Cys Gly Gln His Asp Asn Asp Asp Asn Pro Phe Glu Val Trp
 65                  70                  75                  80

Ser Asp Gly Asp Ser Asp Ala Ser Leu Ile Arg Thr Lys Ala Tyr Val
                 85                  90                  95

Ala Glu His His Pro Glu Leu Ile Phe Asp Ile Ser Ala Lys Thr Ile
            100                 105                 110

Thr Gly Tyr Ser Gln Gly Asp Trp Leu Asp Val Val Cys Val Thr Thr
        115                 120                 125

Ala Ala Thr Cys Asp Glu Leu Ile Pro Ala Asp Ser Leu Ile Asp Ile
    130                 135                 140

Tyr Arg Gln Trp Ala Phe Gly Asp Val Trp Thr Val Ile Pro Asp Ser
145                 150                 155                 160

Gln Pro Gly Leu Ala Gly Ile Tyr Ala Asp Asp Pro Ala Asp Ala Leu
                165                 170                 175

Ala Tyr Tyr Gln Glu Asn Phe Glu Asp Glu Pro Ile Trp Asp Leu Leu
            180                 185                 190

Ser Arg His Asp Ala Asp Lys Asp Ala Ala Ala Leu Ala Ala Ala Ser
        195                 200                 205

Ala Ala Glu Asn His Ala Leu Ala Arg Gly Thr Thr Pro Val Val Ile
    210                 215                 220

Arg Thr Gln Asp Ile Ile Thr Asn Ala Arg Tyr Leu Met Ser Asp Ser
225                 230                 235                 240

Ala Asp Asp Asn Pro Glu Tyr Asp Arg Ala Leu Val Glu Leu Ser Ala
```

```
                245                 250                 255

Tyr Leu Leu Ser Ile Asp Leu Asp Asp Arg Val Ala Ala Glu Met Thr
            260                 265                 270

Ile Leu Gly Arg Pro Val Pro Lys Glu Gly
        275                 280


<210> 881
<211> 583
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(583)
<223> FRXA01908

<400> 881
tccacgacat ctgacacaga aagaagattc accatgtcta agaacaacgc agctcacccg 60

cagtctgtct tccatatttc atatcccagc acataccact atg cac tct gac cgc   115
                                            Met His Ser Asp Arg
                                              1               5

ttt gag cac cca gac aac ggc tat ggc tac acc att cgt cag gac act   163
Phe Glu His Pro Asp Asn Gly Tyr Gly Tyr Thr Ile Arg Gln Asp Thr
                10                  15                  20

gat gca gag aac ccg atg acc cat cac gat acg aaa gat gca gct ctc   211
Asp Ala Glu Asn Pro Met Thr His His Asp Thr Lys Asp Ala Ala Leu
            25                  30                  35

tgg gtt cac aac cga cca cga cgc gga gat acc gtc gcc gat aag cca   259
Trp Val His Asn Arg Pro Arg Arg Gly Asp Thr Val Ala Asp Lys Pro
        40                  45                  50

gaa ggc aat gag att ctc gac atc ttt gcc aag ttc atc tgc ggc cag   307
Glu Gly Asn Glu Ile Leu Asp Ile Phe Ala Lys Phe Ile Cys Gly Gln
    55                  60                  65

cac gat aat gat gac aac ccg ttc gaa gtc tgg tcc gac ggt gac tcg   355
His Asp Asn Asp Asp Asn Pro Phe Glu Val Trp Ser Asp Gly Asp Ser
70                  75                  80                  85

gat gca tca ctc atc cgc acc aag gcg tat gtt gcc gag cac cac ccc   403
Asp Ala Ser Leu Ile Arg Thr Lys Ala Tyr Val Ala Glu His His Pro
                90                  95                  100

gaa ctt ata ttc gac atc tct gcg aaa acc atc acg ggt tat tcc caa   451
Glu Leu Ile Phe Asp Ile Ser Ala Lys Thr Ile Thr Gly Tyr Ser Gln
            105                 110                 115

ggc gat tgg ctc gat gtg gtc tgt gtt act act gcc gcc act tgc gac   499
Gly Asp Trp Leu Asp Val Val Cys Val Thr Thr Ala Ala Thr Cys Asp
        120                 125                 130

gaa ctt atc cct gct gac agt ctt att gac atc tac cgc cag tgg gct   547
Glu Leu Ile Pro Ala Asp Ser Leu Ile Asp Ile Tyr Arg Gln Trp Ala
    135                 140                 145
```

```
ttt ggt gat gtg tgg aca gtg att cct gat tct cag                    583
Phe Gly Asp Val Trp Thr Val Ile Pro Asp Ser Gln
150                 155                 160


<210> 882
<211> 161
<212> PRT
<213> Corynebacterium glutamicum

<400> 882
Met His Ser Asp Arg Phe Glu His Pro Asp Asn Gly Tyr Gly Tyr Thr
  1               5                  10                  15

Ile Arg Gln Asp Thr Asp Ala Glu Asn Pro Met Thr His His Asp Thr
             20                  25                  30

Lys Asp Ala Ala Leu Trp Val His Asn Arg Pro Arg Arg Gly Asp Thr
         35                  40                  45

Val Ala Asp Lys Pro Glu Gly Asn Glu Ile Leu Asp Ile Phe Ala Lys
     50                  55                  60

Phe Ile Cys Gly Gln His Asp Asn Asp Asp Asn Pro Phe Glu Val Trp
 65                  70                  75                  80

Ser Asp Gly Asp Ser Asp Ala Ser Leu Ile Arg Thr Lys Ala Tyr Val
                 85                  90                  95

Ala Glu His His Pro Glu Leu Ile Phe Asp Ile Ser Ala Lys Thr Ile
            100                 105                 110

Thr Gly Tyr Ser Gln Gly Asp Trp Leu Asp Val Val Cys Val Thr Thr
        115                 120                 125

Ala Ala Thr Cys Asp Glu Leu Ile Pro Ala Asp Ser Leu Ile Asp Ile
    130                 135                 140

Tyr Arg Gln Trp Ala Phe Gly Asp Val Trp Thr Val Ile Pro Asp Ser
145                 150                 155                 160

Gln


<210> 883
<211> 970
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (69)..(947)
<223> RXN01909

<400> 883
ttaataagaa ttgttctggg aagtaatata aaaagtcccg aacaaattag tgtgaaaggg 60

tttgtatcatg gct aat ttt cga agc aag gat aaa gat ggc aat gtc atc   110
        Met Ala Asn Phe Arg Ser Lys Asp Lys Asp Gly Asn Val Ile
```

```
          1               5                  10

aat ccg aac gcg tct act aaa ggt gta gat ctt gtt gtc aac gtc tac   158
Asn Pro Asn Ala Ser Thr Lys Gly Val Asp Leu Val Val Asn Val Tyr
 15                  20                  25                  30

gac agc gcc aag cat gtg acc gaa aag ggt aac act gtc cac ttt gtg   206
Asp Ser Ala Lys His Val Thr Glu Lys Gly Asn Thr Val His Phe Val
                 35                  40                  45

gat gtt cag gta gcg caa att ccg att gac gct gac ggc act cgt gcg   254
Asp Val Gln Val Ala Gln Ile Pro Ile Asp Ala Asp Gly Thr Arg Ala
             50                  55                  60

aat gcg aat ctt gca cca cag act atg cct cat ctg cat ctt gac act   302
Asn Ala Asn Leu Ala Pro Gln Thr Met Pro His Leu His Leu Asp Thr
         65                  70                  75

aag gac ggt cag cgc aac aca ggt gtt gcg tat tct gat gcg cag att   350
Lys Asp Gly Gln Arg Asn Thr Gly Val Ala Tyr Ser Asp Ala Gln Ile
     80                  85                  90

caa gcg atg cag acg gtg gca gca cag ggg cgc aac cat atg acc ccg   398
Gln Ala Met Gln Thr Val Ala Ala Gln Gly Arg Asn His Met Thr Pro
 95                 100                 105                 110

ctc ttg agc aaa gac ggt gag aca gtt ggt tac tcc atg ttg gtc aag   446
Leu Leu Ser Lys Asp Gly Glu Thr Val Gly Tyr Ser Met Leu Val Lys
                115                 120                 125

gct gat gtc atg ttc ccg aag acc aag gac ggc aag tct ctc cct gcg   494
Ala Asp Val Met Phe Pro Lys Thr Lys Asp Gly Lys Ser Leu Pro Ala
            130                 135                 140

gtc atg aac act aag tct ctg cag cca tct ggg gtt cct att tcg gac   542
Val Met Asn Thr Lys Ser Leu Gln Pro Ser Gly Val Pro Ile Ser Asp
        145                 150                 155

gcg atg aat att cag cag cag cag ttt atg gct gtg gca atg aat cgc   590
Ala Met Asn Ile Gln Gln Gln Gln Phe Met Ala Val Ala Met Asn Arg
    160                 165                 170

caa gca gca gaa gcg cag aag gct gca caa gcc caa gcg acc cag gct   638
Gln Ala Ala Glu Ala Gln Lys Ala Ala Gln Ala Gln Ala Thr Gln Ala
175                 180                 185                 190

caa gca cca cag gtg gca ccg cag cca gtt atg cag aat cag caa ttc   686
Gln Ala Pro Gln Val Ala Pro Gln Pro Val Met Gln Asn Gln Gln Phe
                195                 200                 205

cag gca cca gtg cca cag ggc cag cag cca gca tat gca gga gcc cct   734
Gln Ala Pro Val Pro Gln Gly Gln Gln Pro Ala Tyr Ala Gly Ala Pro
            210                 215                 220

gtc tat gca gac gcg gta gct cat gca acc gcg cag cag cag gca gca   782
Val Tyr Ala Asp Ala Val Ala His Ala Thr Ala Gln Gln Gln Ala Ala
        225                 230                 235

gca gct cag gca ccg cag gca cct gct ggg aat ccg ttt aac cag ccg   830
Ala Ala Gln Ala Pro Gln Ala Pro Ala Gly Asn Pro Phe Asn Gln Pro
    240                 245                 250
```

```
cca gca gta gca gca gct ctg gca ccg cag acg cag ccg cca gca gta   878
Pro Ala Val Ala Ala Ala Leu Ala Pro Gln Thr Gln Pro Pro Ala Val
255                 260                 265                 270

gca gca gct ctg gca ccg cag acg cag cag ccg gca gca caa cct cag   926
Ala Ala Ala Leu Ala Pro Gln Thr Gln Gln Pro Ala Ala Gln Pro Gln
                275                 280                 285

atg gat aac gag cca ccg ttt taaaggcgca atacaccaca ccc             970
Met Asp Asn Glu Pro Pro Phe
            290
```

<210> 884
<211> 293
<212> PRT
<213> Corynebacterium glutamicum

<400> 884

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Met Ala Asn Phe Arg Ser Lys Asp Lys Asp Gly Asn Val Ile Asn Pro
  1               5                  10                  15

Asn Ala Ser Thr Lys Gly Val Asp Leu Val Val Asn Val Tyr Asp Ser
             20                  25                  30

Ala Lys His Val Thr Glu Lys Gly Asn Thr Val His Phe Val Asp Val
         35                  40                  45

Gln Val Ala Gln Ile Pro Ile Asp Ala Asp Gly Thr Arg Ala Asn Ala
     50                  55                  60

Asn Leu Ala Pro Gln Thr Met Pro His Leu His Leu Asp Thr Lys Asp
 65                  70                  75                  80

Gly Gln Arg Asn Thr Gly Val Ala Tyr Ser Asp Ala Gln Ile Gln Ala
                 85                  90                  95

Met Gln Thr Val Ala Ala Gln Gly Arg Asn His Met Thr Pro Leu Leu
            100                 105                 110

Ser Lys Asp Gly Glu Thr Val Gly Tyr Ser Met Leu Val Lys Ala Asp
        115                 120                 125

Val Met Phe Pro Lys Thr Lys Asp Gly Lys Ser Leu Pro Ala Val Met
    130                 135                 140

Asn Thr Lys Ser Leu Gln Pro Ser Gly Val Pro Ile Ser Asp Ala Met
145                 150                 155                 160

Asn Ile Gln Gln Gln Gln Phe Met Ala Val Ala Met Asn Arg Gln Ala
                165                 170                 175

Ala Glu Ala Gln Lys Ala Ala Gln Ala Gln Ala Thr Gln Ala Gln Ala
            180                 185                 190

Pro Gln Val Ala Pro Gln Pro Val Met Gln Asn Gln Gln Phe Gln Ala
        195                 200                 205

Pro Val Pro Gln Gly Gln Gln Pro Ala Tyr Ala Gly Ala Pro Val Tyr
    210                 215                 220
```

```
Ala Asp Ala Val Ala His Ala Thr Ala Gln Gln Gln Ala Ala Ala Ala
225                 230                 235                 240

Gln Ala Pro Gln Ala Pro Ala Gly Asn Pro Phe Asn Gln Pro Pro Ala
                245                 250                 255

Val Ala Ala Ala Leu Ala Pro Gln Thr Gln Pro Pro Ala Val Ala Ala
            260                 265                 270

Ala Leu Ala Pro Gln Thr Gln Gln Pro Ala Ala Gln Pro Gln Met Asp
        275                 280                 285

Asn Glu Pro Pro Phe
    290
```

<210> 885
<211> 960
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (59)..(937)
<223> FRXA01909

<400> 885

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ttgttctggg aagtaatata aaaagtcccg aacaaattag tgtgaaaggg tttgtatcatg 61
                                                              Met
                                                               1

gct aat ttt cga agc aag gat aaa gat ggc aat gtc atc aat ccg aac  109
Ala Asn Phe Arg Ser Lys Asp Lys Asp Gly Asn Val Ile Asn Pro Asn
              5                  10                  15

gcg tct act aaa ggt gta gat ctt gtt gtc aac gtc tac gac agc gcc  157
Ala Ser Thr Lys Gly Val Asp Leu Val Val Asn Val Tyr Asp Ser Ala
         20                  25                  30

aag cat gtg acc gaa aag ggt aac act gtc cac ttt gtg gat gtt cag  205
Lys His Val Thr Glu Lys Gly Asn Thr Val His Phe Val Asp Val Gln
     35                  40                  45

gta gcg caa att ccg att gac gct gac ggc act cgt gcg aat gcg aat  253
Val Ala Gln Ile Pro Ile Asp Ala Asp Gly Thr Arg Ala Asn Ala Asn
 50                  55                  60                  65

ctt gca cca cag act atg cct cat ctg cat ctt gac act aag gac ggt  301
Leu Ala Pro Gln Thr Met Pro His Leu His Leu Asp Thr Lys Asp Gly
                 70                  75                  80

cag cgc aac aca ggt gtt gcg tat tct gat gcg cag att caa gcg atg  349
Gln Arg Asn Thr Gly Val Ala Tyr Ser Asp Ala Gln Ile Gln Ala Met
             85                  90                  95

cag acg gtg gca gca cag ggg cgc aac cat atg acc ccg ctc ttg agc  397
Gln Thr Val Ala Ala Gln Gly Arg Asn His Met Thr Pro Leu Leu Ser
        100                 105                 110

aaa gac ggt gag aca gtt ggt tac tcc atg ttg gtc aag gct gat gtc  445
```

```
Lys Asp Gly Glu Thr Val Gly Tyr Ser Met Leu Val Lys Ala Asp Val
    115                 120                 125

atg ttc ccg aag acc aag gac ggc aag tct ctc cct gcg gtc atg aac   493
Met Phe Pro Lys Thr Lys Asp Gly Lys Ser Leu Pro Ala Val Met Asn
130                 135                 140                 145

act aag tct ctg cag cca tct ggg gtt cct att tcg gac gcg atg aat   541
Thr Lys Ser Leu Gln Pro Ser Gly Val Pro Ile Ser Asp Ala Met Asn
                150                 155                 160

att cag cag cag cag ttt atg gct gtg gca atg aat cgc caa gca gca   589
Ile Gln Gln Gln Gln Phe Met Ala Val Ala Met Asn Arg Gln Ala Ala
            165                 170                 175

gaa gcg cag aag gct gca caa gcc caa gcg acc cag gct caa gca cca   637
Glu Ala Gln Lys Ala Ala Gln Ala Gln Ala Thr Gln Ala Gln Ala Pro
        180                 185                 190

cag gtg gca ccg cag cca gtt atg cag aat cag caa ttc cag gca cca   685
Gln Val Ala Pro Gln Pro Val Met Gln Asn Gln Gln Phe Gln Ala Pro
    195                 200                 205

gtg cca cag ggc cag cag cca gca tat gca gga gcc cct gtc tat gca   733
Val Pro Gln Gly Gln Gln Pro Ala Tyr Ala Gly Ala Pro Val Tyr Ala
210                 215                 220                 225

gac gcg gta gct cat gca acc gcg cag cag cag gca gca gca gct cag   781
Asp Ala Val Ala His Ala Thr Ala Gln Gln Gln Ala Ala Ala Ala Gln
                230                 235                 240

gca ccg cag gca cct gct ggg aat ccg ttt aac cag ccg cca gca gta   829
Ala Pro Gln Ala Pro Ala Gly Asn Pro Phe Asn Gln Pro Pro Ala Val
            245                 250                 255

gca gca gct ctg gca ccg cag acg cag ccg cca gca gta gca gca gct   877
Ala Ala Ala Leu Ala Pro Gln Thr Gln Pro Pro Ala Val Ala Ala Ala
        260                 265                 270

ctg gca ccg cag acg cag cag ccg gca gca caa cct cag atg gat aac   925
Leu Ala Pro Gln Thr Gln Gln Pro Ala Ala Gln Pro Gln Met Asp Asn
    275                 280                 285

gag cca ccg ttt taaaggcgca atacaccaca ccc                        960
Glu Pro Pro Phe
290
```

<210> 886
<211> 293
<212> PRT
<213> Corynebacterium glutamicum

<400> 886

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Met Ala Asn Phe Arg Ser Lys Asp Lys Asp Gly Asn Val Ile Asn Pro
  1               5                  10                  15

Asn Ala Ser Thr Lys Gly Val Asp Leu Val Val Asn Val Tyr Asp Ser
             20                  25                  30

Ala Lys His Val Thr Glu Lys Gly Asn Thr Val His Phe Val Asp Val
```

```
         35                  40                  45

Gln Val Ala Gln Ile Pro Ile Asp Ala Asp Gly Thr Arg Ala Asn Ala
     50                  55                  60

Asn Leu Ala Pro Gln Thr Met Pro His Leu His Leu Asp Thr Lys Asp
 65                  70                  75                  80

Gly Gln Arg Asn Thr Gly Val Ala Tyr Ser Asp Ala Gln Ile Gln Ala
                 85                  90                  95

Met Gln Thr Val Ala Ala Gln Gly Arg Asn His Met Thr Pro Leu Leu
            100                 105                 110

Ser Lys Asp Gly Glu Thr Val Gly Tyr Ser Met Leu Val Lys Ala Asp
        115                 120                 125

Val Met Phe Pro Lys Thr Lys Asp Gly Lys Ser Leu Pro Ala Val Met
    130                 135                 140

Asn Thr Lys Ser Leu Gln Pro Ser Gly Val Pro Ile Ser Asp Ala Met
145                 150                 155                 160

Asn Ile Gln Gln Gln Gln Phe Met Ala Val Ala Met Asn Arg Gln Ala
                165                 170                 175

Ala Glu Ala Gln Lys Ala Ala Gln Ala Gln Ala Thr Gln Ala Gln Ala
            180                 185                 190

Pro Gln Val Ala Pro Gln Pro Val Met Gln Asn Gln Gln Phe Gln Ala
        195                 200                 205

Pro Val Pro Gln Gly Gln Gln Pro Ala Tyr Ala Gly Ala Pro Val Tyr
    210                 215                 220

Ala Asp Ala Val Ala His Ala Thr Ala Gln Gln Gln Ala Ala Ala Ala
225                 230                 235                 240

Gln Ala Pro Gln Ala Pro Ala Gly Asn Pro Phe Asn Gln Pro Pro Ala
                245                 250                 255

Val Ala Ala Ala Leu Ala Pro Gln Thr Gln Pro Pro Ala Val Ala Ala
            260                 265                 270

Ala Leu Ala Pro Gln Thr Gln Gln Pro Ala Ala Gln Pro Gln Met Asp
        275                 280                 285

Asn Glu Pro Pro Phe
    290
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<210> 887
<211> 969
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(946)
<223> RXN01910

<400> 887
caccgtttta aaggcgcaat acaccacacc ccaacaaact ttttgattgt tggggtgttt 60

gtctcagatc atgaacagca caatgtagga gaagattgat atg gca ttt ccg ctt 115
Met Ala Phe Pro Leu
1 5

cta gcg gtt gct ggc aca gtt gcc ccc gtt gca gca gga tgg gca aaa 163
Leu Ala Val Ala Gly Thr Val Ala Pro Val Ala Ala Gly Trp Ala Lys
10 15 20

gat aag ttt ctc agc aac tct cag aat aat cag cag gcc cag aat cag 211
Asp Lys Phe Leu Ser Asn Ser Gln Asn Asn Gln Gln Ala Gln Asn Gln
25 30 35

cag atg agt ttt gga cag gtc aac aac agc gca cag aat tct gga tca 259
Gln Met Ser Phe Gly Gln Val Asn Asn Ser Ala Gln Asn Ser Gly Ser
40 45 50

gaa aac agc ggt ttc atg ggt caa tac ggc aat ctg ggt gca ggt ttg 307
Glu Asn Ser Gly Phe Met Gly Gln Tyr Gly Asn Leu Gly Ala Gly Leu
55 60 65

gca ggt gct gct aca ggc gca ggg ctt gcg tat agc gat ttt gaa gat 355
Ala Gly Ala Ala Thr Gly Ala Gly Leu Ala Tyr Ser Asp Phe Glu Asp
70 75 80 85

ggt caa agt ttg tcc tcg aag gcc cgc aac atg gtc ggc aaa ggg ctc 403
Gly Gln Ser Leu Ser Ser Lys Ala Arg Asn Met Val Gly Lys Gly Leu
90 95 100

gct ggt gcc gga gct ggt gtg ttc acc aag ctt gcc aat gat gca att 451
Ala Gly Ala Gly Ala Gly Val Phe Thr Lys Leu Ala Asn Asp Ala Ile
105 110 115

cag gcc gag ggt ggc tcg atg aag gct agt gct tat tct gcc att gca 499
Gln Ala Glu Gly Gly Ser Met Lys Ala Ser Ala Tyr Ser Ala Ile Ala
120 125 130

ggc ggc ttg gga tcg tat ctc aaa gac ggc ggt ccg ggt gtg att aaa 547
Gly Gly Leu Gly Ser Tyr Leu Lys Asp Gly Gly Pro Gly Val Ile Lys
135 140 145

tcc gcg atg gcc agc ggt gca gcc ggt ttt ggt gcg gat aaa gtg cac 595
Ser Ala Met Ala Ser Gly Ala Ala Gly Phe Gly Ala Asp Lys Val His
150 155 160 165

gat aaa tta gct gag tct ggt cat gag ggg ttg gct gat tcc ttg tcg 643
Asp Lys Leu Ala Glu Ser Gly His Glu Gly Leu Ala Asp Ser Leu Ser
170 175 180

ggc gct att caa gga ggt ggt ctt ggt tac tcc acg ctt ggc ggt gtc 691
Gly Ala Ile Gln Gly Gly Gly Leu Gly Tyr Ser Thr Leu Gly Gly Val
185 190 195

act ggt gct ggt att ggc ggt gcg acg ggc ggt ctc gca gga cta gca 739
Thr Gly Ala Gly Ile Gly Gly Ala Thr Gly Gly Leu Ala Gly Leu Ala
200 205 210

caa aac tac ttt ggt ggt ggc gat gac tac agc aac gct ggg gca tct 787
Gln Asn Tyr Phe Gly Gly Gly Asp Asp Tyr Ser Asn Ala Gly Ala Ser

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    215                 220                 225

gca tcg ggg ttt agt gcc aac cag gtt aat agt gag atc agc acc gag   835
Ala Ser Gly Phe Ser Ala Asn Gln Val Asn Ser Glu Ile Ser Thr Glu
230                 235                 240                 245

att ccg cag ttt gcg aat ctt ggt caa cca cag cga tcc gag ctt gaa   883
Ile Pro Gln Phe Ala Asn Leu Gly Gln Pro Gln Arg Ser Glu Leu Glu
                250                 255                 260

caa tta gcg cta cct caa gaa tca cgg tct gta gat aag agc tac gac   931
Gln Leu Ala Leu Pro Gln Glu Ser Arg Ser Val Asp Lys Ser Tyr Asp
            265                 270                 275

caa ggc tac gaa gcg taagcgcttt ataacaaccc cgt                    969
Gln Gly Tyr Glu Ala
        280


<210> 888
<211> 282
<212> PRT
<213> Corynebacterium glutamicum

<400> 888
Met Ala Phe Pro Leu Leu Ala Val Ala Gly Thr Val Ala Pro Val Ala
  1               5                  10                  15

Ala Gly Trp Ala Lys Asp Lys Phe Leu Ser Asn Ser Gln Asn Asn Gln
             20                  25                  30

Gln Ala Gln Asn Gln Gln Met Ser Phe Gly Gln Val Asn Asn Ser Ala
         35                  40                  45

Gln Asn Ser Gly Ser Glu Asn Ser Gly Phe Met Gly Gln Tyr Gly Asn
     50                  55                  60

Leu Gly Ala Gly Leu Ala Gly Ala Ala Thr Gly Ala Gly Leu Ala Tyr
 65                  70                  75                  80

Ser Asp Phe Glu Asp Gly Gln Ser Leu Ser Ser Lys Ala Arg Asn Met
                 85                  90                  95

Val Gly Lys Gly Leu Ala Gly Ala Gly Ala Gly Val Phe Thr Lys Leu
            100                 105                 110

Ala Asn Asp Ala Ile Gln Ala Glu Gly Gly Ser Met Lys Ala Ser Ala
        115                 120                 125

Tyr Ser Ala Ile Ala Gly Gly Leu Gly Ser Tyr Leu Lys Asp Gly Gly
    130                 135                 140

Pro Gly Val Ile Lys Ser Ala Met Ala Ser Gly Ala Ala Gly Phe Gly
145                 150                 155                 160

Ala Asp Lys Val His Asp Lys Leu Ala Glu Ser Gly His Glu Gly Leu
                165                 170                 175

Ala Asp Ser Leu Ser Gly Ala Ile Gln Gly Gly Gly Leu Gly Tyr Ser
            180                 185                 190
```

```
Thr Leu Gly Gly Val Thr Gly Ala Gly Ile Gly Gly Ala Thr Gly Gly
        195                 200                 205

Leu Ala Gly Leu Ala Gln Asn Tyr Phe Gly Gly Gly Asp Asp Tyr Ser
    210                 215                 220

Asn Ala Gly Ala Ser Ala Ser Gly Phe Ser Ala Asn Gln Val Asn Ser
225                 230                 235                 240

Glu Ile Ser Thr Glu Ile Pro Gln Phe Ala Asn Leu Gly Gln Pro Gln
                245                 250                 255

Arg Ser Glu Leu Glu Gln Leu Ala Leu Pro Gln Glu Ser Arg Ser Val
            260                 265                 270

Asp Lys Ser Tyr Asp Gln Gly Tyr Glu Ala
        275                 280


<210> 889
<211> 969
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(946)
<223> FRXA01910

<400> 889
caccgtttta aaggcgcaat acaccacacc ccaacaaact ttttgattgt tggggtgttt 60

gtctcagatc atgaacagca caatgtagga gaagattgat atg gca ttt ccg ctt   115
                                            Met Ala Phe Pro Leu
                                              1               5

cta gcg gtt gct ggc aca gtt gcc ccc gtt gca gca gga tgg gca aaa   163
Leu Ala Val Ala Gly Thr Val Ala Pro Val Ala Ala Gly Trp Ala Lys
                10                  15                  20

gat aag ttt ctc agc aac tct cag aat aat cag cag gcc cag aat cag   211
Asp Lys Phe Leu Ser Asn Ser Gln Asn Asn Gln Gln Ala Gln Asn Gln
            25                  30                  35

cag atg agt ttt gga cag gtc aac aac agc gca cag aat tct gga tca   259
Gln Met Ser Phe Gly Gln Val Asn Asn Ser Ala Gln Asn Ser Gly Ser
        40                  45                  50

gaa aac agc ggt ttc atg ggt caa tac ggc aat ctg ggt gca ggt ttg   307
Glu Asn Ser Gly Phe Met Gly Gln Tyr Gly Asn Leu Gly Ala Gly Leu
    55                  60                  65

gca ggt gct gct aca ggc gca ggg ctt gcg tat agc gat ttt gaa gat   355
Ala Gly Ala Ala Thr Gly Ala Gly Leu Ala Tyr Ser Asp Phe Glu Asp
70                  75                  80                  85

ggt caa agt ttg tcc tcg aag gcc cgc aac atg gtc ggc aaa ggg ctc   403
Gly Gln Ser Leu Ser Ser Lys Ala Arg Asn Met Val Gly Lys Gly Leu
                90                  95                  100

gct ggt gcc gga gct ggt gtg ttc acc aag ctt gcc aat gat gca att   451
```

```
Ala Gly Ala Gly Ala Gly Val Phe Thr Lys Leu Ala Asn Asp Ala Ile
            105                 110                 115

cag gcc gag ggt ggc tcg atg aag gct agt gct tat tct gcc att gca   499
Gln Ala Glu Gly Gly Ser Met Lys Ala Ser Ala Tyr Ser Ala Ile Ala
        120                 125                 130

agc ggc ttg gga tcg tat ctc aaa aac ggc ggt ccg ggt gtg att aaa   547
Ser Gly Leu Gly Ser Tyr Leu Lys Asn Gly Gly Pro Gly Val Ile Lys
    135                 140                 145

tcc gcg atg gcc agc ggt gca gcc ggt ttt ggt gcg gat aaa gtg cac   595
Ser Ala Met Ala Ser Gly Ala Ala Gly Phe Gly Ala Asp Lys Val His
150                 155                 160                 165

gat aaa tta gct gag tct ggt cat gag ggg ttg gct gat tcc ttg tcg   643
Asp Lys Leu Ala Glu Ser Gly His Glu Gly Leu Ala Asp Ser Leu Ser
                170                 175                 180

ggc gct att caa gga ggt ggt ctt ggt tac tcc acg ctt ggc ggt gtc   691
Gly Ala Ile Gln Gly Gly Gly Leu Gly Tyr Ser Thr Leu Gly Gly Val
            185                 190                 195

act ggt gct ggt att ggc ggt gcg acg ggc ggt ctc gca gga cta gca   739
Thr Gly Ala Gly Ile Gly Gly Ala Thr Gly Gly Leu Ala Gly Leu Ala
        200                 205                 210

caa aac tac ttt ggt ggt ggc gat gac tac agc aac gct ggg gca tct   787
Gln Asn Tyr Phe Gly Gly Gly Asp Asp Tyr Ser Asn Ala Gly Ala Ser
    215                 220                 225

gca tcg ggg ttt agt gcc aac cag gtt aat agt gag atc agc acc gag   835
Ala Ser Gly Phe Ser Ala Asn Gln Val Asn Ser Glu Ile Ser Thr Glu
230                 235                 240                 245

att ccg cag ttt gcg aat ctt ggt caa cca cag cga tcc gag ctt gaa   883
Ile Pro Gln Phe Ala Asn Leu Gly Gln Pro Gln Arg Ser Glu Leu Glu
                250                 255                 260

caa tta gcg cta cct caa gaa tca cgg tct gta gat aag agc tac gac   931
Gln Leu Ala Leu Pro Gln Glu Ser Arg Ser Val Asp Lys Ser Tyr Asp
            265                 270                 275

caa ggc tac gaa gcg taagcgcttt ataacaaccc cgt                     969
Gln Gly Tyr Glu Ala
        280


<210> 890
<211> 282
<212> PRT
<213> Corynebacterium glutamicum

<400> 890
Met Ala Phe Pro Leu Leu Ala Val Ala Gly Thr Val Ala Pro Val Ala
  1               5                  10                  15

Ala Gly Trp Ala Lys Asp Lys Phe Leu Ser Asn Ser Gln Asn Asn Gln
             20                  25                  30

Gln Ala Gln Asn Gln Gln Met Ser Phe Gly Gln Val Asn Asn Ser Ala
```

```
         35                  40                  45

Gln Asn Ser Gly Ser Glu Asn Ser Gly Phe Met Gly Gln Tyr Gly Asn
     50                  55                  60

Leu Gly Ala Gly Leu Ala Gly Ala Ala Thr Gly Ala Gly Leu Ala Tyr
 65                  70                  75                  80

Ser Asp Phe Glu Asp Gly Gln Ser Leu Ser Ser Lys Ala Arg Asn Met
                 85                  90                  95

Val Gly Lys Gly Leu Ala Gly Ala Gly Ala Gly Val Phe Thr Lys Leu
            100                 105                 110

Ala Asn Asp Ala Ile Gln Ala Glu Gly Gly Ser Met Lys Ala Ser Ala
        115                 120                 125

Tyr Ser Ala Ile Ala Ser Gly Leu Gly Ser Tyr Leu Lys Asn Gly Gly
    130                 135                 140

Pro Gly Val Ile Lys Ser Ala Met Ala Ser Gly Ala Ala Gly Phe Gly
145                 150                 155                 160

Ala Asp Lys Val His Asp Lys Leu Ala Glu Ser Gly His Glu Gly Leu
                165                 170                 175

Ala Asp Ser Leu Ser Gly Ala Ile Gln Gly Gly Gly Leu Gly Tyr Ser
            180                 185                 190

Thr Leu Gly Gly Val Thr Gly Ala Gly Ile Gly Gly Ala Thr Gly Gly
        195                 200                 205

Leu Ala Gly Leu Ala Gln Asn Tyr Phe Gly Gly Gly Asp Asp Tyr Ser
    210                 215                 220

Asn Ala Gly Ala Ser Ala Ser Gly Phe Ser Ala Asn Gln Val Asn Ser
225                 230                 235                 240

Glu Ile Ser Thr Glu Ile Pro Gln Phe Ala Asn Leu Gly Gln Pro Gln
                245                 250                 255

Arg Ser Glu Leu Glu Gln Leu Ala Leu Pro Gln Glu Ser Arg Ser Val
            260                 265                 270

Asp Lys Ser Tyr Asp Gln Gly Tyr Glu Ala
        275                 280


<210> 891
<211> 1062
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1039)
<223> RXN01911

<400> 891
agatgccgca gatcaccgag tgagcgttac tgagatcact gagtctcgat gggtaatcca 60
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tataattgtg agcgggattc ttagtgcgct cgcggttctg gtg ttt att att ggc   115
                                             Val Phe Ile Ile Gly
                                               1               5

gcc ggc ttg cca ctg ttg tac gtg ccg att ttt gtg act gtc atc gtc   163
Ala Gly Leu Pro Leu Leu Tyr Val Pro Ile Phe Val Thr Val Ile Val
                10                  15                  20

atg gtg gtg tat gcg cta ttg cgc tat gag cag cgc atg tca ggc aca   211
Met Val Val Tyr Ala Leu Leu Arg Tyr Glu Gln Arg Met Ser Gly Thr
            25                  30                  35

gtc tac gag gaa gca gat cct gtc gaa atg gat tca gtg atc tgg gag   259
Val Tyr Glu Glu Ala Asp Pro Val Glu Met Asp Ser Val Ile Trp Glu
        40                  45                  50

ggc atc aag tgc gat att gcc tcg gat att gca gcc cga gca gaa gcg   307
Gly Ile Lys Cys Asp Ile Ala Ser Asp Ile Ala Ala Arg Ala Glu Ala
    55                  60                  65

aaa aaa gcg aaa aag cca gtt gcg tca gat gct gtt gct gtt ggt aac   355
Lys Lys Ala Lys Lys Pro Val Ala Ser Asp Ala Val Ala Val Gly Asn
70                  75                  80                  85

tat atc gcg tcc ttg cgt cag cat atg ttg gta gaa acc cag cga cgt   403
Tyr Ile Ala Ser Leu Arg Gln His Met Leu Val Glu Thr Gln Arg Arg
                90                  95                  100

tat cac cac aag ctt ggt cgt gag ctg cat aat gat cca gcg caa cta   451
Tyr His His Lys Leu Gly Arg Glu Leu His Asn Asp Pro Ala Gln Leu
            105                 110                 115

gag gat tat ggc tct ggt ctg cgt gac tgt gag tgt cgg gca tgt gtg   499
Glu Asp Tyr Gly Ser Gly Leu Arg Asp Cys Glu Cys Arg Ala Cys Val
        120                 125                 130

gtg gct cag aaa ttg ggt gtc acg gtg cac gct cat ggt gtg gtg cag   547
Val Ala Gln Lys Leu Gly Val Thr Val His Ala His Gly Val Val Gln
    135                 140                 145

gcg agc gca cgt aaa aaa gat cgc gtc att att ggg cga gcc gat ggt   595
Ala Ser Ala Arg Lys Lys Asp Arg Val Ile Ile Gly Arg Ala Asp Gly
150                 155                 160                 165

att gat gtg gcc ggc tgg tgg aac cac cgc caa gaa gct cga cgt aaa   643
Ile Asp Val Ala Gly Trp Trp Asn His Arg Gln Glu Ala Arg Arg Lys
                170                 175                 180

acg agc gcg gct aag cag ttg gag cgc gat gca caa cgc aag cga acc   691
Thr Ser Ala Ala Lys Gln Leu Glu Arg Asp Ala Gln Arg Lys Arg Thr
            185                 190                 195

caa gct gag cgc gat aaa gag att gag cgt aag cgt aag gct caa gaa   739
Gln Ala Glu Arg Asp Lys Glu Ile Glu Arg Lys Arg Lys Ala Gln Glu
        200                 205                 210

ttt gta gcg gag cag tca ggg aaa gct gct gca gca caa cgg cgg gcc   787
Phe Val Ala Glu Gln Ser Gly Lys Ala Ala Ala Ala Gln Arg Arg Ala
    215                 220                 225

gag aaa aag gct gcg aag caa gcg cgt gta gat gaa ctg gtg gcg cag   835
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```
Glu Lys Lys Ala Ala Lys Gln Ala Arg Val Asp Glu Leu Val Ala Gln
230                 235                 240                 245

aaa cag gct gct cag gag cag aaa act cac tgt aag cgg gac aag cag   883
Lys Gln Ala Ala Gln Glu Gln Lys Thr His Cys Lys Arg Asp Lys Gln
                250                 255                 260

cgt gcg aag aaa gca caa ggg cgc aaa gtt ggt gcc gtt gat aat tcc   931
Arg Ala Lys Lys Ala Gln Gly Arg Lys Val Gly Ala Val Asp Asn Ser
            265                 270                 275

gct gtg gac gat gtg ttg gcg tat gcg gag aaa acc cgc agt ata gct   979
Ala Val Asp Asp Val Leu Ala Tyr Ala Glu Lys Thr Arg Ser Ile Ala
        280                 285                 290

ggc tgt aga gat gac gac agc gtt gtg cac gtt gat atg gca gcg ggt   1027
Gly Cys Arg Asp Asp Asp Ser Val Val His Val Asp Met Ala Ala Gly
    295                 300                 305

gtc cgc gat gtc taaatcgcag gatgatcgaa aaa                        1062
Val Arg Asp Val
310
```

<210> 892
<211> 313
<212> PRT
<213> Corynebacterium glutamicum

<400> 892

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Val Phe Ile Ile Gly Ala Gly Leu Pro Leu Leu Tyr Val Pro Ile Phe
  1               5                  10                  15

Val Thr Val Ile Val Met Val Val Tyr Ala Leu Leu Arg Tyr Glu Gln
             20                  25                  30

Arg Met Ser Gly Thr Val Tyr Glu Glu Ala Asp Pro Val Glu Met Asp
         35                  40                  45

Ser Val Ile Trp Glu Gly Ile Lys Cys Asp Ile Ala Ser Asp Ile Ala
     50                  55                  60

Ala Arg Ala Glu Ala Lys Lys Ala Lys Lys Pro Val Ala Ser Asp Ala
 65                  70                  75                  80

Val Ala Val Gly Asn Tyr Ile Ala Ser Leu Arg Gln His Met Leu Val
                 85                  90                  95

Glu Thr Gln Arg Arg Tyr His His Lys Leu Gly Arg Glu Leu His Asn
            100                 105                 110

Asp Pro Ala Gln Leu Glu Asp Tyr Gly Ser Gly Leu Arg Asp Cys Glu
        115                 120                 125

Cys Arg Ala Cys Val Val Ala Gln Lys Leu Gly Val Thr Val His Ala
    130                 135                 140

His Gly Val Val Gln Ala Ser Ala Arg Lys Lys Asp Arg Val Ile Ile
145                 150                 155                 160

Gly Arg Ala Asp Gly Ile Asp Val Ala Gly Trp Trp Asn His Arg Gln
```

```
                165                 170                 175

Glu Ala Arg Arg Lys Thr Ser Ala Ala Lys Gln Leu Glu Arg Asp Ala
            180                 185                 190

Gln Arg Lys Arg Thr Gln Ala Glu Arg Asp Lys Glu Ile Glu Arg Lys
        195                 200                 205

Arg Lys Ala Gln Glu Phe Val Ala Glu Gln Ser Gly Lys Ala Ala Ala
    210                 215                 220

Ala Gln Arg Arg Ala Glu Lys Lys Ala Ala Lys Gln Ala Arg Val Asp
225                 230                 235                 240

Glu Leu Val Ala Gln Lys Gln Ala Ala Gln Glu Gln Lys Thr His Cys
                245                 250                 255

Lys Arg Asp Lys Gln Arg Ala Lys Lys Ala Gln Gly Arg Lys Val Gly
            260                 265                 270

Ala Val Asp Asn Ser Ala Val Asp Asp Val Leu Ala Tyr Ala Glu Lys
        275                 280                 285

Thr Arg Ser Ile Ala Gly Cys Arg Asp Asp Asp Ser Val Val His Val
    290                 295                 300

Asp Met Ala Ala Gly Val Arg Asp Val
305                 310


<210> 893
<211> 946
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(946)
<223> FRXA01911

<400> 893
agatgccgca gatcaccgag tgagcgttac tgagatcact gagtctcgat gggtaatcca 60

tataattgtg agcgggattc ttagtgcgct cgcggttctg gtg ttt att att ggc   115
                                              Val Phe Ile Ile Gly
                                                1               5

gcc ggc ttg cca ctg ttg tac gtg ccg att ttt gtg act gtc atc gtc   163
Ala Gly Leu Pro Leu Leu Tyr Val Pro Ile Phe Val Thr Val Ile Val
                10                  15                  20

atg gtg gtg tat gcg cta ttg cgc tat gag cag cgc atg tca ggc aca   211
Met Val Val Tyr Ala Leu Leu Arg Tyr Glu Gln Arg Met Ser Gly Thr
            25                  30                  35

gtc tac gag gaa gca gat cct gtc gaa atg gat tca gtg atc tgg gag   259
Val Tyr Glu Glu Ala Asp Pro Val Glu Met Asp Ser Val Ile Trp Glu
        40                  45                  50

ggc atc aag tgc gat att gcc tcg gat att gca gcc cga gca gaa gcg   307
Gly Ile Lys Cys Asp Ile Ala Ser Asp Ile Ala Ala Arg Ala Glu Ala
```

```
     55                  60                  65

aaa aaa gcg aaa aag cca gtt gcg tca gat gct gtt gct gtt ggt aac   355
Lys Lys Ala Lys Lys Pro Val Ala Ser Asp Ala Val Ala Val Gly Asn
 70                  75                  80                  85

tat atc gcg tcc ttg cgt cag cat atg ttg gta gaa acc cag cga cgt   403
Tyr Ile Ala Ser Leu Arg Gln His Met Leu Val Glu Thr Gln Arg Arg
                 90                  95                 100

tat cac cac aag ctt ggt cgt gag ctg cat aat gat cca gcg caa cta   451
Tyr His His Lys Leu Gly Arg Glu Leu His Asn Asp Pro Ala Gln Leu
            105                 110                 115

gag gat tat ggc tct ggt ctg cgt gac tgt gag tgt cgg gca tgt gtg   499
Glu Asp Tyr Gly Ser Gly Leu Arg Asp Cys Glu Cys Arg Ala Cys Val
        120                 125                 130

gtg gct cag aaa ttg ggt gtc acg gtg cac gct cat ggt gtg gtg cag   547
Val Ala Gln Lys Leu Gly Val Thr Val His Ala His Gly Val Val Gln
    135                 140                 145

gcg agc gca cgt aaa aaa gat cgc gtc att att ggg cga gcc gat ggt   595
Ala Ser Ala Arg Lys Lys Asp Arg Val Ile Ile Gly Arg Ala Asp Gly
150                 155                 160                 165

att gat gtg gcc ggc tgg tgg aac cac cgc caa gaa gct cga cgt aaa   643
Ile Asp Val Ala Gly Trp Trp Asn His Arg Gln Glu Ala Arg Arg Lys
                170                 175                 180

acg agc gcg gct aag cag ttg gag cgc gat gca caa cgc aag cga acc   691
Thr Ser Ala Ala Lys Gln Leu Glu Arg Asp Ala Gln Arg Lys Arg Thr
            185                 190                 195

caa gct gag cgc gat aaa gag att gag cgt aag cgt aag gct caa gaa   739
Gln Ala Glu Arg Asp Lys Glu Ile Glu Arg Lys Arg Lys Ala Gln Glu
        200                 205                 210

ttt gta gcg gag cag tca ggg aaa gct gct gca gca caa cgg cgg gcc   787
Phe Val Ala Glu Gln Ser Gly Lys Ala Ala Ala Ala Gln Arg Arg Ala
    215                 220                 225

gag aaa aag gct gcg aag caa gcg cgt gta gat gaa ctg gtg gcg cag   835
Glu Lys Lys Ala Ala Lys Gln Ala Arg Val Asp Glu Leu Val Ala Gln
230                 235                 240                 245

aaa cag gct gct cag gag cag aaa act cac tgt aag cgg gac aag cag   883
Lys Gln Ala Ala Gln Glu Gln Lys Thr His Cys Lys Arg Asp Lys Gln
                250                 255                 260

cgt gcg aag aaa gca caa ggg cgc aaa gtt ggt gcc gtt gat aat tcc   931
Arg Ala Lys Lys Ala Gln Gly Arg Lys Val Gly Ala Val Asp Asn Ser
            265                 270                 275

gct gtg gac gat gtg                                              946
Ala Val Asp Asp Val
        280
```

<210> 894
<211> 282

<212> PRT
<213> Corynebacterium glutamicum

<400> 894

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Val Phe Ile Ile Gly Ala Gly Leu Pro Leu Leu Tyr Val Pro Ile Phe
  1               5                  10                  15

Val Thr Val Ile Val Met Val Val Tyr Ala Leu Leu Arg Tyr Glu Gln
             20                  25                  30

Arg Met Ser Gly Thr Val Tyr Glu Glu Ala Asp Pro Val Glu Met Asp
         35                  40                  45

Ser Val Ile Trp Glu Gly Ile Lys Cys Asp Ile Ala Ser Asp Ile Ala
     50                  55                  60

Ala Arg Ala Glu Ala Lys Lys Ala Lys Lys Pro Val Ala Ser Asp Ala
 65                  70                  75                  80

Val Ala Val Gly Asn Tyr Ile Ala Ser Leu Arg Gln His Met Leu Val
                 85                  90                  95

Glu Thr Gln Arg Arg Tyr His His Lys Leu Gly Arg Glu Leu His Asn
            100                 105                 110

Asp Pro Ala Gln Leu Glu Asp Tyr Gly Ser Gly Leu Arg Asp Cys Glu
        115                 120                 125

Cys Arg Ala Cys Val Val Ala Gln Lys Leu Gly Val Thr Val His Ala
    130                 135                 140

His Gly Val Val Gln Ala Ser Ala Arg Lys Lys Asp Arg Val Ile Ile
145                 150                 155                 160

Gly Arg Ala Asp Gly Ile Asp Val Ala Gly Trp Trp Asn His Arg Gln
                165                 170                 175

Glu Ala Arg Arg Lys Thr Ser Ala Ala Lys Gln Leu Glu Arg Asp Ala
            180                 185                 190

Gln Arg Lys Arg Thr Gln Ala Glu Arg Asp Lys Glu Ile Glu Arg Lys
        195                 200                 205

Arg Lys Ala Gln Glu Phe Val Ala Glu Gln Ser Gly Lys Ala Ala Ala
    210                 215                 220

Ala Gln Arg Arg Ala Glu Lys Lys Ala Ala Lys Gln Ala Arg Val Asp
225                 230                 235                 240

Glu Leu Val Ala Gln Lys Gln Ala Ala Gln Glu Gln Lys Thr His Cys
                245                 250                 255

Lys Arg Asp Lys Gln Arg Ala Lys Lys Ala Gln Gly Arg Lys Val Gly
            260                 265                 270

Ala Val Asp Asn Ser Ala Val Asp Asp Val
        275                 280
```

<210> 895
<211> 1074

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1051)
<223> RXN01930

<400> 895
cgaaagaagc cataatttag agaggacaat tctctactat tggtcaaggc tcccacccgg 60

tgtcattcga cattattacc gctcactcac aatcgatgaa gtg att tca aca aat 115
Val Ile Ser Thr Asn
1 5

gag att gaa aat att cac tca act cgt cgg gat att gaa ata gcg ctt 163
Glu Ile Glu Asn Ile His Ser Thr Arg Arg Asp Ile Glu Ile Ala Leu
10 15 20

gat gaa tct tcc act agt gag cca aag aga ttt tcg gaa att tca cac 211
Asp Glu Ser Ser Thr Ser Glu Pro Lys Arg Phe Ser Glu Ile Ser His
25 30 35

ctt tac ctc gca ctt gcc gaa ggt aaa ata tcc ttt ccg gaa agc cca 259
Leu Tyr Leu Ala Leu Ala Glu Gly Lys Ile Ser Phe Pro Glu Ser Pro
40 45 50

agt gaa ctt cga gaa ctc tat gac cat tta atg cac ggc gag cta ggt 307
Ser Glu Leu Arg Glu Leu Tyr Asp His Leu Met His Gly Glu Leu Gly
55 60 65

aaa gaa aat gaa tta gat ggt gag att ttc cgc caa gga ccc gtg gaa 355
Lys Glu Asn Glu Leu Asp Gly Glu Ile Phe Arg Gln Gly Pro Val Glu
70 75 80 85

atc cgc gat agt cgg caa aaa gtg att cat tca ggt ttt tct cca gaa 403
Ile Arg Asp Ser Arg Gln Lys Val Ile His Ser Gly Phe Ser Pro Glu
90 95 100

tca cag atc atc gaa gga atc aac gca att att aag ctg gcg cac tca 451
Ser Gln Ile Ile Glu Gly Ile Asn Ala Ile Ile Lys Leu Ala His Ser
105 110 115

gaa gag gaa tcc aac ctt gtt ggc atc atg atg tca cac ttc atg ttt 499
Glu Glu Glu Ser Asn Leu Val Gly Ile Met Met Ser His Phe Met Phe
120 125 130

gaa tca att cac ccg ttt tat gat gga aac gga aga act ggg cgc tac 547
Glu Ser Ile His Pro Phe Tyr Asp Gly Asn Gly Arg Thr Gly Arg Tyr
135 140 145

ctt ctc ggg ata caa tta agc aaa att ctc tcc cct gct aca gca ctg 595
Leu Leu Gly Ile Gln Leu Ser Lys Ile Leu Ser Pro Ala Thr Ala Leu
150 155 160 165

aca atg tct tcg gca att aat caa ttt cga aac aag tac tac aaa gcg 643
Thr Met Ser Ser Ala Ile Asn Gln Phe Arg Asn Lys Tyr Tyr Lys Ala
170 175 180

ttt cat gcc gta gaa cac cga tta aat cgc gga gac gga aca ccg ttt 691
Phe His Ala Val Glu His Arg Leu Asn Arg Gly Asp Gly Thr Pro Phe

```
            185                 190                 195

gtt att tcc atg ctt gag ctg tta att gca gcg caa gaa ggt ctc att   739
Val Ile Ser Met Leu Glu Leu Leu Ile Ala Ala Gln Glu Gly Leu Ile
        200                 205                 210

gag aat ata aaa caa aga atc gac ttt ttg gca agc ctt gag gac gcc   787
Glu Asn Ile Lys Gln Arg Ile Asp Phe Leu Ala Ser Leu Glu Asp Ala
    215                 220                 225

att aaa acg ctt cgg ggt acc aat tcc ttt aag aac cat cag atc aat   835
Ile Lys Thr Leu Arg Gly Thr Asn Ser Phe Lys Asn His Gln Ile Asn
230                 235                 240                 245

ctg ttg tac att ctc ggc cag att cag ctt ttc ggt aag gac gaa aca   883
Leu Leu Tyr Ile Leu Gly Gln Ile Gln Leu Phe Gly Lys Asp Glu Thr
                250                 255                 260

ctt tca ctt gaa tcg gca gca aag ttt ctt aaa gtt tct aag gca act   931
Leu Ser Leu Glu Ser Ala Ala Lys Phe Leu Lys Val Ser Lys Ala Thr
            265                 270                 275

gca acg agg tat ttt aga act ctc cga gaa atg gaa tta gtt cac gag   979
Ala Thr Arg Tyr Phe Arg Thr Leu Arg Glu Met Glu Leu Val His Glu
        280                 285                 290

gtc agc aaa cgc cct ttg cgg ttt gcg ctc acg gat aaa ggt cgt gag   1027
Val Ser Lys Arg Pro Leu Arg Phe Ala Leu Thr Asp Lys Gly Arg Glu
    295                 300                 305

ata gta ggt ctt gag gta aaa att tgactccata acgagaactt aat         1074
Ile Val Gly Leu Glu Val Lys Ile
310                 315


<210> 896
<211> 317
<212> PRT
<213> Corynebacterium glutamicum

<400> 896
Val Ile Ser Thr Asn Glu Ile Glu Asn Ile His Ser Thr Arg Arg Asp
  1               5                  10                  15

Ile Glu Ile Ala Leu Asp Glu Ser Ser Thr Ser Glu Pro Lys Arg Phe
             20                  25                  30

Ser Glu Ile Ser His Leu Tyr Leu Ala Leu Ala Glu Gly Lys Ile Ser
         35                  40                  45

Phe Pro Glu Ser Pro Ser Glu Leu Arg Glu Leu Tyr Asp His Leu Met
     50                  55                  60

His Gly Glu Leu Gly Lys Glu Asn Glu Leu Asp Gly Glu Ile Phe Arg
 65                  70                  75                  80

Gln Gly Pro Val Glu Ile Arg Asp Ser Arg Gln Lys Val Ile His Ser
                 85                  90                  95

Gly Phe Ser Pro Glu Ser Gln Ile Ile Glu Gly Ile Asn Ala Ile Ile
            100                 105                 110
```

```
Lys Leu Ala His Ser Glu Glu Glu Ser Asn Leu Val Gly Ile Met Met
        115                 120                 125

Ser His Phe Met Phe Glu Ser Ile His Pro Phe Tyr Asp Gly Asn Gly
    130                 135                 140

Arg Thr Gly Arg Tyr Leu Leu Gly Ile Gln Leu Ser Lys Ile Leu Ser
145                 150                 155                 160

Pro Ala Thr Ala Leu Thr Met Ser Ser Ala Ile Asn Gln Phe Arg Asn
                165                 170                 175

Lys Tyr Tyr Lys Ala Phe His Ala Val Glu His Arg Leu Asn Arg Gly
            180                 185                 190

Asp Gly Thr Pro Phe Val Ile Ser Met Leu Glu Leu Leu Ile Ala Ala
        195                 200                 205

Gln Glu Gly Leu Ile Glu Asn Ile Lys Gln Arg Ile Asp Phe Leu Ala
    210                 215                 220

Ser Leu Glu Asp Ala Ile Lys Thr Leu Arg Gly Thr Asn Ser Phe Lys
225                 230                 235                 240

Asn His Gln Ile Asn Leu Leu Tyr Ile Leu Gly Gln Ile Gln Leu Phe
                245                 250                 255

Gly Lys Asp Glu Thr Leu Ser Leu Glu Ser Ala Ala Lys Phe Leu Lys
            260                 265                 270

Val Ser Lys Ala Thr Ala Thr Arg Tyr Phe Arg Thr Leu Arg Glu Met
        275                 280                 285

Glu Leu Val His Glu Val Ser Lys Arg Pro Leu Arg Phe Ala Leu Thr
    290                 295                 300

Asp Lys Gly Arg Glu Ile Val Gly Leu Glu Val Lys Ile
305                 310                 315
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<210> 897
<211> 1074
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1051)
<223> FRXA01930

<400> 897
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tgtcattcga cattattacc gctcactcac aatcgatgaa gtg att tca aca aat   115
                                            Val Ile Ser Thr Asn
                                              1               5

gag att gaa aat att cac tca act cgt cgg gat att gaa ata gcg ctt   163
Glu Ile Glu Asn Ile His Ser Thr Arg Arg Asp Ile Glu Ile Ala Leu
                  10                  15                  20
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gat gaa tct tcc act agt gag cca aag aga ttt tcg gaa att tca cac   211
Asp Glu Ser Ser Thr Ser Glu Pro Lys Arg Phe Ser Glu Ile Ser His
            25                  30                  35

ctt tac ctc gca ctt gcc gaa ggt aaa ata tcc ttt ccg gaa agc cca   259
Leu Tyr Leu Ala Leu Ala Glu Gly Lys Ile Ser Phe Pro Glu Ser Pro
        40                  45                  50

agt gaa ctt cga gaa ctc tat gac cat tta atg cac ggc gag cta ggt   307
Ser Glu Leu Arg Glu Leu Tyr Asp His Leu Met His Gly Glu Leu Gly
    55                  60                  65

aaa gaa aat gaa tta gat ggt gag att ttc cgc caa gga ccc gtg gaa   355
Lys Glu Asn Glu Leu Asp Gly Glu Ile Phe Arg Gln Gly Pro Val Glu
70                  75                  80                  85

atc cgc gat agt cgg caa aaa gtg att cat tca ggt ttt tct cca gaa   403
Ile Arg Asp Ser Arg Gln Lys Val Ile His Ser Gly Phe Ser Pro Glu
                90                  95                  100

tca cag atc atc gaa gga atc aac gca att att aag ctg gcg cac tca   451
Ser Gln Ile Ile Glu Gly Ile Asn Ala Ile Ile Lys Leu Ala His Ser
            105                 110                 115

gaa gag gaa tcc aac ctt gtt ggc atc atg atg tca cac ttc atg ttt   499
Glu Glu Glu Ser Asn Leu Val Gly Ile Met Met Ser His Phe Met Phe
        120                 125                 130

gaa tca att cac ccg ttt tat gat gga aac gga aga act ggg cgc tac   547
Glu Ser Ile His Pro Phe Tyr Asp Gly Asn Gly Arg Thr Gly Arg Tyr
    135                 140                 145

ctt ctc ggg ata caa tta agc aaa att ctc tcc cct gct aca gca ctg   595
Leu Leu Gly Ile Gln Leu Ser Lys Ile Leu Ser Pro Ala Thr Ala Leu
150                 155                 160                 165

aca atg tct tcg gca att aat caa ttt cga aac aag tac tac aaa gcg   643
Thr Met Ser Ser Ala Ile Asn Gln Phe Arg Asn Lys Tyr Tyr Lys Ala
                170                 175                 180

ttt cat gcc gta gaa cac cga tta aat cgc gga gac gga aca ccg ttt   691
Phe His Ala Val Glu His Arg Leu Asn Arg Gly Asp Gly Thr Pro Phe
            185                 190                 195

gtt att tcc atg ctt gag ctg tta att gca gcg caa gaa ggt ctc att   739
Val Ile Ser Met Leu Glu Leu Leu Ile Ala Ala Gln Glu Gly Leu Ile
        200                 205                 210

gag aat ata aaa caa aga atc gac ttt ttg gca agc ctt gag gac gcc   787
Glu Asn Ile Lys Gln Arg Ile Asp Phe Leu Ala Ser Leu Glu Asp Ala
    215                 220                 225

att aaa acg ctt cgg ggt acc aat tcc ttt aag aac cat cag atc aat   835
Ile Lys Thr Leu Arg Gly Thr Asn Ser Phe Lys Asn His Gln Ile Asn
230                 235                 240                 245

ctg ttg tac att ctc ggc cag att cag ctt ttc ggt aag gac gaa aca   883
Leu Leu Tyr Ile Leu Gly Gln Ile Gln Leu Phe Gly Lys Asp Glu Thr
                250                 255                 260
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ctt tca ctt gaa tcg gca gca aag ttt ctt aaa gtt tct aag gca act   931
Leu Ser Leu Glu Ser Ala Ala Lys Phe Leu Lys Val Ser Lys Ala Thr
            265                 270                 275

gca acg agg tat ttt aga act ctc cga gaa atg gaa tta gtt cac gag   979
Ala Thr Arg Tyr Phe Arg Thr Leu Arg Glu Met Glu Leu Val His Glu
        280                 285                 290

gtc agc aaa cgc cct ttg cgg ttt gcg ctc acg gat aaa ggt cgt gag   1027
Val Ser Lys Arg Pro Leu Arg Phe Ala Leu Thr Asp Lys Gly Arg Glu
    295                 300                 305

ata gta ggt ctt gag gta aaa att tgactccata acgagaactt aat         1074
Ile Val Gly Leu Glu Val Lys Ile
310                 315
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<210> 898
<211> 317
<212> PRT
<213> Corynebacterium glutamicum

<400> 898

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Val Ile Ser Thr Asn Glu Ile Glu Asn Ile His Ser Thr Arg Arg Asp
  1               5                  10                  15

Ile Glu Ile Ala Leu Asp Glu Ser Ser Thr Ser Glu Pro Lys Arg Phe
             20                  25                  30

Ser Glu Ile Ser His Leu Tyr Leu Ala Leu Ala Glu Gly Lys Ile Ser
         35                  40                  45

Phe Pro Glu Ser Pro Ser Glu Leu Arg Glu Leu Tyr Asp His Leu Met
     50                  55                  60

His Gly Glu Leu Gly Lys Glu Asn Glu Leu Asp Gly Glu Ile Phe Arg
 65                  70                  75                  80

Gln Gly Pro Val Glu Ile Arg Asp Ser Arg Gln Lys Val Ile His Ser
                 85                  90                  95

Gly Phe Ser Pro Glu Ser Gln Ile Ile Glu Gly Ile Asn Ala Ile Ile
            100                 105                 110

Lys Leu Ala His Ser Glu Glu Glu Ser Asn Leu Val Gly Ile Met Met
        115                 120                 125

Ser His Phe Met Phe Glu Ser Ile His Pro Phe Tyr Asp Gly Asn Gly
    130                 135                 140

Arg Thr Gly Arg Tyr Leu Leu Gly Ile Gln Leu Ser Lys Ile Leu Ser
145                 150                 155                 160

Pro Ala Thr Ala Leu Thr Met Ser Ser Ala Ile Asn Gln Phe Arg Asn
                165                 170                 175

Lys Tyr Tyr Lys Ala Phe His Ala Val Glu His Arg Leu Asn Arg Gly
            180                 185                 190

Asp Gly Thr Pro Phe Val Ile Ser Met Leu Glu Leu Leu Ile Ala Ala
        195                 200                 205
```

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Gln Glu Gly Leu Ile Glu Asn Ile Lys Gln Arg Ile Asp Phe Leu Ala
    210                 215                 220

Ser Leu Glu Asp Ala Ile Lys Thr Leu Arg Gly Thr Asn Ser Phe Lys
225                 230                 235                 240

Asn His Gln Ile Asn Leu Leu Tyr Ile Leu Gly Gln Ile Gln Leu Phe
                245                 250                 255

Gly Lys Asp Glu Thr Leu Ser Leu Glu Ser Ala Ala Lys Phe Leu Lys
            260                 265                 270

Val Ser Lys Ala Thr Ala Thr Arg Tyr Phe Arg Thr Leu Arg Glu Met
        275                 280                 285

Glu Leu Val His Glu Val Ser Lys Arg Pro Leu Arg Phe Ala Leu Thr
    290                 295                 300

Asp Lys Gly Arg Glu Ile Val Gly Leu Glu Val Lys Ile
305                 310                 315
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Sequence Listing as filed with the application

<210> 899
<211> 1095
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1072)
<223> RXN01944

<400> 899

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ccgtttacct tcgccttcaa atatcaccga tgatgtccag gtg cgc acg gca aca   115
                                            Val Arg Thr Ala Thr
                                              1               5

ctg cat gtt act tcc agt gct ggc gaa gcc gcg aca acc atc aac ctc   163
Leu His Val Thr Ser Ser Ala Gly Glu Ala Ala Thr Thr Ile Asn Leu
                  10                  15                  20

acc gag gat gac ggc tct ttc aat tgg gct ctg cct gca gcg gat ctc   211
Thr Glu Asp Asp Gly Ser Phe Asn Trp Ala Leu Pro Ala Ala Asp Leu
              25                  30                  35

acc gga aaa tcc tgg ttc gaa tac acc gta acc gcc acc gac gga ttc   259
Thr Gly Lys Ser Trp Phe Glu Tyr Thr Val Thr Ala Thr Asp Gly Phe
          40                  45                  50

aac agc gtt acc acc gag ccg gta cgc gtc acc gtc gac ggc gcc aac   307
Asn Ser Val Thr Thr Glu Pro Val Arg Val Thr Val Asp Gly Ala Asn
      55                  60                  65

acc gac ccg ctg cgc ctc aac ctg gaa gaa aac caa tgg gtc agt ggc   355
Thr Asp Pro Leu Arg Leu Asn Leu Glu Glu Asn Gln Trp Val Ser Gly
  70                  75                  80                  85

acc acc gat gtt atc ggt gct tca gat gtc ttc ggc gac aag ctt gaa   403
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Thr Thr Asp Val Ile Gly Ala Ser Asp Val Phe Gly Asp Lys Leu Glu
                 90                  95                 100

ttg ctt atc gac gac gcg cct gca gtc acc aac tcc agc ctg tct gcg   451
Leu Leu Ile Asp Asp Ala Pro Ala Val Thr Asn Ser Ser Leu Ser Ala
            105                 110                 115

gcc ccg acg ttt gcg atg gaa gta acc caa act gat gtg ttc ttc cgc   499
Ala Pro Thr Phe Ala Met Glu Val Thr Gln Thr Asp Val Phe Phe Arg
        120                 125                 130

aac ggc atc ctt gcc ggt ggg gaa gaa ctc cgc att ttc gat caa gga   547
Asn Gly Ile Leu Ala Gly Gly Glu Glu Leu Arg Ile Phe Asp Gln Gly
    135                 140                 145

act tac gcc aac acc gaa acc atc tcc aca cca gtc ccg ctg tat cac   595
Thr Tyr Ala Asn Thr Glu Thr Ile Ser Thr Pro Val Pro Leu Tyr His
150                 155                 160                 165

atc aat gag gac ggt acc ctc aca gtc agt gtg tat gcg gga act aaa   643
Ile Asn Glu Asp Gly Thr Leu Thr Val Ser Val Tyr Ala Gly Thr Lys
                170                 175                 180

gca gca cca gaa att gac ctc aac gag aac aat gac gat ttc cag atc   691
Ala Ala Pro Glu Ile Asp Leu Asn Glu Asn Asn Asp Asp Phe Gln Ile
            185                 190                 195

aga aac ctt cga cta att ctg cct gat ggc cgg acc ctc acc cct gcc   739
Arg Asn Leu Arg Leu Ile Leu Pro Asp Gly Arg Thr Leu Thr Pro Ala
        200                 205                 210

gga att tcc gat tct aat gcg tgg ctc aac atg gga gac agc gct gga   787
Gly Ile Ser Asp Ser Asn Ala Trp Leu Asn Met Gly Asp Ser Ala Gly
    215                 220                 225

aaa ctc gat ttc ttc gat gcc acc ttc gcc ctc cct gag gat gct ttc   835
Lys Leu Asp Phe Phe Asp Ala Thr Phe Ala Leu Pro Glu Asp Ala Phe
230                 235                 240                 245

acc ggt gtg gca cac gca tgg gat acc acc caa agc aca gat gga gaa   883
Thr Gly Val Ala His Ala Trp Asp Thr Thr Gln Ser Thr Asp Gly Glu
                250                 255                 260

cac cac atc acc att tcc cgc gaa gac ggc ggg gaa atc agc cgc acc   931
His His Ile Thr Ile Ser Arg Glu Asp Gly Gly Glu Ile Ser Arg Thr
            265                 270                 275

atc cgg gtt gat aat act gcc cca gaa ctc acc gtt tct gga gtt gaa   979
Ile Arg Val Asp Asn Thr Ala Pro Glu Leu Thr Val Ser Gly Val Glu
        280                 285                 290

gaa gga caa gaa ctg cgc ggc acc gta gaa att gat gcc cag gca acc   1027
Glu Gly Gln Glu Leu Arg Gly Thr Val Glu Ile Asp Ala Gln Ala Thr
    295                 300                 305

gat gcg ggt gcg ggc gtg aag agc gtc gag acg ctt ctc gac ggc       1072
Asp Ala Gly Ala Gly Val Lys Ser Val Glu Thr Leu Leu Asp Gly
310                 315                 320

taacgcgtgc aacttccact aac                                        1095
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<210> 900
<211> 324
<212> PRT
<213> Corynebacterium glutamicum

<400> 900
Val Arg Thr Ala Thr Leu His Val Thr Ser Ser Ala Gly Glu Ala Ala
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20 25 30

Pro Ala Ala Asp Leu Thr Gly Lys Ser Trp Phe Glu Tyr Thr Val Thr
35 40 45

Ala Thr Asp Gly Phe Asn Ser Val Thr Thr Glu Pro Val Arg Val Thr
50 55 60

Val Asp Gly Ala Asn Thr Asp Pro Leu Arg Leu Asn Leu Glu Glu Asn
65 70 75 80

Gln Trp Val Ser Gly Thr Thr Asp Val Ile Gly Ala Ser Asp Val Phe
85 90 95

Gly Asp Lys Leu Glu Leu Leu Ile Asp Asp Ala Pro Ala Val Thr Asn
100 105 110

Ser Ser Leu Ser Ala Ala Pro Thr Phe Ala Met Glu Val Thr Gln Thr
115 120 125

Asp Val Phe Phe Arg Asn Gly Ile Leu Ala Gly Gly Glu Glu Leu Arg
130 135 140

Ile Phe Asp Gln Gly Thr Tyr Ala Asn Thr Glu Thr Ile Ser Thr Pro
145 150 155 160

Val Pro Leu Tyr His Ile Asn Glu Asp Gly Thr Leu Thr Val Ser Val
165 170 175

Tyr Ala Gly Thr Lys Ala Ala Pro Glu Ile Asp Leu Asn Glu Asn Asn
180 185 190

Asp Asp Phe Gln Ile Arg Asn Leu Arg Leu Ile Leu Pro Asp Gly Arg
195 200 205

Thr Leu Thr Pro Ala Gly Ile Ser Asp Ser Asn Ala Trp Leu Asn Met
210 215 220

Gly Asp Ser Ala Gly Lys Leu Asp Phe Phe Asp Ala Thr Phe Ala Leu
225 230 235 240

Pro Glu Asp Ala Phe Thr Gly Val Ala His Ala Trp Asp Thr Thr Gln
245 250 255

Ser Thr Asp Gly Glu His His Ile Thr Ile Ser Arg Glu Asp Gly Gly
260 265 270

Glu Ile Ser Arg Thr Ile Arg Val Asp Asn Thr Ala Pro Glu Leu Thr
275 280 285

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Val Ser Gly Val Glu Glu Gly Gln Glu Leu Arg Gly Thr Val Glu Ile
    290                 295                 300

Asp Ala Gln Ala Thr Asp Ala Gly Ala Gly Val Lys Ser Val Glu Thr
305                 310                 315                 320

Leu Leu Asp Gly
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<210> 901
<211> 407
<212> DNA
<213> Corynebacterium glutamicum

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<222> (1)..(384)
<223> FRXA01944

<400> 901

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  1               5                  10                  15

gcc gga att tcc gat tct aat gcg tgg ctc aac atg gga gac agc gct   96
Ala Gly Ile Ser Asp Ser Asn Ala Trp Leu Asn Met Gly Asp Ser Ala
             20                  25                  30

gga aaa ctc gat ttc ttc gat gcc acc ttc gcc ctc cct gag gat gct  144
Gly Lys Leu Asp Phe Phe Asp Ala Thr Phe Ala Leu Pro Glu Asp Ala
         35                  40                  45

ttc acc ggt gtg gca cac gca tgg gat acc acc caa agc aca gat gga  192
Phe Thr Gly Val Ala His Ala Trp Asp Thr Thr Gln Ser Thr Asp Gly
     50                  55                  60

gaa cac cac atc acc att tcc cgc gaa gac ggc ggg gaa atc agc cgc  240
Glu His His Ile Thr Ile Ser Arg Glu Asp Gly Gly Glu Ile Ser Arg
 65                  70                  75                  80

acc atc cgg gtt gat aat act gcc cca gaa ctc acc gtt tct gga gtt  288
Thr Ile Arg Val Asp Asn Thr Ala Pro Glu Leu Thr Val Ser Gly Val
                 85                  90                  95

gaa gaa gga caa gaa ctg cgc ggc acc gta gaa att gat gcc cag gca  336
Glu Glu Gly Gln Glu Leu Arg Gly Thr Val Glu Ile Asp Ala Gln Ala
            100                 105                 110

acc gat gcg ggt gcg ggc gtg aag agc gtc gag acg ctt ctc gac ggc  384
Thr Asp Ala Gly Ala Gly Val Lys Ser Val Glu Thr Leu Leu Asp Gly
        115                 120                 125

taacgcgtgc aacttccact aac                                       407
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<210> 902
<211> 128
<212> PRT
<213> Corynebacterium glutamicum

<400> 902
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20 25 30

Gly Lys Leu Asp Phe Phe Asp Ala Thr Phe Ala Leu Pro Glu Asp Ala
35 40 45

Phe Thr Gly Val Ala His Ala Trp Asp Thr Thr Gln Ser Thr Asp Gly
50 55 60

Glu His His Ile Thr Ile Ser Arg Glu Asp Gly Gly Glu Ile Ser Arg
65 70 75 80

Thr Ile Arg Val Asp Asn Thr Ala Pro Glu Leu Thr Val Ser Gly Val
85 90 95

Glu Glu Gly Gln Glu Leu Arg Gly Thr Val Glu Ile Asp Ala Gln Ala
100 105 110

Thr Asp Ala Gly Ala Gly Val Lys Ser Val Glu Thr Leu Leu Asp Gly
115 120 125

<210> 903
<211> 673
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(673)
<223> FRXA01636

<400> 903
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ccgtttacct tcgccttcaa atatcaccga tgatgtccag gtg cgc acg gca aca 115
Val Arg Thr Ala Thr
1 5

ctg cat gtt act tcc agt gct ggc gaa gcc gcg aca acc atc aac ctc 163
Leu His Val Thr Ser Ser Ala Gly Glu Ala Ala Thr Thr Ile Asn Leu
10 15 20

acc gag gat gac ggc tct ttc aat tgg gct ctg cct gca gcg gat ctc 211
Thr Glu Asp Asp Gly Ser Phe Asn Trp Ala Leu Pro Ala Ala Asp Leu
25 30 35

acc gga aaa tcc tgg ttc gaa tac acc gta acc gcc acc gac gga ttc 259
Thr Gly Lys Ser Trp Phe Glu Tyr Thr Val Thr Ala Thr Asp Gly Phe
40 45 50

aac agc gtt acc acc gag ccg gta cgc gtc acc gtc gac ggc gcc aac 307
Asn Ser Val Thr Thr Glu Pro Val Arg Val Thr Val Asp Gly Ala Asn
55 60 65

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acc gac ccg ctg cgc ctc aac ctg gaa gaa aac caa tgg gtc agt ggc   355
Thr Asp Pro Leu Arg Leu Asn Leu Glu Glu Asn Gln Trp Val Ser Gly
 70                  75                  80                  85

acc acc gat gtt atc ggt gct tca gat gtc ttc ggc gac aag ctt gaa   403
Thr Thr Asp Val Ile Gly Ala Ser Asp Val Phe Gly Asp Lys Leu Glu
                90                  95                 100

ttg ctt atc gac gac gcg cct gca gtc acc aac tcc agc ctg tct gcg   451
Leu Leu Ile Asp Asp Ala Pro Ala Val Thr Asn Ser Ser Leu Ser Ala
            105                 110                 115

gcc ccg acg ttt gcg atg gaa gta acc caa act gat gtg ttc ttc cgc   499
Ala Pro Thr Phe Ala Met Glu Val Thr Gln Thr Asp Val Phe Phe Arg
        120                 125                 130

aac ggc atc ctt gcc ggt ggg gaa gaa ctc cgc att ttc gat caa gga   547
Asn Gly Ile Leu Ala Gly Gly Glu Glu Leu Arg Ile Phe Asp Gln Gly
    135                 140                 145

act tac gcc aac acc gaa acc atc tcc aca cca gtc ccg ctg tat cac   595
Thr Tyr Ala Asn Thr Glu Thr Ile Ser Thr Pro Val Pro Leu Tyr His
150                 155                 160                 165

atc aat gag gac ggt acc ctc aca gtc agt gtg tat gcg gga act aaa   643
Ile Asn Glu Asp Gly Thr Leu Thr Val Ser Val Tyr Ala Gly Thr Lys
                170                 175                 180

gca gca cca gaa att gac ctc aac gag aac                          673
Ala Ala Pro Glu Ile Asp Leu Asn Glu Asn
            185                 190
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Application Filed with the European Patent Office on 2007-08-30

<210> 904
<211> 191
<212> PRT
<213> Corynebacterium glutamicum

<400> 904

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Val Arg Thr Ala Thr Leu His Val Thr Ser Ser Ala Gly Glu Ala Ala
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             20                  25                  30

Pro Ala Ala Asp Leu Thr Gly Lys Ser Trp Phe Glu Tyr Thr Val Thr
         35                  40                  45

Ala Thr Asp Gly Phe Asn Ser Val Thr Thr Glu Pro Val Arg Val Thr
     50                  55                  60

Val Asp Gly Ala Asn Thr Asp Pro Leu Arg Leu Asn Leu Glu Glu Asn
 65                  70                  75                  80

Gln Trp Val Ser Gly Thr Thr Asp Val Ile Gly Ala Ser Asp Val Phe
                 85                  90                  95

Gly Asp Lys Leu Glu Leu Leu Ile Asp Asp Ala Pro Ala Val Thr Asn
            100                 105                 110
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Ser Ser Leu Ser Ala Ala Pro Thr Phe Ala Met Glu Val Thr Gln Thr
        115                 120                 125

Asp Val Phe Phe Arg Asn Gly Ile Leu Ala Gly Gly Glu Glu Leu Arg
    130                 135                 140

Ile Phe Asp Gln Gly Thr Tyr Ala Asn Thr Glu Thr Ile Ser Thr Pro
145                 150                 155                 160

Val Pro Leu Tyr His Ile Asn Glu Asp Gly Thr Leu Thr Val Ser Val
                165                 170                 175

Tyr Ala Gly Thr Lys Ala Ala Pro Glu Ile Asp Leu Asn Glu Asn
            180                 185                 190


<210> 905
<211> 2115
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2092)
<223> RXN01945

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gggcgtgaag agcgtcgaga cgcttctcga cggctaacgc gtg caa ctt cca cta   115
                                            Val Gln Leu Pro Leu
                                              1               5

acc acc ggt tcc atc gct ttg gat aaa ggt gaa cac acc ttg gtt atc   163
Thr Thr Gly Ser Ile Ala Leu Asp Lys Gly Glu His Thr Leu Val Ile
                10                  15                  20

cgt gca gaa gat gaa gta gga aac cgc acc gag aaa acc atc acg ttt   211
Arg Ala Glu Asp Glu Val Gly Asn Arg Thr Glu Lys Thr Ile Thr Phe
            25                  30                  35

agc act ccg gat gaa aac ccc atc agt ggt gac tac gct cca agc aat   259
Ser Thr Pro Asp Glu Asn Pro Ile Ser Gly Asp Tyr Ala Pro Ser Asn
        40                  45                  50

ggg gcc acc gtg ggc gtc ggt gac gtt aag tta tct gca cga gca agt   307
Gly Ala Thr Val Gly Val Gly Asp Val Lys Leu Ser Ala Arg Ala Ser
    55                  60                  65

gat cca agt ggc gat act gtc aag atg acg ttc ctg gaa gcc gat tca   355
Asp Pro Ser Gly Asp Thr Val Lys Met Thr Phe Leu Glu Ala Asp Ser
70                  75                  80                  85

cca aaa tta gat agt ggt cgc gtc cga atg tca tca gga acg gta gaa   403
Pro Lys Leu Asp Ser Gly Arg Val Arg Met Ser Ser Gly Thr Val Glu
                90                  95                  100

gat gcc gga agt gtc tcg cgc gcc gag gcg aaa atg ttg gag agg gga   451
Asp Ala Gly Ser Val Ser Arg Ala Glu Ala Lys Met Leu Glu Arg Gly
            105                 110                 115
```

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gac gtc gag aag cta tcc agc ctg gat ggg ctg ggc atg gaa gtt acc   499
Asp Val Glu Lys Leu Ser Ser Leu Asp Gly Leu Gly Met Glu Val Thr
        120                 125                 130

tcc gac gcc gca ctg ccg tac cag ctt ttt gaa gtc gat gcg gcg gat   547
Ser Asp Ala Ala Leu Pro Tyr Gln Leu Phe Glu Val Asp Ala Ala Asp
    135                 140                 145

gca ctc gcg gcc gac act gaa gtg cgc ctg aat tgg gcg gga tcc gcc   595
Ala Leu Ala Ala Asp Thr Glu Val Arg Leu Asn Trp Ala Gly Ser Ala
150                 155                 160                 165

gat ggt cgc gcg cag gtg atc atg tat gtt ttc gat ggc gag gcg tgg   643
Asp Gly Arg Ala Gln Val Ile Met Tyr Val Phe Asp Gly Glu Ala Trp
                170                 175                 180

gtt gag gtg gat cgt cac ttg acc ggc gat gag ctg gaa gag ttt acg   691
Val Glu Val Asp Arg His Leu Thr Gly Asp Glu Leu Glu Glu Phe Thr
            185                 190                 195

ctg cag ggc gtc gtc aat gcg gaa aaa ttt gca atc ggc ggc act gtc   739
Leu Gln Gly Val Val Asn Ala Glu Lys Phe Ala Ile Gly Gly Thr Val
        200                 205                 210

acc gta ttg att cag cac tcc gaa ggc ttc gcc ggt gcg gat cat tca   787
Thr Val Leu Ile Gln His Ser Glu Gly Phe Ala Gly Ala Asp His Ser
    215                 220                 225

act aga aat tcc gac gtg acc gca gcg cac ccg gat gat gtg gct cgc   835
Thr Arg Asn Ser Asp Val Thr Ala Ala His Pro Asp Asp Val Ala Arg
230                 235                 240                 245

tct gag tac gat ttc acc ctc gcg tgg gaa tct gac acc cag tac tac   883
Ser Glu Tyr Asp Phe Thr Leu Ala Trp Glu Ser Asp Thr Gln Tyr Tyr
                250                 255                 260

aac gag gaa ttc cac gag cac caa acc aac atc cat gac tac gtg ctc   931
Asn Glu Glu Phe His Glu His Gln Thr Asn Ile His Asp Tyr Val Leu
            265                 270                 275

gcc gaa cgg gag aac aag aat att cag ttc atg ttc cac act ggc gat   979
Ala Glu Arg Glu Asn Lys Asn Ile Gln Phe Met Phe His Thr Gly Asp
        280                 285                 290

gtt gtc gac gac tgg gat cag ccc gcg cag tgg gcc aca gcc aac ccc   1027
Val Val Asp Asp Trp Asp Gln Pro Ala Gln Trp Ala Thr Ala Asn Pro
    295                 300                 305

gaa tac cag cgc ctc gac gac gcc ggc ctg cca tat tct gtc ctt gcc   1075
Glu Tyr Gln Arg Leu Asp Asp Ala Gly Leu Pro Tyr Ser Val Leu Ala
310                 315                 320                 325

gga aac cac gat gtt ggc cac acc agc aat gac tac acc gaa ttc agc   1123
Gly Asn His Asp Val Gly His Thr Ser Asn Asp Tyr Thr Glu Phe Ser
                330                 335                 340

cga cac ttc ggc gaa cag cgc tac gta gac aac ccg tgg tac ggc gaa   1171
Arg His Phe Gly Glu Gln Arg Tyr Val Asp Asn Pro Trp Tyr Gly Glu
            345                 350                 355

tcc tac caa gac aac cga ggg cac tac gat cta ttt tct gcc ggc gga   1219
```

```
Ser Tyr Gln Asp Asn Arg Gly His Tyr Asp Leu Phe Ser Ala Gly Gly
        360                 365                 370

att gac ttc att aac gta gcg atg ggc tgg ggt cca gac gac gaa gaa   1267
Ile Asp Phe Ile Asn Val Ala Met Gly Trp Gly Pro Asp Asp Glu Glu
    375                 380                 385

atc gcg tgg atg aac gag gtc ctg gcc aag cat ccc gag cgt gtg gcg   1315
Ile Ala Trp Met Asn Glu Val Leu Ala Lys His Pro Glu Arg Val Ala
390                 395                 400                 405

atc ctc aac ctc cac gaa ttc atg ctc acc acc ggc gga ctt ggc ccg   1363
Ile Leu Asn Leu His Glu Phe Met Leu Thr Thr Gly Gly Leu Gly Pro
                410                 415                 420

atc ccg cag cgc att ctc gac gag gtc gca gcc acc aac cca aat gtc   1411
Ile Pro Gln Arg Ile Leu Asp Glu Val Ala Ala Thr Asn Pro Asn Val
            425                 430                 435

agc atg atc atg tcc ggc cac tac cac gac gca ttc caa cgc acc gac   1459
Ser Met Ile Met Ser Gly His Tyr His Asp Ala Phe Gln Arg Thr Asp
        440                 445                 450

tcc ttt gac gac gat ggt gat gga gta gat gac cgc acc gtc acc tct   1507
Ser Phe Asp Asp Asp Gly Asp Gly Val Asp Asp Arg Thr Val Thr Ser
    455                 460                 465

atg ctt ttc gat tac caa ggc cta ccg gag ggc gga cag ggg tac ctc   1555
Met Leu Phe Asp Tyr Gln Gly Leu Pro Glu Gly Gly Gln Gly Tyr Leu
470                 475                 480                 485

cga ctt ctc cac ttt gat aac caa ggc caa aag atg atg gtg cgc acc   1603
Arg Leu Leu His Phe Asp Asn Gln Gly Gln Lys Met Met Val Arg Thr
                490                 495                 500

tat tca cca tcc ctg aag gat tac aac tct gat gaa ccc tca ctg ttg   1651
Tyr Ser Pro Ser Leu Lys Asp Tyr Asn Ser Asp Glu Pro Ser Leu Leu
            505                 510                 515

ggg cct gca gaa gac ccc aac atg tat caa gaa ttc gaa gtg tcc tac   1699
Gly Pro Ala Glu Asp Pro Asn Met Tyr Gln Glu Phe Glu Val Ser Tyr
        520                 525                 530

gag cag ctc ggc atc aaa cca gag ggc cgc acc ctg atc ggc gat tcc   1747
Glu Gln Leu Gly Ile Lys Pro Glu Gly Arg Thr Leu Ile Gly Asp Ser
    535                 540                 545

ttc agc gcc gat ttc ttg acc tcc aat gaa att gga ata gtt gat gag   1795
Phe Ser Ala Asp Phe Leu Thr Ser Asn Glu Ile Gly Ile Val Asp Glu
550                 555                 560                 565

gtt cct tct gga acg atc gct ttc acg aac tgg aag gac gta acc gaa   1843
Val Pro Ser Gly Thr Ile Ala Phe Thr Asn Trp Lys Asp Val Thr Glu
                570                 575                 580

ggt cgc cac agt tgg tat gtt cgc tcc gag gat cct ttc ggc ggc gtc   1891
Gly Arg His Ser Trp Tyr Val Arg Ser Glu Asp Pro Phe Gly Gly Val
            585                 590                 595

gag att tca ccc gtg cag tcc ttc att gcc ggg gaa gag gct ggc ggg   1939
Glu Ile Ser Pro Val Gln Ser Phe Ile Ala Gly Glu Glu Ala Gly Gly
```

```
        600                 605                 610

aac gcg ccc ggc act gga agc tcc aat ggc ggt tca tcc cac gga tta   1987
Asn Ala Pro Gly Thr Gly Ser Ser Asn Gly Gly Ser Ser His Gly Leu
    615                 620                 625

tgg ggt gcg ctt gcg gaa ttc ttt gcc gga gcg gca gcc ctg gct gga   2035
Trp Gly Ala Leu Ala Glu Phe Phe Ala Gly Ala Ala Ala Leu Ala Gly
630                 635                 640                 645

gct gcg atc gca ttt gtc ccc gga att tgg gac tat gtg acc aac gca   2083
Ala Ala Ile Ala Phe Val Pro Gly Ile Trp Asp Tyr Val Thr Asn Ala
                650                 655                 660

ttc aag cga taattatgga taggtaaacg ctc                            2115
Phe Lys Arg
```

<210> 906
<211> 664
<212> PRT
<213> Corynebacterium glutamicum

<400> 906

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Val Gln Leu Pro Leu Thr Thr Gly Ser Ile Ala Leu Asp Lys Gly Glu
  1               5                  10                  15

His Thr Leu Val Ile Arg Ala Glu Asp Glu Val Gly Asn Arg Thr Glu
             20                  25                  30

Lys Thr Ile Thr Phe Ser Thr Pro Asp Glu Asn Pro Ile Ser Gly Asp
         35                  40                  45

Tyr Ala Pro Ser Asn Gly Ala Thr Val Gly Val Gly Asp Val Lys Leu
     50                  55                  60

Ser Ala Arg Ala Ser Asp Pro Ser Gly Asp Thr Val Lys Met Thr Phe
 65                  70                  75                  80

Leu Glu Ala Asp Ser Pro Lys Leu Asp Ser Gly Arg Val Arg Met Ser
                 85                  90                  95

Ser Gly Thr Val Glu Asp Ala Gly Ser Val Ser Arg Ala Glu Ala Lys
            100                 105                 110

Met Leu Glu Arg Gly Asp Val Glu Lys Leu Ser Ser Leu Asp Gly Leu
        115                 120                 125

Gly Met Glu Val Thr Ser Asp Ala Ala Leu Pro Tyr Gln Leu Phe Glu
    130                 135                 140

Val Asp Ala Ala Asp Ala Leu Ala Ala Asp Thr Glu Val Arg Leu Asn
145                 150                 155                 160

Trp Ala Gly Ser Ala Asp Gly Arg Ala Gln Val Ile Met Tyr Val Phe
                165                 170                 175

Asp Gly Glu Ala Trp Val Glu Val Asp Arg His Leu Thr Gly Asp Glu
            180                 185                 190
```

```
Leu Glu Glu Phe Thr Leu Gln Gly Val Val Asn Ala Glu Lys Phe Ala
        195                 200                 205

Ile Gly Gly Thr Val Thr Val Leu Ile Gln His Ser Glu Gly Phe Ala
    210                 215                 220

Gly Ala Asp His Ser Thr Arg Asn Ser Asp Val Thr Ala Ala His Pro
225                 230                 235                 240

Asp Asp Val Ala Arg Ser Glu Tyr Asp Phe Thr Leu Ala Trp Glu Ser
                245                 250                 255

Asp Thr Gln Tyr Tyr Asn Glu Glu Phe His Glu His Gln Thr Asn Ile
            260                 265                 270

His Asp Tyr Val Leu Ala Glu Arg Glu Asn Lys Asn Ile Gln Phe Met
        275                 280                 285

Phe His Thr Gly Asp Val Val Asp Asp Trp Asp Gln Pro Ala Gln Trp
    290                 295                 300

Ala Thr Ala Asn Pro Glu Tyr Gln Arg Leu Asp Asp Ala Gly Leu Pro
305                 310                 315                 320

Tyr Ser Val Leu Ala Gly Asn His Asp Val Gly His Thr Ser Asn Asp
                325                 330                 335

Tyr Thr Glu Phe Ser Arg His Phe Gly Glu Gln Arg Tyr Val Asp Asn
            340                 345                 350

Pro Trp Tyr Gly Glu Ser Tyr Gln Asp Asn Arg Gly His Tyr Asp Leu
        355                 360                 365

Phe Ser Ala Gly Gly Ile Asp Phe Ile Asn Val Ala Met Gly Trp Gly
    370                 375                 380

Pro Asp Asp Glu Glu Ile Ala Trp Met Asn Glu Val Leu Ala Lys His
385                 390                 395                 400

Pro Glu Arg Val Ala Ile Leu Asn Leu His Glu Phe Met Leu Thr Thr
                405                 410                 415

Gly Gly Leu Gly Pro Ile Pro Gln Arg Ile Leu Asp Glu Val Ala Ala
            420                 425                 430

Thr Asn Pro Asn Val Ser Met Ile Met Ser Gly His Tyr His Asp Ala
        435                 440                 445

Phe Gln Arg Thr Asp Ser Phe Asp Asp Asp Gly Asp Gly Val Asp Asp
    450                 455                 460

Arg Thr Val Thr Ser Met Leu Phe Asp Tyr Gln Gly Leu Pro Glu Gly
465                 470                 475                 480

Gly Gln Gly Tyr Leu Arg Leu Leu His Phe Asp Asn Gln Gly Gln Lys
                485                 490                 495

Met Met Val Arg Thr Tyr Ser Pro Ser Leu Lys Asp Tyr Asn Ser Asp
            500                 505                 510

Glu Pro Ser Leu Leu Gly Pro Ala Glu Asp Pro Asn Met Tyr Gln Glu
```

```
        515                 520                 525

Phe Glu Val Ser Tyr Glu Gln Leu Gly Ile Lys Pro Glu Gly Arg Thr
    530                 535                 540

Leu Ile Gly Asp Ser Phe Ser Ala Asp Phe Leu Thr Ser Asn Glu Ile
545                 550                 555                 560

Gly Ile Val Asp Glu Val Pro Ser Gly Thr Ile Ala Phe Thr Asn Trp
                565                 570                 575

Lys Asp Val Thr Glu Gly Arg His Ser Trp Tyr Val Arg Ser Glu Asp
            580                 585                 590

Pro Phe Gly Gly Val Glu Ile Ser Pro Val Gln Ser Phe Ile Ala Gly
        595                 600                 605

Glu Glu Ala Gly Gly Asn Ala Pro Gly Thr Gly Ser Ser Asn Gly Gly
    610                 615                 620

Ser Ser His Gly Leu Trp Gly Ala Leu Ala Glu Phe Phe Ala Gly Ala
625                 630                 635                 640

Ala Ala Leu Ala Gly Ala Ala Ile Ala Phe Val Pro Gly Ile Trp Asp
                645                 650                 655

Tyr Val Thr Asn Ala Phe Lys Arg
            660


<210> 907
<211> 1342
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1342)
<223> FRXA01945

<400> 907
agaaggacaa gaactgcgcg gcaccgtaga aattgatgcc caggcaaccg atgcgggtgc 60

gggcgtgaag agcgtcgaga cgcttctcga cggctaacgc gtg caa ctt cca cta   115
                                            Val Gln Leu Pro Leu
                                              1               5

acc acc ggt tcc atc gct ttg gat aaa ggt gaa cac acc ttg gtt atc   163
Thr Thr Gly Ser Ile Ala Leu Asp Lys Gly Glu His Thr Leu Val Ile
                10                  15                  20

cgt gca gaa gat gaa gta gga aac cgc acc gag aaa acc atc acg ttt   211
Arg Ala Glu Asp Glu Val Gly Asn Arg Thr Glu Lys Thr Ile Thr Phe
            25                  30                  35

agc act ccg gat gaa aac ccc atc agt ggt gac tac gct cca agc aat   259
Ser Thr Pro Asp Glu Asn Pro Ile Ser Gly Asp Tyr Ala Pro Ser Asn
        40                  45                  50

ggg gcc acc gtg ggc gtc ggt gac gtt aag tta tct gca cga gca agt   307
Gly Ala Thr Val Gly Val Gly Asp Val Lys Leu Ser Ala Arg Ala Ser
```

```
     55                  60                  65

gat cca agt ggc gat act gtc aag atg acg ttc ctg gaa gcc gat tca   355
Asp Pro Ser Gly Asp Thr Val Lys Met Thr Phe Leu Glu Ala Asp Ser
 70                  75                  80                  85

cca aaa tta gat agt ggt cgc gtc cga atg tca tca gga acg gta gaa   403
Pro Lys Leu Asp Ser Gly Arg Val Arg Met Ser Ser Gly Thr Val Glu
                90                  95                 100

gat gcc gga agt gtc tcg cgc gcc gag gcg aaa atg ttg gag agg gga   451
Asp Ala Gly Ser Val Ser Arg Ala Glu Ala Lys Met Leu Glu Arg Gly
            105                 110                 115

gac gtc gag aag cta tcc agc ctg gat ggg ctg ggc atg gaa gtt acc   499
Asp Val Glu Lys Leu Ser Ser Leu Asp Gly Leu Gly Met Glu Val Thr
        120                 125                 130

tcc gac gcc gca ctg ccg tac cag ctt ttt gaa gtc gat gcg gcg gat   547
Ser Asp Ala Ala Leu Pro Tyr Gln Leu Phe Glu Val Asp Ala Ala Asp
    135                 140                 145

gca ctc gcg gcc gac act gaa gtg cgc ctg aat tgg gcg gga tcc gcc   595
Ala Leu Ala Ala Asp Thr Glu Val Arg Leu Asn Trp Ala Gly Ser Ala
150                 155                 160                 165

gat ggt cgc gcg cag gtg atc atg tat gtt ttc gat ggc gag gcg tgg   643
Asp Gly Arg Ala Gln Val Ile Met Tyr Val Phe Asp Gly Glu Ala Trp
                170                 175                 180

gtt gag gtg gat cgt cac ttg acc ggc gat gag ctg gaa gag ttt acg   691
Val Glu Val Asp Arg His Leu Thr Gly Asp Glu Leu Glu Glu Phe Thr
            185                 190                 195

ctg cag ggc gtc gtc aat gcg gaa aaa ttt gca atc ggc ggc act gtc   739
Leu Gln Gly Val Val Asn Ala Glu Lys Phe Ala Ile Gly Gly Thr Val
        200                 205                 210

acc gta ttg att cag cac tcc gaa ggc ttc gcc ggt gcg gat cat tca   787
Thr Val Leu Ile Gln His Ser Glu Gly Phe Ala Gly Ala Asp His Ser
    215                 220                 225

act aga aat tcc gac gtg acc gca gcg cac ccg gat gat gtg gct cgc   835
Thr Arg Asn Ser Asp Val Thr Ala Ala His Pro Asp Asp Val Ala Arg
230                 235                 240                 245

tct gag tac gat ttc acc ctc gcg tgg gaa tct gac acc cag tac tac   883
Ser Glu Tyr Asp Phe Thr Leu Ala Trp Glu Ser Asp Thr Gln Tyr Tyr
                250                 255                 260

aac gag gaa ttc cac gag cac caa acc aac atc cat gac tac gtg ctc   931
Asn Glu Glu Phe His Glu His Gln Thr Asn Ile His Asp Tyr Val Leu
            265                 270                 275

gcc gaa cgg gag aac aag aat att cag ttc atg ttc cac act ggc gat   979
Ala Glu Arg Glu Asn Lys Asn Ile Gln Phe Met Phe His Thr Gly Asp
        280                 285                 290

gtt gtc gac gac tgg gat cag ccc gcg cag tgg gcc aca gcc aac ccc  1027
Val Val Asp Asp Trp Asp Gln Pro Ala Gln Trp Ala Thr Ala Asn Pro
    295                 300                 305
```

```
gaa tac cag cgc ctc gac gac gcc ggc ctg cca tat tct gtc ctt gcc   1075
Glu Tyr Gln Arg Leu Asp Asp Ala Gly Leu Pro Tyr Ser Val Leu Ala
310                 315                 320                 325

gga aac cac gat gtt ggc cac acc agc aat gac tac acc gaa ttc agc   1123
Gly Asn His Asp Val Gly His Thr Ser Asn Asp Tyr Thr Glu Phe Ser
                330                 335                 340

cga cac ttc ggc gaa cag cgc tac gta gac aac ccg tgg tac ggc gaa   1171
Arg His Phe Gly Glu Gln Arg Tyr Val Asp Asn Pro Trp Tyr Gly Glu
            345                 350                 355

tcc tac caa gac aac cga ggg cac tac gat cta ttt tct gcc ggc gga   1219
Ser Tyr Gln Asp Asn Arg Gly His Tyr Asp Leu Phe Ser Ala Gly Gly
        360                 365                 370

att gac ttc att aac gta gcg atg ggc tgg ggt cca gac gac gaa gaa   1267
Ile Asp Phe Ile Asn Val Ala Met Gly Trp Gly Pro Asp Asp Glu Glu
    375                 380                 385

atc gcg tgg atg aac gag gtc ctg gcc aag cat ccc gag cgt gtg gcg   1315
Ile Ala Trp Met Asn Glu Val Leu Ala Lys His Pro Glu Arg Val Ala
390                 395                 400                 405

atc ctc aac ctc cac gaa ttc atg ctc                              1342
Ile Leu Asn Leu His Glu Phe Met Leu
                410
```

<210> 908
<211> 414
<212> PRT
<213> Corynebacterium glutamicum

<400> 908

```
Val Gln Leu Pro Leu Thr Thr Gly Ser Ile Ala Leu Asp Lys Gly Glu
  1               5                  10                  15

His Thr Leu Val Ile Arg Ala Glu Asp Glu Val Gly Asn Arg Thr Glu
             20                  25                  30

Lys Thr Ile Thr Phe Ser Thr Pro Asp Glu Asn Pro Ile Ser Gly Asp
         35                  40                  45

Tyr Ala Pro Ser Asn Gly Ala Thr Val Gly Val Gly Asp Val Lys Leu
     50                  55                  60

Ser Ala Arg Ala Ser Asp Pro Ser Gly Asp Thr Val Lys Met Thr Phe
 65                  70                  75                  80

Leu Glu Ala Asp Ser Pro Lys Leu Asp Ser Gly Arg Val Arg Met Ser
                 85                  90                  95

Ser Gly Thr Val Glu Asp Ala Gly Ser Val Ser Arg Ala Glu Ala Lys
            100                 105                 110

Met Leu Glu Arg Gly Asp Val Glu Lys Leu Ser Ser Leu Asp Gly Leu
        115                 120                 125

Gly Met Glu Val Thr Ser Asp Ala Ala Leu Pro Tyr Gln Leu Phe Glu
```

```
    130                 135                 140

Val Asp Ala Ala Asp Ala Leu Ala Ala Asp Thr Glu Val Arg Leu Asn
145                 150                 155                 160

Trp Ala Gly Ser Ala Asp Gly Arg Ala Gln Val Ile Met Tyr Val Phe
                165                 170                 175

Asp Gly Glu Ala Trp Val Glu Val Asp Arg His Leu Thr Gly Asp Glu
            180                 185                 190

Leu Glu Glu Phe Thr Leu Gln Gly Val Val Asn Ala Glu Lys Phe Ala
        195                 200                 205

Ile Gly Gly Thr Val Thr Val Leu Ile Gln His Ser Glu Gly Phe Ala
    210                 215                 220

Gly Ala Asp His Ser Thr Arg Asn Ser Asp Val Thr Ala Ala His Pro
225                 230                 235                 240

Asp Asp Val Ala Arg Ser Glu Tyr Asp Phe Thr Leu Ala Trp Glu Ser
                245                 250                 255

Asp Thr Gln Tyr Tyr Asn Glu Glu Phe His Glu His Gln Thr Asn Ile
            260                 265                 270

His Asp Tyr Val Leu Ala Glu Arg Glu Asn Lys Asn Ile Gln Phe Met
        275                 280                 285

Phe His Thr Gly Asp Val Val Asp Asp Trp Asp Gln Pro Ala Gln Trp
    290                 295                 300

Ala Thr Ala Asn Pro Glu Tyr Gln Arg Leu Asp Asp Ala Gly Leu Pro
305                 310                 315                 320

Tyr Ser Val Leu Ala Gly Asn His Asp Val Gly His Thr Ser Asn Asp
                325                 330                 335

Tyr Thr Glu Phe Ser Arg His Phe Gly Glu Gln Arg Tyr Val Asp Asn
            340                 345                 350

Pro Trp Tyr Gly Glu Ser Tyr Gln Asp Asn Arg Gly His Tyr Asp Leu
        355                 360                 365

Phe Ser Ala Gly Gly Ile Asp Phe Ile Asn Val Ala Met Gly Trp Gly
    370                 375                 380

Pro Asp Asp Glu Glu Ile Ala Trp Met Asn Glu Val Leu Ala Lys His
385                 390                 395                 400

Pro Glu Arg Val Ala Ile Leu Asn Leu His Glu Phe Met Leu
                405                 410
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<210> 909
<211> 518
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (1)..(495)
<223> FRXA01627

<400> 909
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cgc acc tat tca cca tcc ctg aag gat tac aac tct gat gaa ccc tca   48
Arg Thr Tyr Ser Pro Ser Leu Lys Asp Tyr Asn Ser Asp Glu Pro Ser
  1               5                  10                  15

ctg ttg ggg cct gca gaa gac ccc aac atg tat caa gaa ttc gaa gtg   96
Leu Leu Gly Pro Ala Glu Asp Pro Asn Met Tyr Gln Glu Phe Glu Val
             20                  25                  30

tcc tac gag cag ctc ggc atc aaa cca gag ggc cgc acc ctg atc ggc   144
Ser Tyr Glu Gln Leu Gly Ile Lys Pro Glu Gly Arg Thr Leu Ile Gly
         35                  40                  45

gat tcc ttc agc gcc gat ttc ttg acc tcc aat gaa att gga ata gtt   192
Asp Ser Phe Ser Ala Asp Phe Leu Thr Ser Asn Glu Ile Gly Ile Val
     50                  55                  60

gat gag gtt cct tct gga acg atc gct ttc acg aac tgg aag gac gta   240
Asp Glu Val Pro Ser Gly Thr Ile Ala Phe Thr Asn Trp Lys Asp Val
 65                  70                  75                  80

acc gaa ggt cgc cac agt tgg tat gtt cgc tcc gag gat cct ttc ggc   288
Thr Glu Gly Arg His Ser Trp Tyr Val Arg Ser Glu Asp Pro Phe Gly
                 85                  90                  95

ggc gtc gag att tca ccc gtg cag tcc ttc att gcc ggg gaa gag gct   336
Gly Val Glu Ile Ser Pro Val Gln Ser Phe Ile Ala Gly Glu Glu Ala
            100                 105                 110

ggc ggg aac gcg ccc ggc act gga agc tcc aat ggc ggt tca tcc cac   384
Gly Gly Asn Ala Pro Gly Thr Gly Ser Ser Asn Gly Gly Ser Ser His
        115                 120                 125

gga tta tgg ggt gcg ctt gcg gaa ttc ttt gcc gga gcg gca gcc ctg   432
Gly Leu Trp Gly Ala Leu Ala Glu Phe Phe Ala Gly Ala Ala Ala Leu
    130                 135                 140

gct gga gct gcg atc gca ttt gtc ccc gga att tgg gac tat gtg acc   480
Ala Gly Ala Ala Ile Ala Phe Val Pro Gly Ile Trp Asp Tyr Val Thr
145                 150                 155                 160

aac gca ttc aag cga taattatgga taggtaaacg ctc                    518
Asn Ala Phe Lys Arg
                165
```

<210> 910
<211> 165
<212> PRT
<213> Corynebacterium glutamicum

<400> 910
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Arg Thr Tyr Ser Pro Ser Leu Lys Asp Tyr Asn Ser Asp Glu Pro Ser
  1               5                  10                  15

Leu Leu Gly Pro Ala Glu Asp Pro Asn Met Tyr Gln Glu Phe Glu Val
             20                  25                  30
```

```
Ser Tyr Glu Gln Leu Gly Ile Lys Pro Glu Gly Arg Thr Leu Ile Gly
         35                  40                  45

Asp Ser Phe Ser Ala Asp Phe Leu Thr Ser Asn Glu Ile Gly Ile Val
     50                  55                  60

Asp Glu Val Pro Ser Gly Thr Ile Ala Phe Thr Asn Trp Lys Asp Val
 65                  70                  75                  80

Thr Glu Gly Arg His Ser Trp Tyr Val Arg Ser Glu Asp Pro Phe Gly
                 85                  90                  95

Gly Val Glu Ile Ser Pro Val Gln Ser Phe Ile Ala Gly Glu Glu Ala
            100                 105                 110

Gly Gly Asn Ala Pro Gly Thr Gly Ser Ser Asn Gly Gly Ser Ser His
        115                 120                 125

Gly Leu Trp Gly Ala Leu Ala Glu Phe Phe Ala Gly Ala Ala Ala Leu
    130                 135                 140

Ala Gly Ala Ala Ile Ala Phe Val Pro Gly Ile Trp Asp Tyr Val Thr
145                 150                 155                 160

Asn Ala Phe Lys Arg
                165
```

Do not delete, alter, or write over this page

<210> 911
<211> 441
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(418)
<223> RXN01960

<400> 911

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tccagattga tcgtgccaac aaagactaag ccactctagc taaaccaact taccccaccc 60

caacacccca tgaggcatct gcttcatggg gtgttttgct atg ccg caa cac ttt   115
                                              Met Pro Gln His Phe
                                                1               5

tct caa gaa aac tac aga aag gcc ccc gtc att atg tct gca ccg ctc   163
Ser Gln Glu Asn Tyr Arg Lys Ala Pro Val Ile Met Ser Ala Pro Leu
                 10                  15                  20

acc att cat gat ctg ctg tcc acc aat tcg aag ctt aac ctc aag tgg   211
Thr Ile His Asp Leu Leu Ser Thr Asn Ser Lys Leu Asn Leu Lys Trp
             25                  30                  35

ctg acc tgc act gtc ttg aac agc cca aat ctc acc gaa ccc tgc atc   259
Leu Thr Cys Thr Val Leu Asn Ser Pro Asn Leu Thr Glu Pro Cys Ile
         40                  45                  50

acg gtt tct gtg aac cac acc gaa ggc atg tcc ctg gtc tct ttc gaa   307
Thr Val Ser Val Asn His Thr Glu Gly Met Ser Leu Val Ser Phe Glu
     55                  60                  65
```

```
ggt ggt cac ggg ctc acc gag att gcc aac acc cag cta gtg cct gtg   355
Gly Gly His Gly Leu Thr Glu Ile Ala Asn Thr Gln Leu Val Pro Val
 70                  75                  80                  85

ctt gag cta cca aag ttc aat cct ttt gag gca ctt gct atc cac ctt   403
Leu Glu Leu Pro Lys Phe Asn Pro Phe Glu Ala Leu Ala Ile His Leu
                 90                  95                 100

gaa gcc gcc aac aac taagaaagca tccttcatga ctg                    441
Glu Ala Ala Asn Asn
            105
```

<210> 912
<211> 106
<212> PRT
<213> Corynebacterium glutamicum

<400> 912

```
Met Pro Gln His Phe Ser Gln Glu Asn Tyr Arg Lys Ala Pro Val Ile
  1               5                  10                  15

Met Ser Ala Pro Leu Thr Ile His Asp Leu Leu Ser Thr Asn Ser Lys
             20                  25                  30

Leu Asn Leu Lys Trp Leu Thr Cys Thr Val Leu Asn Ser Pro Asn Leu
         35                  40                  45

Thr Glu Pro Cys Ile Thr Val Ser Val Asn His Thr Glu Gly Met Ser
     50                  55                  60

Leu Val Ser Phe Glu Gly Gly His Gly Leu Thr Glu Ile Ala Asn Thr
 65                  70                  75                  80

Gln Leu Val Pro Val Leu Glu Leu Pro Lys Phe Asn Pro Phe Glu Ala
                 85                  90                  95

Leu Ala Ile His Leu Glu Ala Ala Asn Asn
            100                 105
```

<210> 913
<211> 441
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(418)
<223> FRXA01960

<400> 913

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tccagattga tcgtgccaac aaagactaag ccactctagc taaaccaact taccccaccc 60

caacacccca tgaggcatct gcttcatggg gtgttttgct atg ccg caa cac ttt   115
                                               Met Pro Gln His Phe
                                                 1               5

tct caa gaa aac tac aga aag gcc ccc gtc att atg tct gca ccg ctc   163
Ser Gln Glu Asn Tyr Arg Lys Ala Pro Val Ile Met Ser Ala Pro Leu
                 10                  15                  20
```

```
acc att cat gat ctg ctg tcc acc aat tcg aag ctt aac ctc aag tgg   211
Thr Ile His Asp Leu Leu Ser Thr Asn Ser Lys Leu Asn Leu Lys Trp
             25                  30                  35

ctg acc tgc act gtc ttg aac agc cca aat ctc ccc gaa ccc tgc atc   259
Leu Thr Cys Thr Val Leu Asn Ser Pro Asn Leu Pro Glu Pro Cys Ile
         40                  45                  50

acg gtt tct gtg aac cac acc gaa ggc atg tcc ctg gtc tct ttc gaa   307
Thr Val Ser Val Asn His Thr Glu Gly Met Ser Leu Val Ser Phe Glu
     55                  60                  65

ggt ggt cac ggg ctc acc gag att gcc aac acc cag cta gtg cct gtg   355
Gly Gly His Gly Leu Thr Glu Ile Ala Asn Thr Gln Leu Val Pro Val
 70                  75                  80                  85

ctt gag cta cca aag ttc aat cct ttt gag gca ctt gct atc cac ctt   403
Leu Glu Leu Pro Lys Phe Asn Pro Phe Glu Ala Leu Ala Ile His Leu
                 90                  95                 100

gaa gcc gcc aac aac taagaaagca tccttcatga ctg                    441
Glu Ala Ala Asn Asn
            105
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Application Filed

<210> 914
<211> 106
<212> PRT
<213> Corynebacterium glutamicum

<400> 914

```
Met Pro Gln His Phe Ser Gln Glu Asn Tyr Arg Lys Ala Pro Val Ile
  1               5                  10                  15

Met Ser Ala Pro Leu Thr Ile His Asp Leu Leu Ser Thr Asn Ser Lys
             20                  25                  30

Leu Asn Leu Lys Trp Leu Thr Cys Thr Val Leu Asn Ser Pro Asn Leu
         35                  40                  45

Pro Glu Pro Cys Ile Thr Val Ser Val Asn His Thr Glu Gly Met Ser
     50                  55                  60

Leu Val Ser Phe Glu Gly Gly His Gly Leu Thr Glu Ile Ala Asn Thr
 65                  70                  75                  80

Gln Leu Val Pro Val Leu Glu Leu Pro Lys Phe Asn Pro Phe Glu Ala
                 85                  90                  95

Leu Ala Ile His Leu Glu Ala Ala Asn Asn
            100                 105
```

<210> 915
<211> 1173
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(1150)
<223> RXN01985

<400> 915
gacgtgagac atttcctcca atacctctcc agtgatattc tgtcgggcag cctaacctaa 60

gttattccgt tgttgttcga gaaagagaga gaaacttttc atg cgt acg tct cgc 115
Met Arg Thr Ser Arg
1 5

gtt cta gcc ggc att ctt gcc gca acc ctc acg gtg tcc ctc gcg gcc 163
Val Leu Ala Gly Ile Leu Ala Ala Thr Leu Thr Val Ser Leu Ala Ala
10 15 20

tgc tcc cag gat tct tca gaa acg tcc tcc aat tcg tct tca gca gca 211
Cys Ser Gln Asp Ser Ser Glu Thr Ser Ser Asn Ser Ser Ser Ala Ala
25 30 35

tcc caa agc tct gac gtt tcc aac gag gcg ttc cct gtc acc att gag 259
Ser Gln Ser Ser Asp Val Ser Asn Glu Ala Phe Pro Val Thr Ile Glu
40 45 50

cac gct ttc ggc gag acc acc att gag tcc aag cca gaa cgc atc gca 307
His Ala Phe Gly Glu Thr Thr Ile Glu Ser Lys Pro Glu Arg Ile Ala
55 60 65

act gtt ggc tgg tcc aac cat gaa gtc cct ctc gca ttg ggt gtg act 355
Thr Val Gly Trp Ser Asn His Glu Val Pro Leu Ala Leu Gly Val Thr
70 75 80 85

cct gtc ggc ttt gag aag gtc acg tgg ggc gac gat gac aac aac ggc 403
Pro Val Gly Phe Glu Lys Val Thr Trp Gly Asp Asp Asp Asn Asn Gly
90 95 100

atc ttg cca tgg gtg gaa gaa acc ttg agc aag ctc ggc tcc gat gag 451
Ile Leu Pro Trp Val Glu Glu Thr Leu Ser Lys Leu Gly Ser Asp Glu
105 110 115

cct gtg ctt ttc gat gcc acc gat tcc att cct ttt gag gag atc gcc 499
Pro Val Leu Phe Asp Ala Thr Asp Ser Ile Pro Phe Glu Glu Ile Ala
120 125 130

aac act gct ccg gat gtc att ttg gcg tcc tac tct ggc atc acc cag 547
Asn Thr Ala Pro Asp Val Ile Leu Ala Ser Tyr Ser Gly Ile Thr Gln
135 140 145

gaa gac tac gat cag ctg tcc cag atc gca cct gtg gtt gcc tac cca 595
Glu Asp Tyr Asp Gln Leu Ser Gln Ile Ala Pro Val Val Ala Tyr Pro
150 155 160 165

gaa atc gca tgg ggc acc tcc ctg gat gaa atg att gag atg aac tct 643
Glu Ile Ala Trp Gly Thr Ser Leu Asp Glu Met Ile Glu Met Asn Ser
170 175 180

aag gcg att ggc ttg gag caa gaa ggc aag gat ctc atc gca gat ctg 691
Lys Ala Ile Gly Leu Glu Gln Glu Gly Lys Asp Leu Ile Ala Asp Leu
185 190 195

gat gca gag gtt gct tcc gcc atc gat gcc aac cca gag ttg aag gat 739
Asp Ala Glu Val Ala Ser Ala Ile Asp Ala Asn Pro Glu Leu Lys Asp
200 205 210

```
gcg aag cct gta ttc gcg ttc ttc gat gag agc gat ttc tcg cag att   787
Ala Lys Pro Val Phe Ala Phe Phe Asp Glu Ser Asp Phe Ser Gln Ile
    215                 220                 225

ggt gtg tac acc agc att gat cct cgc atg agc ttc ttg ctt gat gcg   835
Gly Val Tyr Thr Ser Ile Asp Pro Arg Met Ser Phe Leu Leu Asp Ala
230                 235                 240                 245

ggt gtc cag gaa gct tca gtc ctc aag gag cac tcc agc cca gat agc   883
Gly Val Gln Glu Ala Ser Val Leu Lys Glu His Ser Ser Pro Asp Ser
                250                 255                 260

ttc tac gag cag gtt tct gca gaa aac cct gaa acc ttc gac gat gtt   931
Phe Tyr Glu Gln Val Ser Ala Glu Asn Pro Glu Thr Phe Asp Asp Val
            265                 270                 275

gat gtg atc atc acc tac ggc acc gaa gat gat gct gca aac gct gag   979
Asp Val Ile Ile Thr Tyr Gly Thr Glu Asp Asp Ala Ala Asn Ala Glu
        280                 285                 290

ctg ttg tcc aag atg cag gct gat cca ctg ctg tct cga atc cca gct   1027
Leu Leu Ser Lys Met Gln Ala Asp Pro Leu Leu Ser Arg Ile Pro Ala
    295                 300                 305

atc gcc gag ggc aag gtt gtg ttc ttg ggt gct aac cca ctg gct gct   1075
Ile Ala Glu Gly Lys Val Val Phe Leu Gly Ala Asn Pro Leu Ala Ala
310                 315                 320                 325

tca gcg aat gaa tcc cca cta tct att cct tgg ggt atc aac gat tac   1123
Ser Ala Asn Glu Ser Pro Leu Ser Ile Pro Trp Gly Ile Asn Asp Tyr
                330                 335                 340

ttt gca aaa ctc gcc gaa cct ctg aag taaaactgct tgatgtcaac         1170
Phe Ala Lys Leu Ala Glu Pro Leu Lys
            345                 350

aac                                                              1173
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<210> 916
<211> 350
<212> PRT
<213> Corynebacterium glutamicum

<400> 916

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Met Arg Thr Ser Arg Val Leu Ala Gly Ile Leu Ala Ala Thr Leu Thr
  1               5                  10                  15

Val Ser Leu Ala Ala Cys Ser Gln Asp Ser Ser Glu Thr Ser Ser Asn
             20                  25                  30

Ser Ser Ser Ala Ala Ser Gln Ser Ser Asp Val Ser Asn Glu Ala Phe
         35                  40                  45

Pro Val Thr Ile Glu His Ala Phe Gly Glu Thr Thr Ile Glu Ser Lys
     50                  55                  60

Pro Glu Arg Ile Ala Thr Val Gly Trp Ser Asn His Glu Val Pro Leu
 65                  70                  75                  80
```

```
Ala Leu Gly Val Thr Pro Val Gly Phe Glu Lys Val Thr Trp Gly Asp
                 85                  90                  95

Asp Asp Asn Asn Gly Ile Leu Pro Trp Val Glu Glu Thr Leu Ser Lys
            100                 105                 110

Leu Gly Ser Asp Glu Pro Val Leu Phe Asp Ala Thr Asp Ser Ile Pro
        115                 120                 125

Phe Glu Glu Ile Ala Asn Thr Ala Pro Asp Val Ile Leu Ala Ser Tyr
    130                 135                 140

Ser Gly Ile Thr Gln Glu Asp Tyr Asp Gln Leu Ser Gln Ile Ala Pro
145                 150                 155                 160

Val Val Ala Tyr Pro Glu Ile Ala Trp Gly Thr Ser Leu Asp Glu Met
                165                 170                 175

Ile Glu Met Asn Ser Lys Ala Ile Gly Leu Glu Gln Glu Gly Lys Asp
            180                 185                 190

Leu Ile Ala Asp Leu Asp Ala Glu Val Ala Ser Ala Ile Asp Ala Asn
        195                 200                 205

Pro Glu Leu Lys Asp Ala Lys Pro Val Phe Ala Phe Phe Asp Glu Ser
    210                 215                 220

Asp Phe Ser Gln Ile Gly Val Tyr Thr Ser Ile Asp Pro Arg Met Ser
225                 230                 235                 240

Phe Leu Leu Asp Ala Gly Val Gln Glu Ala Ser Val Leu Lys Glu His
                245                 250                 255

Ser Ser Pro Asp Ser Phe Tyr Glu Gln Val Ser Ala Glu Asn Pro Glu
            260                 265                 270

Thr Phe Asp Asp Val Asp Val Ile Ile Thr Tyr Gly Thr Glu Asp Asp
        275                 280                 285

Ala Ala Asn Ala Glu Leu Leu Ser Lys Met Gln Ala Asp Pro Leu Leu
    290                 295                 300

Ser Arg Ile Pro Ala Ile Ala Glu Gly Lys Val Val Phe Leu Gly Ala
305                 310                 315                 320

Asn Pro Leu Ala Ala Ser Ala Asn Glu Ser Pro Leu Ser Ile Pro Trp
                325                 330                 335

Gly Ile Asn Asp Tyr Phe Ala Lys Leu Ala Glu Pro Leu Lys
            340                 345                 350
```

<210> 917
<211> 336
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(313)
<223> RXN01987

<400> 917
gggttaggag aggggaaatc cccgatgtgc tctaggttct tattggcgat gattgaagaa 60

gaaagaaaaa ctcaatcagc cataaaggag cttgatcccg atg act ttc cca gca 115
Met Thr Phe Pro Ala
1 5

caa tct cga cga ctc gcc cga agc acc acc gac aaa tgg atc ggc ggc 163
Gln Ser Arg Arg Leu Ala Arg Ser Thr Thr Asp Lys Trp Ile Gly Gly
10 15 20

gtc gct ggt ggc ctc gca gag acc tac ggt tgg aat ccg gcc tat gtg 211
Val Ala Gly Gly Leu Ala Glu Thr Tyr Gly Trp Asn Pro Ala Tyr Val
25 30 35

cgt ctc gcg ttc gtg gcg tcg gtt ctg ttt cca ctg cca ggt tca cag 259
Arg Leu Ala Phe Val Ala Ser Val Leu Phe Pro Leu Pro Gly Ser Gln
40 45 50

atc ctg ttc tac gcc cta gcg tgg ctg atc atc cca tcc cga gaa aat 307
Ile Leu Phe Tyr Ala Leu Ala Trp Leu Ile Ile Pro Ser Arg Glu Asn
55 60 65

cgc ttc taacgtgcgt tgcataacgc aga 336
Arg Phe
70

<210> 918
<211> 71
<212> PRT
<213> Corynebacterium glutamicum

<400> 918
Met Thr Phe Pro Ala Gln Ser Arg Arg Leu Ala Arg Ser Thr Thr Asp
1 5 10 15

Lys Trp Ile Gly Gly Val Ala Gly Gly Leu Ala Glu Thr Tyr Gly Trp
20 25 30

Asn Pro Ala Tyr Val Arg Leu Ala Phe Val Ala Ser Val Leu Phe Pro
35 40 45

Leu Pro Gly Ser Gln Ile Leu Phe Tyr Ala Leu Ala Trp Leu Ile Ile
50 55 60

Pro Ser Arg Glu Asn Arg Phe
65 70

<210> 919
<211> 336
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(313)
<223> FRXA01987

<400> 919
gggttaggag aggggaaatc cccgatgtgc tctaggttct tattggcgat gattgaagaa 60

gaaagaaaaa ctcaatcagc cataaaggag cttgatcccg atg act ttc cca gca 115
Met Thr Phe Pro Ala
1 5

caa tct cga cga ctc gcc cga agc acc acc gac aaa tgg atc ggc ggc 163
Gln Ser Arg Arg Leu Ala Arg Ser Thr Thr Asp Lys Trp Ile Gly Gly
10 15 20

gtc gct ggt ggc ctc gca gag acc tac ggt tgg aat ccg gcc tat gtg 211
Val Ala Gly Gly Leu Ala Glu Thr Tyr Gly Trp Asn Pro Ala Tyr Val
25 30 35

cgt ctc gcg ttc gtg gcg tcg gtt ctg ttt cca ctg cca ggt tca cag 259
Arg Leu Ala Phe Val Ala Ser Val Leu Phe Pro Leu Pro Gly Ser Gln
40 45 50

atc ctg ttc tac gcc cta gcg tgg ctg atc atc cca tcc cga gaa aat 307
Ile Leu Phe Tyr Ala Leu Ala Trp Leu Ile Ile Pro Ser Arg Glu Asn
55 60 65

cgc ttc taacgtgcgt tgcataacgc aga 336
Arg Phe
70

<210> 920
<211> 71
<212> PRT
<213> Corynebacterium glutamicum

<400> 920
Met Thr Phe Pro Ala Gln Ser Arg Arg Leu Ala Arg Ser Thr Thr Asp
1 5 10 15

Lys Trp Ile Gly Gly Val Ala Gly Gly Leu Ala Glu Thr Tyr Gly Trp
20 25 30

Asn Pro Ala Tyr Val Arg Leu Ala Phe Val Ala Ser Val Leu Phe Pro
35 40 45

Leu Pro Gly Ser Gln Ile Leu Phe Tyr Ala Leu Ala Trp Leu Ile Ile
50 55 60

Pro Ser Arg Glu Asn Arg Phe
65 70

<210> 921
<211> 549
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(526)
<223> RXN01988

<400> 921

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ttaagaattg gattcgagtc ggtaccgctt gaaagtactt tgcgtaagtt cccaccgact 60

gcccctagtt gttgcgaata tttatagatt gttgagaaag atg aac atg aag acg   115
                                            Met Asn Met Lys Thr
                                              1               5

cac ccg gct tcc gcc aag cag acc acc gag ctt cga ctc ctg aca gcc   163
His Pro Ala Ser Ala Lys Gln Thr Thr Glu Leu Arg Leu Leu Thr Ala
                 10                  15                  20

acc gtg tac ttc aaa gca ctc aat gaa gtc cac aac gtc atg cag atg   211
Thr Val Tyr Phe Lys Ala Leu Asn Glu Val His Asn Val Met Gln Met
             25                  30                  35

atc gac cca cta act cca gtc gtt ccc atc acc acg ggc acc tca gtt   259
Ile Asp Pro Leu Thr Pro Val Val Pro Ile Thr Thr Gly Thr Ser Val
         40                  45                  50

gcc gag ctt tat gct gac gcc cgc gag cac ctc gac aat ggt gca acc   307
Ala Glu Leu Tyr Ala Asp Ala Arg Glu His Leu Asp Asn Gly Ala Thr
     55                  60                  65

cag gtg atg atc ccc gtc att tca cct tcc aac ctg acc ttg tca gta   355
Gln Val Met Ile Pro Val Ile Ser Pro Ser Asn Leu Thr Leu Ser Val
 70                  75                  80                  85

gtt gcc ctg ggc aat gaa gag gtt gac gca ctg ggc cat tcc gaa gga   403
Val Ala Leu Gly Asn Glu Glu Val Asp Ala Leu Gly His Ser Glu Gly
                 90                  95                 100

caa gca gtt cac tcc ctt ctg gaa att cat acc ccg aag cgc agc tgg   451
Gln Ala Val His Ser Leu Leu Glu Ile His Thr Pro Lys Arg Ser Trp
            105                 110                 115

cct ctt tcc gag ctt tat att gat gac aat gag ggt ttg gct cag gtg   499
Pro Leu Ser Glu Leu Tyr Ile Asp Asp Asn Glu Gly Leu Ala Gln Val
        120                 125                 130

tcg cgc tgc ttc gcc cgc ctt gtt ggc tagtcccacc ccaccaattg         546
Ser Arg Cys Phe Ala Arg Leu Val Gly
    135                 140

cat                                                               549


<210> 922
<211> 142
<212> PRT
<213> Corynebacterium glutamicum

<400> 922
Met Asn Met Lys Thr His Pro Ala Ser Ala Lys Gln Thr Thr Glu Leu
  1               5                  10                  15

Arg Leu Leu Thr Ala Thr Val Tyr Phe Lys Ala Leu Asn Glu Val His
             20                  25                  30

Asn Val Met Gln Met Ile Asp Pro Leu Thr Pro Val Val Pro Ile Thr
         35                  40                  45

Thr Gly Thr Ser Val Ala Glu Leu Tyr Ala Asp Ala Arg Glu His Leu
```

```
     50                  55                  60

Asp Asn Gly Ala Thr Gln Val Met Ile Pro Val Ile Ser Pro Ser Asn
 65                  70                  75                  80

Leu Thr Leu Ser Val Val Ala Leu Gly Asn Glu Glu Val Asp Ala Leu
                 85                  90                  95

Gly His Ser Glu Gly Gln Ala Val His Ser Leu Leu Glu Ile His Thr
            100                 105                 110

Pro Lys Arg Ser Trp Pro Leu Ser Glu Leu Tyr Ile Asp Asp Asn Glu
        115                 120                 125

Gly Leu Ala Gln Val Ser Arg Cys Phe Ala Arg Leu Val Gly
    130                 135                 140


<210> 923
<211> 341
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(318)
<223> FRXA01988

<400> 923
atg atc gac cca cta act cca gtc gtt ccc atc acc acg ggc acc tca   48
Met Ile Asp Pro Leu Thr Pro Val Val Pro Ile Thr Thr Gly Thr Ser
  1               5                  10                  15

gtt gcc gag ctt tat gct gac gcc cgc gag cac ctc gac aat ggt gca   96
Val Ala Glu Leu Tyr Ala Asp Ala Arg Glu His Leu Asp Asn Gly Ala
             20                  25                  30

acc cag gtg atg atc ccc gtc att tca cct tcc aac ctg acc ttg tca   144
Thr Gln Val Met Ile Pro Val Ile Ser Pro Ser Asn Leu Thr Leu Ser
         35                  40                  45

gta gtt gcc ctg ggc aat caa gag gtt gac gca ctg ggc cat tcc gaa   192
Val Val Ala Leu Gly Asn Gln Glu Val Asp Ala Leu Gly His Ser Glu
     50                  55                  60

gga caa gca gtt cac tcc ctt ctg gaa att cat acc ccg aag cgc agc   240
Gly Gln Ala Val His Ser Leu Leu Glu Ile His Thr Pro Lys Arg Ser
 65                  70                  75                  80

tgg cct ctt tcc gag ctt tat att gat gac aat gag ggt ttg gct cag   288
Trp Pro Leu Ser Glu Leu Tyr Ile Asp Asp Asn Glu Gly Leu Ala Gln
                 85                  90                  95

gtg tcg cgc tgc ttc gcc cgc ctt gtt ggc tagtcccacc ccaccaattg     338
Val Ser Arg Cys Phe Ala Arg Leu Val Gly
            100                 105

cat                                                               341


<210> 924
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<211> 106
<212> PRT
<213> Corynebacterium glutamicum

<400> 924
Met Ile Asp Pro Leu Thr Pro Val Val Pro Ile Thr Thr Gly Thr Ser
1 5 10 15

Val Ala Glu Leu Tyr Ala Asp Ala Arg Glu His Leu Asp Asn Gly Ala
20 25 30

Thr Gln Val Met Ile Pro Val Ile Ser Pro Ser Asn Leu Thr Leu Ser
35 40 45

Val Val Ala Leu Gly Asn Gln Glu Val Asp Ala Leu Gly His Ser Glu
50 55 60

Gly Gln Ala Val His Ser Leu Leu Glu Ile His Thr Pro Lys Arg Ser
65 70 75 80

Trp Pro Leu Ser Glu Leu Tyr Ile Asp Asp Asn Glu Gly Leu Ala Gln
85 90 95

Val Ser Arg Cys Phe Ala Arg Leu Val Gly
100 105

<210> 925
<211> 996
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(973)
<223> RXN01991

<400> 925
tccggaggtg gatttgagga tttcgacgtt ttctcggaag ttcctcgggt agaggaaaca 60

tcgacgagga tcagctattc ttacaaaaat tcatttgaat atg acg aat ttg ttg 115
Met Thr Asn Leu Leu
1 5

ccg cat ttc ccg agt acc gac gta gct gcg tgg gaa cca acc gtt gtg 163
Pro His Phe Pro Ser Thr Asp Val Ala Ala Trp Glu Pro Thr Val Val
10 15 20

tat tca gcg gat aag acc aca gca aca gcg acg ttt aag aat att cct 211
Tyr Ser Ala Asp Lys Thr Thr Ala Thr Ala Thr Phe Lys Asn Ile Pro
25 30 35

tcg gat att tcc ttt agt tgg act ggt att gaa gca cta gag cca ttt 259
Ser Asp Ile Ser Phe Ser Trp Thr Gly Ile Glu Ala Leu Glu Pro Phe
40 45 50

agc cct ggt aaa acc ttc gaa cat aag gtg caa ggt tct gtt ggt gaa 307
Ser Pro Gly Lys Thr Phe Glu His Lys Val Gln Gly Ser Val Gly Glu
55 60 65

cca gcg ggg gcg ttc act agg gat aac tat ttc act gag ggt gag ctc 355

```
Pro Ala Gly Ala Phe Thr Arg Asp Asn Tyr Phe Thr Glu Gly Glu Leu
 70                  75                  80                  85

tac aaa cat cgc cac gca gac gat ctg ctt tcc ggt gat ggc ttg ttt   403
Tyr Lys His Arg His Ala Asp Asp Leu Leu Ser Gly Asp Gly Leu Phe
                 90                  95                 100

ggc ccc aac atc acc gat ggc gat ggc aac ctc ccc tct gtt gat gac   451
Gly Pro Asn Ile Thr Asp Gly Asp Gly Asn Leu Pro Ser Val Asp Asp
            105                 110                 115

ggc aag gac ggt gac gat ggg tct gat ggc tca gac ggc cga gac ggt   499
Gly Lys Asp Gly Asp Asp Gly Ser Asp Gly Ser Asp Gly Arg Asp Gly
        120                 125                 130

gtt gtc gcc att gat gtt gtt gac aat gct gac ggc acg gtg act gtc   547
Val Val Ala Ile Asp Val Val Asp Asn Ala Asp Gly Thr Val Thr Val
    135                 140                 145

acc ttg tcc gat ggc act acg ttt act ctt gat gct ggt caa gac ggc   595
Thr Leu Ser Asp Gly Thr Thr Phe Thr Leu Asp Ala Gly Gln Asp Gly
150                 155                 160                 165

aaa gat ggt ctt gac ggg ctt gat ggt act ggc cta acg ctg gaa tct   643
Lys Asp Gly Leu Asp Gly Leu Asp Gly Thr Gly Leu Thr Leu Glu Ser
                170                 175                 180

gct acc cct gat gag gac ggc aac atc acc tat gtt ctt tct gac ggt   691
Ala Thr Pro Asp Glu Asp Gly Asn Ile Thr Tyr Val Leu Ser Asp Gly
            185                 190                 195

act gag ttc act gtg cgc aac ggt gtt gat ggg tca gac ggt aag gac   739
Thr Glu Phe Thr Val Arg Asn Gly Val Asp Gly Ser Asp Gly Lys Asp
        200                 205                 210

ggc aaa gat gga gtc aat ggc aca gat ggc gta gac ggg tca gac ggt   787
Gly Lys Asp Gly Val Asn Gly Thr Asp Gly Val Asp Gly Ser Asp Gly
    215                 220                 225

aaa ggt ctg gta gag gtg tcc cga gtt acc aac gac aac ggc tca gtg   835
Lys Gly Leu Val Glu Val Ser Arg Val Thr Asn Asp Asn Gly Ser Val
230                 235                 240                 245

acc att acc tac gag gac ggt tca cag atc acc acg aag cca acg ccg   883
Thr Ile Thr Tyr Glu Asp Gly Ser Gln Ile Thr Thr Lys Pro Thr Pro
                250                 255                 260

aca aac tgg ctg tcc aag ctg ctt gat ttg ctt ctc ccg ctg ttt aat   931
Thr Asn Trp Leu Ser Lys Leu Leu Asp Leu Leu Leu Pro Leu Phe Asn
            265                 270                 275

ctg ttc ggt ctt ggt ggc ggc tcc gtc att agt tcc agt aag           973
Leu Phe Gly Leu Gly Gly Gly Ser Val Ile Ser Ser Ser Lys
        280                 285                 290

tagttttttc actccctgtt ttg                                        996
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<210> 926
<211> 291
<212> PRT

<213> Corynebacterium glutamicum

<400> 926

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Met Thr Asn Leu Leu Pro His Phe Pro Ser Thr Asp Val Ala Ala Trp
  1               5                  10                  15

Glu Pro Thr Val Val Tyr Ser Ala Asp Lys Thr Thr Ala Thr Ala Thr
             20                  25                  30

Phe Lys Asn Ile Pro Ser Asp Ile Ser Phe Ser Trp Thr Gly Ile Glu
         35                  40                  45

Ala Leu Glu Pro Phe Ser Pro Gly Lys Thr Phe Glu His Lys Val Gln
     50                  55                  60

Gly Ser Val Gly Glu Pro Ala Gly Ala Phe Thr Arg Asp Asn Tyr Phe
 65                  70                  75                  80

Thr Glu Gly Glu Leu Tyr Lys His Arg His Ala Asp Asp Leu Leu Ser
                 85                  90                  95

Gly Asp Gly Leu Phe Gly Pro Asn Ile Thr Asp Gly Asp Gly Asn Leu
            100                 105                 110

Pro Ser Val Asp Asp Gly Lys Asp Gly Asp Asp Gly Ser Asp Gly Ser
        115                 120                 125

Asp Gly Arg Asp Gly Val Val Ala Ile Asp Val Val Asp Asn Ala Asp
    130                 135                 140

Gly Thr Val Thr Val Thr Leu Ser Asp Gly Thr Thr Phe Thr Leu Asp
145                 150                 155                 160

Ala Gly Gln Asp Gly Lys Asp Gly Leu Asp Gly Leu Asp Gly Thr Gly
                165                 170                 175

Leu Thr Leu Glu Ser Ala Thr Pro Asp Glu Asp Gly Asn Ile Thr Tyr
            180                 185                 190

Val Leu Ser Asp Gly Thr Glu Phe Thr Val Arg Asn Gly Val Asp Gly
        195                 200                 205

Ser Asp Gly Lys Asp Gly Lys Asp Gly Val Asn Gly Thr Asp Gly Val
    210                 215                 220

Asp Gly Ser Asp Gly Lys Gly Leu Val Glu Val Ser Arg Val Thr Asn
225                 230                 235                 240

Asp Asn Gly Ser Val Thr Ile Thr Tyr Glu Asp Gly Ser Gln Ile Thr
                245                 250                 255

Thr Lys Pro Thr Pro Thr Asn Trp Leu Ser Lys Leu Leu Asp Leu Leu
            260                 265                 270

Leu Pro Leu Phe Asn Leu Phe Gly Leu Gly Gly Gly Ser Val Ile Ser
        275                 280                 285

Ser Ser Lys
    290
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<210> 927
<211> 895
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(895)
<223> FRXA01991

<400> 927
tccggaggtg gatttgagga tttcgacgtt ttctcggaag ttcctcgggt agaggaaaca 60

tcgacgagga tcagctattc ttacaaaaat tcatttgaat atg acg aat ttg ttg 115
Met Thr Asn Leu Leu
1 5

ccg cat ttc ccg agt acc gac gta gct gcg tgg gaa cca acc gtt gtg 163
Pro His Phe Pro Ser Thr Asp Val Ala Ala Trp Glu Pro Thr Val Val
10 15 20

tat tca gcg gat aag acc aca gca aca gcg acg ttt aag aat att cct 211
Tyr Ser Ala Asp Lys Thr Thr Ala Thr Ala Thr Phe Lys Asn Ile Pro
25 30 35

tcg gat att tcc ttt agt tgg act ggt att gaa gca cta gag cca ttt 259
Ser Asp Ile Ser Phe Ser Trp Thr Gly Ile Glu Ala Leu Glu Pro Phe
40 45 50

agc cct ggt aaa acc ttc gaa cat aag gtg caa ggt tct gtt ggt gaa 307
Ser Pro Gly Lys Thr Phe Glu His Lys Val Gln Gly Ser Val Gly Glu
55 60 65

cca gcg ggg gcg ttc act agg gat aac tat ttc act gag ggt gag ctc 355
Pro Ala Gly Ala Phe Thr Arg Asp Asn Tyr Phe Thr Glu Gly Glu Leu
70 75 80 85

tac aaa cat cgc cac gca gac gat ctg ctt tcc ggt gat ggc ttg ttt 403
Tyr Lys His Arg His Ala Asp Asp Leu Leu Ser Gly Asp Gly Leu Phe
90 95 100

ggc ccc aac atc acc gat ggc gat ggc aac ctc ccc tct gtt gat gac 451
Gly Pro Asn Ile Thr Asp Gly Asp Gly Asn Leu Pro Ser Val Asp Asp
105 110 115

ggc aag gac ggt gac gat ggg tct gat ggc tca gac ggc cga gac ggt 499
Gly Lys Asp Gly Asp Asp Gly Ser Asp Gly Ser Asp Gly Arg Asp Gly
120 125 130

gtt gtc gcc att gat gtt gtt gac aat gct gac ggc acg gtg act gtc 547
Val Val Ala Ile Asp Val Val Asp Asn Ala Asp Gly Thr Val Thr Val
135 140 145

acc ttg tcc gat ggc act acg ttt act ctt gat gct ggt caa gac ggc 595
Thr Leu Ser Asp Gly Thr Thr Phe Thr Leu Asp Ala Gly Gln Asp Gly
150 155 160 165

aaa gat ggt ctt gac ggg ctt gat ggt act ggc cta acg ctg gaa tct 643
Lys Asp Gly Leu Asp Gly Leu Asp Gly Thr Gly Leu Thr Leu Glu Ser
170 175 180

```
gct acc cct gat gag gac ggc aac atc acc tat gtt ctt tct gac ggt   691
Ala Thr Pro Asp Glu Asp Gly Asn Ile Thr Tyr Val Leu Ser Asp Gly
            185                 190                 195

act gag ttc act gtg cgc aac ggt gtt gat ggg tca gac ggt aag gac   739
Thr Glu Phe Thr Val Arg Asn Gly Val Asp Gly Ser Asp Gly Lys Asp
        200                 205                 210

ggc aaa gat gga gtc aat ggc aca gat ggc gta gac ggg tca gac ggt   787
Gly Lys Asp Gly Val Asn Gly Thr Asp Gly Val Asp Gly Ser Asp Gly
    215                 220                 225

aaa ggt ctg gta gag gtg tcc cga gtt acc aac gac aac ggc tca gtg   835
Lys Gly Leu Val Glu Val Ser Arg Val Thr Asn Asp Asn Gly Ser Val
230                 235                 240                 245

acc att acc tac gag gac ggt tca cag atc acc acg aag cca acg ccg   883
Thr Ile Thr Tyr Glu Asp Gly Ser Gln Ile Thr Thr Lys Pro Thr Pro
                250                 255                 260

aca aac tgg ctg                                                  895
Thr Asn Trp Leu
            265
```

<210> 928
<211> 265
<212> PRT
<213> Corynebacterium glutamicum

<400> 928

```
Met Thr Asn Leu Leu Pro His Phe Pro Ser Thr Asp Val Ala Ala Trp
  1               5                  10                  15

Glu Pro Thr Val Val Tyr Ser Ala Asp Lys Thr Thr Ala Thr Ala Thr
             20                  25                  30

Phe Lys Asn Ile Pro Ser Asp Ile Ser Phe Ser Trp Thr Gly Ile Glu
         35                  40                  45

Ala Leu Glu Pro Phe Ser Pro Gly Lys Thr Phe Glu His Lys Val Gln
     50                  55                  60

Gly Ser Val Gly Glu Pro Ala Gly Ala Phe Thr Arg Asp Asn Tyr Phe
 65                  70                  75                  80

Thr Glu Gly Glu Leu Tyr Lys His Arg His Ala Asp Asp Leu Leu Ser
                 85                  90                  95

Gly Asp Gly Leu Phe Gly Pro Asn Ile Thr Asp Gly Asp Gly Asn Leu
            100                 105                 110

Pro Ser Val Asp Asp Gly Lys Asp Gly Asp Asp Gly Ser Asp Gly Ser
        115                 120                 125

Asp Gly Arg Asp Gly Val Val Ala Ile Asp Val Val Asp Asn Ala Asp
    130                 135                 140

Gly Thr Val Thr Val Thr Leu Ser Asp Gly Thr Thr Phe Thr Leu Asp
145                 150                 155                 160
```

```
Ala Gly Gln Asp Gly Lys Asp Gly Leu Asp Gly Leu Asp Gly Thr Gly
                165                 170                 175

Leu Thr Leu Glu Ser Ala Thr Pro Asp Glu Asp Gly Asn Ile Thr Tyr
            180                 185                 190

Val Leu Ser Asp Gly Thr Glu Phe Thr Val Arg Asn Gly Val Asp Gly
        195                 200                 205

Ser Asp Gly Lys Asp Gly Lys Asp Gly Val Asn Gly Thr Asp Gly Val
    210                 215                 220

Asp Gly Ser Asp Gly Lys Gly Leu Val Glu Val Ser Arg Val Thr Asn
225                 230                 235                 240

Asp Asn Gly Ser Val Thr Ile Thr Tyr Glu Asp Gly Ser Gln Ile Thr
                245                 250                 255

Thr Lys Pro Thr Pro Thr Asn Trp Leu
            260                 265
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<210> 929
<211> 660
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(637)
<223> RXN01996

<400> 929

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ctagtataga acggaacacg gcagcgacac aaactgcaca gatgcaagag tgtcggtacc 60

gttaaaaacg aaacacactt tcaccgaaaa ggacttccca atg agc aag ttg act   115
                                              Met Ser Lys Leu Thr
                                                1               5

ggc acc tgg acc ctc gac cct gca cac acc gaa atc aag ttc gtg gct   163
Gly Thr Trp Thr Leu Asp Pro Ala His Thr Glu Ile Lys Phe Val Ala
                10                  15                  20

cgc cac gca atg gtt acc aag gtt cgc ggt gaa ttc acc gag tac acc   211
Arg His Ala Met Val Thr Lys Val Arg Gly Glu Phe Thr Glu Tyr Thr
            25                  30                  35

gac tcc att gtc gta gat gct gaa aac cca gag aac tcc tct gca aag   259
Asp Ser Ile Val Val Asp Ala Glu Asn Pro Glu Asn Ser Ser Ala Lys
        40                  45                  50

gtt gtt atc aag acc gct tcc gtt acc acc ggc aac gca gac cgc gat   307
Val Val Ile Lys Thr Ala Ser Val Thr Thr Gly Asn Ala Asp Arg Asp
    55                  60                  65

gca cac gtt aag ggc gac gac ttc ttc gca gta gac aag ttc cct gaa   355
Ala His Val Lys Gly Asp Asp Phe Phe Ala Val Asp Lys Phe Pro Glu
70                  75                  80                  85

atg act ttc gaa gct act tcc ttt gtt atc aag aac gaa aac gaa ggc   403
Met Thr Phe Glu Ala Thr Ser Phe Val Ile Lys Asn Glu Asn Glu Gly
```

```
                90                  95                 100

acc gtt acc ggc gac ctc aca att cgt gac acc acc aag tcc gtc acc   451
Thr Val Thr Gly Asp Leu Thr Ile Arg Asp Thr Thr Lys Ser Val Thr
            105                 110                 115

ctg gac gtt gag gtt ggt ggc gtt gct gag gat cca ttc ggc aac acc   499
Leu Asp Val Glu Val Gly Gly Val Ala Glu Asp Pro Phe Gly Asn Thr
        120                 125                 130

cgc ctt ggc ttc gaa gcc tcc acc gaa atc aac cgc aag gac ttc ggc   547
Arg Leu Gly Phe Glu Ala Ser Thr Glu Ile Asn Arg Lys Asp Phe Gly
    135                 140                 145

gta gat ttc cag gct cca ctc tcc acc ggt ggc gtt ctg gtt tct gag   595
Val Asp Phe Gln Ala Pro Leu Ser Thr Gly Gly Val Leu Val Ser Glu
150                 155                 160                 165

aag atc aag atc gag atc gac ggc tcc gca atc aag gct gct           637
Lys Ile Lys Ile Glu Ile Asp Gly Ser Ala Ile Lys Ala Ala
                170                 175

taagcgccca caaacaaaaa gcc                                        660


<210> 930
<211> 179
<212> PRT
<213> Corynebacterium glutamicum

<400> 930
Met Ser Lys Leu Thr Gly Thr Trp Thr Leu Asp Pro Ala His Thr Glu
  1               5                  10                  15

Ile Lys Phe Val Ala Arg His Ala Met Val Thr Lys Val Arg Gly Glu
             20                  25                  30

Phe Thr Glu Tyr Thr Asp Ser Ile Val Val Asp Ala Glu Asn Pro Glu
         35                  40                  45

Asn Ser Ser Ala Lys Val Val Ile Lys Thr Ala Ser Val Thr Thr Gly
     50                  55                  60

Asn Ala Asp Arg Asp Ala His Val Lys Gly Asp Asp Phe Phe Ala Val
 65                  70                  75                  80

Asp Lys Phe Pro Glu Met Thr Phe Glu Ala Thr Ser Phe Val Ile Lys
                 85                  90                  95

Asn Glu Asn Glu Gly Thr Val Thr Gly Asp Leu Thr Ile Arg Asp Thr
            100                 105                 110

Thr Lys Ser Val Thr Leu Asp Val Glu Val Gly Gly Val Ala Glu Asp
        115                 120                 125

Pro Phe Gly Asn Thr Arg Leu Gly Phe Glu Ala Ser Thr Glu Ile Asn
    130                 135                 140

Arg Lys Asp Phe Gly Val Asp Phe Gln Ala Pro Leu Ser Thr Gly Gly
145                 150                 155                 160
```

```
Val Leu Val Ser Glu Lys Ile Lys Ile Glu Ile Asp Gly Ser Ala Ile
                165                 170                 175

Lys Ala Ala
```

<210> 931
<211> 647
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (88)..(624)
<223> FRXA01996

<400> 931

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gaacacggca gcgacacaaa ctgcacagat gcaagagtgt cggtaccgtt aaaaacgaaa 60

cacactttca ccgaaaagga cttcccaatg agc aag ttg act ggc acc tgg acc  114
                           Met Ser Lys Leu Thr Gly Thr Trp Thr
                             1               5

ctc gac cct gca cac acc gaa atc aag ttc gtg gct cgc cac gca atg   162
Leu Asp Pro Ala His Thr Glu Ile Lys Phe Val Ala Arg His Ala Met
 10                  15                  20                  25

gtt acc aag gtt cgc ggt gaa ttc acc gag tac acc gac tcc att gtc   210
Val Thr Lys Val Arg Gly Glu Phe Thr Glu Tyr Thr Asp Ser Ile Val
                 30                  35                  40

gta gat gct gaa aac cca gag aac tcc tct gca aag gtt gtt atc aag   258
Val Asp Ala Glu Asn Pro Glu Asn Ser Ser Ala Lys Val Val Ile Lys
             45                  50                  55

acc gct tcc gtt acc acc ggc aac gca gac cgc gat gca cac gtt aag   306
Thr Ala Ser Val Thr Thr Gly Asn Ala Asp Arg Asp Ala His Val Lys
         60                  65                  70

ggc gac gac ttc ttc gca gta gac aag ttc cct gaa atg act ttc gaa   354
Gly Asp Asp Phe Phe Ala Val Asp Lys Phe Pro Glu Met Thr Phe Glu
     75                  80                  85

gct act tcc ttt gtt atc aag aac gaa aac gaa ggc acc gtt acc ggc   402
Ala Thr Ser Phe Val Ile Lys Asn Glu Asn Glu Gly Thr Val Thr Gly
 90                  95                 100                 105

gac ctc aca att cgt gac acc acc aag tcc gtc acc ctg gac gtt gag   450
Asp Leu Thr Ile Arg Asp Thr Thr Lys Ser Val Thr Leu Asp Val Glu
                110                 115                 120

gtt ggt ggc gtt gct gag gat cca ttc ggc aac acc cgc ctt ggc ttc   498
Val Gly Gly Val Ala Glu Asp Pro Phe Gly Asn Thr Arg Leu Gly Phe
            125                 130                 135

gaa gcc tcc acc gaa atc aac cgc aag gac ttc ggc gta gat ttc cag   546
Glu Ala Ser Thr Glu Ile Asn Arg Lys Asp Phe Gly Val Asp Phe Gln
        140                 145                 150

gct cca ctc tcc acc ggt ggc gtt ctg gtt tct gag aag atc aag atc   594
```

```
Ala Pro Leu Ser Thr Gly Gly Val Leu Val Ser Glu Lys Ile Lys Ile
    155                 160                 165

gag atc gac ggc tcc gca atc aag gct gct taagcgccca caaacaaaaa     644
Glu Ile Asp Gly Ser Ala Ile Lys Ala Ala
170                 175

gcc                                                               647
```

<210> 932
<211> 179
<212> PRT
<213> Corynebacterium glutamicum

<400> 932

```
Met Ser Lys Leu Thr Gly Thr Trp Thr Leu Asp Pro Ala His Thr Glu
  1               5                  10                  15

Ile Lys Phe Val Ala Arg His Ala Met Val Thr Lys Val Arg Gly Glu
             20                  25                  30

Phe Thr Glu Tyr Thr Asp Ser Ile Val Val Asp Ala Glu Asn Pro Glu
         35                  40                  45

Asn Ser Ser Ala Lys Val Val Ile Lys Thr Ala Ser Val Thr Thr Gly
     50                  55                  60

Asn Ala Asp Arg Asp Ala His Val Lys Gly Asp Asp Phe Phe Ala Val
 65                  70                  75                  80

Asp Lys Phe Pro Glu Met Thr Phe Glu Ala Thr Ser Phe Val Ile Lys
                 85                  90                  95

Asn Glu Asn Glu Gly Thr Val Thr Gly Asp Leu Thr Ile Arg Asp Thr
            100                 105                 110

Thr Lys Ser Val Thr Leu Asp Val Glu Val Gly Gly Val Ala Glu Asp
        115                 120                 125

Pro Phe Gly Asn Thr Arg Leu Gly Phe Glu Ala Ser Thr Glu Ile Asn
    130                 135                 140

Arg Lys Asp Phe Gly Val Asp Phe Gln Ala Pro Leu Ser Thr Gly Gly
145                 150                 155                 160

Val Leu Val Ser Glu Lys Ile Lys Ile Glu Ile Asp Gly Ser Ala Ile
                165                 170                 175

Lys Ala Ala
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<210> 933
<211> 756
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(733)

<223> RXN02007

<400> 933

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tggaagcccc agccgcggtc caagagacag ttgcgccgac gtccacccct taggacgctg 60

attacagacg tgtcccattt ctttactact attggaaatt atg agt tca gac gca   115
                                            Met Ser Ser Asp Ala
                                              1               5

gaa aag gca tcc gtg gag ctt tcc gaa aaa ttt cac cca gaa cgc acc   163
Glu Lys Ala Ser Val Glu Leu Ser Glu Lys Phe His Pro Glu Arg Thr
                 10                  15                  20

cat att ttg ggc gcc gtt gtt ttt ggc ctg atc tca tta tta gtc atc   211
His Ile Leu Gly Ala Val Val Phe Gly Leu Ile Ser Leu Leu Val Ile
             25                  30                  35

ggc gca gcc cct cag tac ctg ttt tgg ctg ctc gcg ctc cct gtc atc   259
Gly Ala Ala Pro Gln Tyr Leu Phe Trp Leu Leu Ala Leu Pro Val Ile
         40                  45                  50

ttc ggt tac tgg gtt cta aaa tca tcc acg atc gtt gat gaa cag ggc   307
Phe Gly Tyr Trp Val Leu Lys Ser Ser Thr Ile Val Asp Glu Gln Gly
     55                  60                  65

atc acc gca aac tac gcc ttc aag ggc aaa aag gtt gtg gcc tgg gaa   355
Ile Thr Ala Asn Tyr Ala Phe Lys Gly Lys Lys Val Val Ala Trp Glu
 70                  75                  80                  85

gac ctc gca gga atc gga ttc aag ggt gcc cgc act ttc gct cgc acc   403
Asp Leu Ala Gly Ile Gly Phe Lys Gly Ala Arg Thr Phe Ala Arg Thr
                 90                  95                 100

acc tcc gat gca gaa gtc acc ctc ccg ggc gtc acc ttc aac tcc ctt   451
Thr Ser Asp Ala Glu Val Thr Leu Pro Gly Val Thr Phe Asn Ser Leu
            105                 110                 115

ccc cgc ctt gaa gct gct tcc cac ggc cgc atc ccc gat gcg atc acc   499
Pro Arg Leu Glu Ala Ala Ser His Gly Arg Ile Pro Asp Ala Ile Thr
        120                 125                 130

gca agc aag gaa gca gcc gac ggc aag gtt gta gtc gtt caa gaa gac   547
Ala Ser Lys Glu Ala Ala Asp Gly Lys Val Val Val Val Gln Glu Asp
    135                 140                 145

ggc tac tcc gtg atg atg tcc aag gaa gag tac ttg gag cgc caa aag   595
Gly Tyr Ser Val Met Met Ser Lys Glu Glu Tyr Leu Glu Arg Gln Lys
150                 155                 160                 165

gca ctg ggc aag cca gtt cag ttg aac ttc gat gac gac acc gat ggg   643
Ala Leu Gly Lys Pro Val Gln Leu Asn Phe Asp Asp Asp Thr Asp Gly
                170                 175                 180

aat aca aca caa aca gaa agc gtt gaa tcc caa gag acc gga caa gcc   691
Asn Thr Thr Gln Thr Glu Ser Val Glu Ser Gln Glu Thr Gly Gln Ala
            185                 190                 195

gcg tct gaa acc tca cat cgt gat aac cct gcg tca cag cac           733
Ala Ser Glu Thr Ser His Arg Asp Asn Pro Ala Ser Gln His
        200                 205                 210
```

tagagtgtaa taagccgtcc gaa 756

<210> 934
<211> 211
<212> PRT
<213> Corynebacterium glutamicum

<400> 934
Met Ser Ser Asp Ala Glu Lys Ala Ser Val Glu Leu Ser Glu Lys Phe
1 5 10 15

His Pro Glu Arg Thr His Ile Leu Gly Ala Val Val Phe Gly Leu Ile
20 25 30

Ser Leu Leu Val Ile Gly Ala Ala Pro Gln Tyr Leu Phe Trp Leu Leu
35 40 45

Ala Leu Pro Val Ile Phe Gly Tyr Trp Val Leu Lys Ser Ser Thr Ile
50 55 60

Val Asp Glu Gln Gly Ile Thr Ala Asn Tyr Ala Phe Lys Gly Lys Lys
65 70 75 80

Val Val Ala Trp Glu Asp Leu Ala Gly Ile Gly Phe Lys Gly Ala Arg
85 90 95

Thr Phe Ala Arg Thr Thr Ser Asp Ala Glu Val Thr Leu Pro Gly Val
100 105 110

Thr Phe Asn Ser Leu Pro Arg Leu Glu Ala Ala Ser His Gly Arg Ile
115 120 125

Pro Asp Ala Ile Thr Ala Ser Lys Glu Ala Ala Asp Gly Lys Val Val
130 135 140

Val Val Gln Glu Asp Gly Tyr Ser Val Met Met Ser Lys Glu Glu Tyr
145 150 155 160

Leu Glu Arg Gln Lys Ala Leu Gly Lys Pro Val Gln Leu Asn Phe Asp
165 170 175

Asp Asp Thr Asp Gly Asn Thr Thr Gln Thr Glu Ser Val Glu Ser Gln
180 185 190

Glu Thr Gly Gln Ala Ala Ser Glu Thr Ser His Arg Asp Asn Pro Ala
195 200 205

Ser Gln His
210

<210> 935
<211> 452
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(429)
<223> FRXA02007

<400> 935

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ggc atc acc gca aac tac gcc ttc aag ggc aaa aag gtt gtg gct tgg   48
Gly Ile Thr Ala Asn Tyr Ala Phe Lys Gly Lys Lys Val Val Ala Trp
  1               5                  10                  15

aaa gac ctc gca gga atc gga ttc aag ggt gcc cgc act ttc gct cgc   96
Lys Asp Leu Ala Gly Ile Gly Phe Lys Gly Ala Arg Thr Phe Ala Arg
             20                  25                  30

ccc acc tcc gat gca gaa gtc acc ctc ccg ggc gtc acc ttc aac tcc   144
Pro Thr Ser Asp Ala Glu Val Thr Leu Pro Gly Val Thr Phe Asn Ser
         35                  40                  45

ctt ccc cgc ctt gaa gct gct tcc cac ggc cgc atc ccc gat gcg atc   192
Leu Pro Arg Leu Glu Ala Ala Ser His Gly Arg Ile Pro Asp Ala Ile
     50                  55                  60

acc gca agc aag gaa gca gcc gac ggc aag gtt gta gtc gtt caa gaa   240
Thr Ala Ser Lys Glu Ala Ala Asp Gly Lys Val Val Val Val Gln Glu
 65                  70                  75                  80

gac ggc tac tcc gtg atg atg tcc aag gaa gag tac ttg gag cgc caa   288
Asp Gly Tyr Ser Val Met Met Ser Lys Glu Glu Tyr Leu Glu Arg Gln
                 85                  90                  95

aag gca ctg ggc aag cca gtt cag ttg aac ttc gat gac gac acc gat   336
Lys Ala Leu Gly Lys Pro Val Gln Leu Asn Phe Asp Asp Asp Thr Asp
            100                 105                 110

ggg aat aca aca caa aca gaa agc gtt gaa tcc caa gag acc gga caa   384
Gly Asn Thr Thr Gln Thr Glu Ser Val Glu Ser Gln Glu Thr Gly Gln
        115                 120                 125

gcc gcg tct gaa acc tca cat cgt gat aac cct gcg tca cag cac       429
Ala Ala Ser Glu Thr Ser His Arg Asp Asn Pro Ala Ser Gln His
    130                 135                 140

tagagtgtaa taagccgtcc gaa                                        452
```

<210> 936
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 936

```
Gly Ile Thr Ala Asn Tyr Ala Phe Lys Gly Lys Lys Val Val Ala Trp
  1               5                  10                  15

Lys Asp Leu Ala Gly Ile Gly Phe Lys Gly Ala Arg Thr Phe Ala Arg
             20                  25                  30

Pro Thr Ser Asp Ala Glu Val Thr Leu Pro Gly Val Thr Phe Asn Ser
         35                  40                  45

Leu Pro Arg Leu Glu Ala Ala Ser His Gly Arg Ile Pro Asp Ala Ile
     50                  55                  60

Thr Ala Ser Lys Glu Ala Ala Asp Gly Lys Val Val Val Val Gln Glu
 65                  70                  75                  80
```

```
Asp Gly Tyr Ser Val Met Met Ser Lys Glu Glu Tyr Leu Glu Arg Gln
                 85                  90                  95

Lys Ala Leu Gly Lys Pro Val Gln Leu Asn Phe Asp Asp Asp Thr Asp
            100                 105                 110

Gly Asn Thr Thr Gln Thr Glu Ser Val Glu Ser Gln Glu Thr Gly Gln
        115                 120                 125

Ala Ala Ser Glu Thr Ser His Arg Asp Asn Pro Ala Ser Gln His
    130                 135                 140


<210> 937
<211> 630
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(607)
<223> RXN02014

<400> 937
agaggacaac aacatgagag cagacgcact aaaacgccgc gaacacatca taaccacaac 60

ctgcaatctc taccgcacac accatcacga ttcgctcacc atg gaa aac att gca   115
                                            Met Glu Asn Ile Ala
                                              1               5

gaa cag gca gga gtg ggt gtt gca act tta tac cga aac ttc ccc gat   163
Glu Gln Ala Gly Val Gly Val Ala Thr Leu Tyr Arg Asn Phe Pro Asp
                10                  15                  20

cgc ttc aca ctg gac atg gca tgc gcc caa tac ctt ttc aac gtg gtg   211
Arg Phe Thr Leu Asp Met Ala Cys Ala Gln Tyr Leu Phe Asn Val Val
            25                  30                  35

atc tcc ctc caa ctc caa gcc atc agc acc ttc ccc acc gac cca gaa   259
Ile Ser Leu Gln Leu Gln Ala Ile Ser Thr Phe Pro Thr Asp Pro Glu
        40                  45                  50

ggc gtg tgg acc tcc ttc aac caa cta ctt ttc gac cgc ggc cta ggc   307
Gly Val Trp Thr Ser Phe Asn Gln Leu Leu Phe Asp Arg Gly Leu Gly
    55                  60                  65

tcc ctc gtc cca gca ctt gcc cca gaa tcc tta gac gac ctc ccc gac   355
Ser Leu Val Pro Ala Leu Ala Pro Glu Ser Leu Asp Asp Leu Pro Asp
70                  75                  80                  85

gag gtc tcc gcc ctg cgt cgc acc aca gag aaa aac acc aca aca ctc   403
Glu Val Ser Ala Leu Arg Arg Thr Thr Glu Lys Asn Thr Thr Thr Leu
                90                  95                  100

atc aac cta gcc aag cag cac gga ctc gta cac cac gac atc gcg ccg   451
Ile Asn Leu Ala Lys Gln His Gly Leu Val His His Asp Ile Ala Pro
            105                 110                 115

ggc acc tac atc gtc ggt ttg atc acc att tcc cgc cca cct atc acc   499
Gly Thr Tyr Ile Val Gly Leu Ile Thr Ile Ser Arg Pro Pro Ile Thr
```

```
        120                 125                 130

gcg ctg gcg aca att tca gaa aac tcc cac aaa gca ctg ctt ggc ctt   547
Ala Leu Ala Thr Ile Ser Glu Asn Ser His Lys Ala Leu Leu Gly Leu
    135                 140                 145

tat ttg tcc ggt ctt aaa cac ggc atg atg gct aac atc gga gaa cat   595
Tyr Leu Ser Gly Leu Lys His Gly Met Met Ala Asn Ile Gly Glu His
150                 155                 160                 165

gac gga aag tcc tgatctagca gtttccttt tag                          630
Asp Gly Lys Ser
```

<210> 938
<211> 169
<212> PRT
<213> Corynebacterium glutamicum

<400> 938

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Met Glu Asn Ile Ala Glu Gln Ala Gly Val Gly Val Ala Thr Leu Tyr
  1               5                  10                  15

Arg Asn Phe Pro Asp Arg Phe Thr Leu Asp Met Ala Cys Ala Gln Tyr
             20                  25                  30

Leu Phe Asn Val Val Ile Ser Leu Gln Leu Gln Ala Ile Ser Thr Phe
         35                  40                  45

Pro Thr Asp Pro Glu Gly Val Trp Thr Ser Phe Asn Gln Leu Leu Phe
     50                  55                  60

Asp Arg Gly Leu Gly Ser Leu Val Pro Ala Leu Ala Pro Glu Ser Leu
 65                  70                  75                  80

Asp Asp Leu Pro Asp Glu Val Ser Ala Leu Arg Arg Thr Thr Glu Lys
                 85                  90                  95

Asn Thr Thr Thr Leu Ile Asn Leu Ala Lys Gln His Gly Leu Val His
            100                 105                 110

His Asp Ile Ala Pro Gly Thr Tyr Ile Val Gly Leu Ile Thr Ile Ser
        115                 120                 125

Arg Pro Pro Ile Thr Ala Leu Ala Thr Ile Ser Glu Asn Ser His Lys
    130                 135                 140

Ala Leu Leu Gly Leu Tyr Leu Ser Gly Leu Lys His Gly Met Met Ala
145                 150                 155                 160

Asn Ile Gly Glu His Asp Gly Lys Ser
                165
```

<210> 939
<211> 419
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (1)..(396)
<223> FRXA02014

<400> 939
atc tcc ctc caa ctc caa gcc atc agc acc ttc ccc acc gac cca gaa 48
Ile Ser Leu Gln Leu Gln Ala Ile Ser Thr Phe Pro Thr Asp Pro Glu
1 5 10 15

ggc gtg tgg acc tcc ttc aac caa cta ctt ttc gac cgc ggc cta ggc 96
Gly Val Trp Thr Ser Phe Asn Gln Leu Leu Phe Asp Arg Gly Leu Gly
20 25 30

tcc ctc gtc cca gca ctt gcc cca gaa tcc tta gac gac ctc ccc gac 144
Ser Leu Val Pro Ala Leu Ala Pro Glu Ser Leu Asp Asp Leu Pro Asp
35 40 45

gag gtc tcc gcc ctg cgt cgc acc aca gag aaa aac acc aca aca ctc 192
Glu Val Ser Ala Leu Arg Arg Thr Thr Glu Lys Asn Thr Thr Thr Leu
50 55 60

atc aac cta gcc aag cag cac gga ctc gta cac cac gac atc gcg ccg 240
Ile Asn Leu Ala Lys Gln His Gly Leu Val His His Asp Ile Ala Pro
65 70 75 80

ggc acc tac atc gtc ggt ttg atc acc att tcc cgc cca cct atc acc 288
Gly Thr Tyr Ile Val Gly Leu Ile Thr Ile Ser Arg Pro Pro Ile Thr
85 90 95

gcg ctg gcg aca att tca gaa aac tcc cac aaa gca ctg ctt ggc ctt 336
Ala Leu Ala Thr Ile Ser Glu Asn Ser His Lys Ala Leu Leu Gly Leu
100 105 110

tat ttg tcc ggt ctt aaa cac ggc atg atg gct aac atc gga gaa cat 384
Tyr Leu Ser Gly Leu Lys His Gly Met Met Ala Asn Ile Gly Glu His
115 120 125

gac gga aag tcc tgatctagca gtttcctttt tag 419
Asp Gly Lys Ser
130

<210> 940
<211> 132
<212> PRT
<213> Corynebacterium glutamicum

<400> 940
Ile Ser Leu Gln Leu Gln Ala Ile Ser Thr Phe Pro Thr Asp Pro Glu
1 5 10 15

Gly Val Trp Thr Ser Phe Asn Gln Leu Leu Phe Asp Arg Gly Leu Gly
20 25 30

Ser Leu Val Pro Ala Leu Ala Pro Glu Ser Leu Asp Asp Leu Pro Asp
35 40 45

Glu Val Ser Ala Leu Arg Arg Thr Thr Glu Lys Asn Thr Thr Thr Leu
50 55 60

Ile Asn Leu Ala Lys Gln His Gly Leu Val His His Asp Ile Ala Pro

```
 65                  70                  75                  80

Gly Thr Tyr Ile Val Gly Leu Ile Thr Ile Ser Arg Pro Pro Ile Thr
                85                  90                  95

Ala Leu Ala Thr Ile Ser Glu Asn Ser His Lys Ala Leu Leu Gly Leu
            100                 105                 110

Tyr Leu Ser Gly Leu Lys His Gly Met Met Ala Asn Ile Gly Glu His
        115                 120                 125

Asp Gly Lys Ser
    130
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<210> 941
<211> 524
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(501)
<223> RXN02019

<400> 941

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gaa att cct gct ggc acc aag gtt gag gcc tct gac ctt gga ctt cag   48
Glu Ile Pro Ala Gly Thr Lys Val Glu Ala Ser Asp Leu Gly Leu Gln
  1               5                  10                  15

gca atc cct act tcc cta ctg ccc agc acc tcc tac gat tcg att gac   96
Ala Ile Pro Thr Ser Leu Leu Pro Ser Thr Ser Tyr Asp Ser Ile Asp
             20                  25                  30

gat gta gtt ggg ctc gtt gcg gcc tcc aca tta agt tcc ggg gaa ata   144
Asp Val Val Gly Leu Val Ala Ala Ser Thr Leu Ser Ser Gly Glu Ile
         35                  40                  45

gcc aca aag cct cga ttc gtg ggc acc gaa ttg ata aac tcc att gcg   192
Ala Thr Lys Pro Arg Phe Val Gly Thr Glu Leu Ile Asn Ser Ile Ala
     50                  55                  60

aca aac gtc act gat agc tct ttg gtg gaa gaa att aac atg gtt cca   240
Thr Asn Val Thr Asp Ser Ser Leu Val Glu Glu Ile Asn Met Val Pro
 65                  70                  75                  80

ctc agt ttg gct gaa cct tcc gtc atc ccc cta ctg cag cat ggg gac   288
Leu Ser Leu Ala Glu Pro Ser Val Ile Pro Leu Leu Gln His Gly Asp
                85                  90                  95

acc att tcg gtt gtt tcc caa gac cca gac acc ggt ctc cca gag aac   336
Thr Ile Ser Val Val Ser Gln Asp Pro Asp Thr Gly Leu Pro Glu Asn
            100                 105                 110

att gct gca ggt gga aca gta att ctg gcg ggt ggt aca gac ccc tca   384
Ile Ala Ala Gly Gly Thr Val Ile Leu Ala Gly Gly Thr Asp Pro Ser
        115                 120                 125

acc atc ttg att gcg ctt cca caa tca atc gct gaa aag gtt gca gca   432
Thr Ile Leu Ile Ala Leu Pro Gln Ser Ile Ala Glu Lys Val Ala Ala
    130                 135                 140
```

caa tcg ctc aat acc cct ctg gcg gta gtc ctg acc gga gac aga gca 480
Gln Ser Leu Asn Thr Pro Leu Ala Val Val Leu Thr Gly Asp Arg Ala
145 150 155 160

gat aat tac aca acc gaa gaa tagttcccta ttcaaaaaaa agg 524
Asp Asn Tyr Thr Thr Glu Glu
165

<210> 942
<211> 167
<212> PRT
<213> Corynebacterium glutamicum

<400> 942
Glu Ile Pro Ala Gly Thr Lys Val Glu Ala Ser Asp Leu Gly Leu Gln
1 5 10 15

Ala Ile Pro Thr Ser Leu Leu Pro Ser Thr Ser Tyr Asp Ser Ile Asp
20 25 30

Asp Val Val Gly Leu Val Ala Ala Ser Thr Leu Ser Ser Gly Glu Ile
35 40 45

Ala Thr Lys Pro Arg Phe Val Gly Thr Glu Leu Ile Asn Ser Ile Ala
50 55 60

Thr Asn Val Thr Asp Ser Ser Leu Val Glu Glu Ile Asn Met Val Pro
65 70 75 80

Leu Ser Leu Ala Glu Pro Ser Val Ile Pro Leu Leu Gln His Gly Asp
85 90 95

Thr Ile Ser Val Val Ser Gln Asp Pro Asp Thr Gly Leu Pro Glu Asn
100 105 110

Ile Ala Ala Gly Gly Thr Val Ile Leu Ala Gly Gly Thr Asp Pro Ser
115 120 125

Thr Ile Leu Ile Ala Leu Pro Gln Ser Ile Ala Glu Lys Val Ala Ala
130 135 140

Gln Ser Leu Asn Thr Pro Leu Ala Val Val Leu Thr Gly Asp Arg Ala
145 150 155 160

Asp Asn Tyr Thr Thr Glu Glu
165

<210> 943
<211> 515
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(492)
<223> FRXA02019

<400> 943

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gct ggc acc aag gtt gag gcc tct gac ctt gga ctt cag gca atc cct   48
Ala Gly Thr Lys Val Glu Ala Ser Asp Leu Gly Leu Gln Ala Ile Pro
  1               5                  10                  15

act tcc cta ctg ccc agc acc tcc tac gat tcg att gac gat gta gtt   96
Thr Ser Leu Leu Pro Ser Thr Ser Tyr Asp Ser Ile Asp Asp Val Val
             20                  25                  30

ggg ctc gtt gcg gcc tcc aca tta agt tcc ggg gaa ata gcc aca aag   144
Gly Leu Val Ala Ala Ser Thr Leu Ser Ser Gly Glu Ile Ala Thr Lys
         35                  40                  45

cct cga ttc gtg ggc acc gaa ttg ata aac tcc att gcg aca aac gtc   192
Pro Arg Phe Val Gly Thr Glu Leu Ile Asn Ser Ile Ala Thr Asn Val
     50                  55                  60

act gat agc tct ttg gtg gaa gaa att aac atg gtt cca ctc agt ttg   240
Thr Asp Ser Ser Leu Val Glu Glu Ile Asn Met Val Pro Leu Ser Leu
 65                  70                  75                  80

gct gaa cct tcc gtc atc ccc cta ctg cag cat ggg gac acc att tcg   288
Ala Glu Pro Ser Val Ile Pro Leu Leu Gln His Gly Asp Thr Ile Ser
                 85                  90                  95

gtt gtt tcc caa gac cca gac acc ggt ctc cca gag aac att gct gca   336
Val Val Ser Gln Asp Pro Asp Thr Gly Leu Pro Glu Asn Ile Ala Ala
            100                 105                 110

ggt gga aca gta att ctg gcg ggt ggt aca gac ccc tca acc atc ttg   384
Gly Gly Thr Val Ile Leu Ala Gly Gly Thr Asp Pro Ser Thr Ile Leu
        115                 120                 125

att gcg ctt cca caa tca atc gct gaa aag gtt gca gca caa tcg ctc   432
Ile Ala Leu Pro Gln Ser Ile Ala Glu Lys Val Ala Ala Gln Ser Leu
    130                 135                 140

aat acc cct ctg gcg gta gtc ctg acc gga gac aga gca aat aat tac   480
Asn Thr Pro Leu Ala Val Val Leu Thr Gly Asp Arg Ala Asn Asn Tyr
145                 150                 155                 160

aca acc gaa gaa tagttcccta ttcaaaaaaa agg                        515
Thr Thr Glu Glu
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<210> 944
<211> 164
<212> PRT
<213> Corynebacterium glutamicum

<400> 944

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Ala Gly Thr Lys Val Glu Ala Ser Asp Leu Gly Leu Gln Ala Ile Pro
  1               5                  10                  15

Thr Ser Leu Leu Pro Ser Thr Ser Tyr Asp Ser Ile Asp Asp Val Val
             20                  25                  30

Gly Leu Val Ala Ala Ser Thr Leu Ser Ser Gly Glu Ile Ala Thr Lys
         35                  40                  45

Pro Arg Phe Val Gly Thr Glu Leu Ile Asn Ser Ile Ala Thr Asn Val
```

```
     50                  55                  60

Thr Asp Ser Ser Leu Val Glu Glu Ile Asn Met Val Pro Leu Ser Leu
 65                  70                  75                  80

Ala Glu Pro Ser Val Ile Pro Leu Leu Gln His Gly Asp Thr Ile Ser
                85                  90                  95

Val Val Ser Gln Asp Pro Asp Thr Gly Leu Pro Glu Asn Ile Ala Ala
            100                 105                 110

Gly Gly Thr Val Ile Leu Ala Gly Gly Thr Asp Pro Ser Thr Ile Leu
        115                 120                 125

Ile Ala Leu Pro Gln Ser Ile Ala Glu Lys Val Ala Ala Gln Ser Leu
    130                 135                 140

Asn Thr Pro Leu Ala Val Val Leu Thr Gly Asp Arg Ala Asn Asn Tyr
145                 150                 155                 160

Thr Thr Glu Glu
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CURRENT SEQUENCE LISTING

<210> 945
<211> 891
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(868)
<223> RXN02023

<400> 945

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gatgtggcag caattttgaa gcagtacctg agcgagtaac cgcattcggg gttatcgtgg 60

gacttccgaa atgtaactag agactagagg aggaaacacg atg gct cct aaa caa   115
                                            Met Ala Pro Lys Gln
                                              1               5

act ccc agc cca gag aag aat cga aac ctg gtg gga cca gtt ctg caa   163
Thr Pro Ser Pro Glu Lys Asn Arg Asn Leu Val Gly Pro Val Leu Gln
                10                  15                  20

cgt cgg cag aca gag ggt act ttt gat caa cgc ttg cta gaa atg cgc   211
Arg Arg Gln Thr Glu Gly Thr Phe Asp Gln Arg Leu Leu Glu Met Arg
            25                  30                  35

gct gat cac aat tgg aag cac gcc gat cca tgg cgt gta ctg cgt att   259
Ala Asp His Asn Trp Lys His Ala Asp Pro Trp Arg Val Leu Arg Ile
        40                  45                  50

cag tct gag ttt gtg gcg ggt ttt gat gcc ctc cac gag atg cca aag   307
Gln Ser Glu Phe Val Ala Gly Phe Asp Ala Leu His Glu Met Pro Lys
    55                  60                  65

gcc gta acc gtc ttt ggt tcc gca cgc att aaa gag gat cac ccg tac   355
Ala Val Thr Val Phe Gly Ser Ala Arg Ile Lys Glu Asp His Pro Tyr
 70                  75                  80                  85
```

```
tac aag gcg ggt gta gaa ctt ggt gaa aag ctc gtt gca gcg gac tac   403
Tyr Lys Ala Gly Val Glu Leu Gly Glu Lys Leu Val Ala Ala Asp Tyr
                 90                  95                 100

gca gtt gtc acc ggt ggc ggt cca ggt ctg atg gaa gcc ccc aat aag   451
Ala Val Val Thr Gly Gly Gly Pro Gly Leu Met Glu Ala Pro Asn Lys
            105                 110                 115

ggg gca agc gag gcc aat ggt tta tca gtt ggt ctg ggc att gag ttg   499
Gly Ala Ser Glu Ala Asn Gly Leu Ser Val Gly Leu Gly Ile Glu Leu
        120                 125                 130

cca cat gaa cag cat ctg aac cct tat gtg gat ttg ggt ctg aac ttc   547
Pro His Glu Gln His Leu Asn Pro Tyr Val Asp Leu Gly Leu Asn Phe
    135                 140                 145

cgg tac ttc ttc gca cgc aag acc atg ttc ctg aaa tac tcc cag gct   595
Arg Tyr Phe Phe Ala Arg Lys Thr Met Phe Leu Lys Tyr Ser Gln Ala
150                 155                 160                 165

ttt gtg tgt ctg cct ggt ggt ttc ggc acg ctc gat gag ctt ttc gag   643
Phe Val Cys Leu Pro Gly Gly Phe Gly Thr Leu Asp Glu Leu Phe Glu
                170                 175                 180

gtc ctc tgc atg gta caa acc ggc aag gta ccc aac ttt ccc atc gtg   691
Val Leu Cys Met Val Gln Thr Gly Lys Val Pro Asn Phe Pro Ile Val
            185                 190                 195

ctg atc ggc act gag ttc tgg gca ggt ttg gtg gat tgg atc cgt cac   739
Leu Ile Gly Thr Glu Phe Trp Ala Gly Leu Val Asp Trp Ile Arg His
        200                 205                 210

cgc ctg gta gag gaa ggc atg atc gat gag aag gat gtt gac cgg atg   787
Arg Leu Val Glu Glu Gly Met Ile Asp Glu Lys Asp Val Asp Arg Met
    215                 220                 225

ttg gtc act gat gac ctg gat cag gcc gtc aaa ttc atc gtc gat gca   835
Leu Val Thr Asp Asp Leu Asp Gln Ala Val Lys Phe Ile Val Asp Ala
230                 235                 240                 245

cac gct gga ttg gac gta gcg cgt ctc cac aat taagcagtgg ctacattagg 888
His Ala Gly Leu Asp Val Ala Arg Leu His Asn
                250                 255

tgt                                                               891


<210> 946
<211> 256
<212> PRT
<213> Corynebacterium glutamicum

<400> 946
Met Ala Pro Lys Gln Thr Pro Ser Pro Glu Lys Asn Arg Asn Leu Val
  1               5                  10                  15

Gly Pro Val Leu Gln Arg Arg Gln Thr Glu Gly Thr Phe Asp Gln Arg
             20                  25                  30

Leu Leu Glu Met Arg Ala Asp His Asn Trp Lys His Ala Asp Pro Trp
         35                  40                  45
```

```
Arg Val Leu Arg Ile Gln Ser Glu Phe Val Ala Gly Phe Asp Ala Leu
     50                  55                  60

His Glu Met Pro Lys Ala Val Thr Val Phe Gly Ser Ala Arg Ile Lys
 65                  70                  75                  80

Glu Asp His Pro Tyr Tyr Lys Ala Gly Val Glu Leu Gly Glu Lys Leu
                 85                  90                  95

Val Ala Ala Asp Tyr Ala Val Val Thr Gly Gly Gly Pro Gly Leu Met
            100                 105                 110

Glu Ala Pro Asn Lys Gly Ala Ser Glu Ala Asn Gly Leu Ser Val Gly
        115                 120                 125

Leu Gly Ile Glu Leu Pro His Glu Gln His Leu Asn Pro Tyr Val Asp
    130                 135                 140

Leu Gly Leu Asn Phe Arg Tyr Phe Phe Ala Arg Lys Thr Met Phe Leu
145                 150                 155                 160

Lys Tyr Ser Gln Ala Phe Val Cys Leu Pro Gly Gly Phe Gly Thr Leu
                165                 170                 175

Asp Glu Leu Phe Glu Val Leu Cys Met Val Gln Thr Gly Lys Val Pro
            180                 185                 190

Asn Phe Pro Ile Val Leu Ile Gly Thr Glu Phe Trp Ala Gly Leu Val
        195                 200                 205

Asp Trp Ile Arg His Arg Leu Val Glu Glu Gly Met Ile Asp Glu Lys
    210                 215                 220

Asp Val Asp Arg Met Leu Val Thr Asp Asp Leu Asp Gln Ala Val Lys
225                 230                 235                 240

Phe Ile Val Asp Ala His Ala Gly Leu Asp Val Ala Arg Leu His Asn
                245                 250                 255
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<210> 947
<211> 891
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(868)
<223> FRXA02023

<400> 947
gatgtggcag caattttgaa gcagtacctg agcgagtaac cgcattcggg gttatcgtgg 60

gacttccgaa atgtaactag agactagagg aggaaacacg atg gct cct aaa caa 115
                                                Met Ala Pro Lys Gln
                                                  1   5

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act ccc agc cca gag aag aat cga aac ctg gtg gga cca gtt ctg caa   163
Thr Pro Ser Pro Glu Lys Asn Arg Asn Leu Val Gly Pro Val Leu Gln
                 10                  15                  20

cgt cgg cag aca gag ggt act ttt gat caa cgc ttg cta gaa atg cgc   211
Arg Arg Gln Thr Glu Gly Thr Phe Asp Gln Arg Leu Leu Glu Met Arg
             25                  30                  35

gct gat cac aat tgg aag cac gcc gat cca tgg cgt gta ctg cgt att   259
Ala Asp His Asn Trp Lys His Ala Asp Pro Trp Arg Val Leu Arg Ile
         40                  45                  50

cag tct gag ttt gtg gcg ggt ttt gat gcc ctc cac gag atg cca aag   307
Gln Ser Glu Phe Val Ala Gly Phe Asp Ala Leu His Glu Met Pro Lys
     55                  60                  65

gcc gta acc gtc ttt ggt tcc gca cgc att aaa gag gat cac ccg tac   355
Ala Val Thr Val Phe Gly Ser Ala Arg Ile Lys Glu Asp His Pro Tyr
 70                  75                  80                  85

tac aag gcg ggt gta gaa ctt ggt gaa aag ctc gtt gct gct gac tac   403
Tyr Lys Ala Gly Val Glu Leu Gly Glu Lys Leu Val Ala Ala Asp Tyr
                 90                  95                 100

gca gtt gtc acc ggt ggc ggt cca ggt ctg atg gaa gcc ccc aat aag   451
Ala Val Val Thr Gly Gly Gly Pro Gly Leu Met Glu Ala Pro Asn Lys
            105                 110                 115

ggg gca agc gag gcc aat ggt tta tca gtt ggt ctg ggc att gag ttg   499
Gly Ala Ser Glu Ala Asn Gly Leu Ser Val Gly Leu Gly Ile Glu Leu
        120                 125                 130

cca cat gaa cag cac ctg aac cct tat gtg gat ttg ggt ctg aac ttc   547
Pro His Glu Gln His Leu Asn Pro Tyr Val Asp Leu Gly Leu Asn Phe
    135                 140                 145

cgg tac ttc ttc gca cgc aag acc atg ttc ctg aaa tac tcc cag gct   595
Arg Tyr Phe Phe Ala Arg Lys Thr Met Phe Leu Lys Tyr Ser Gln Ala
150                 155                 160                 165

ttt gtg tgt ctg cct ggc ggt ttc ggc acg ctc gat gag ctt ttc gag   643
Phe Val Cys Leu Pro Gly Gly Phe Gly Thr Leu Asp Glu Leu Phe Glu
                170                 175                 180

gtc ctc tgc atg gta caa acc ggc aag gta acc aac ttt ccc atc gtg   691
Val Leu Cys Met Val Gln Thr Gly Lys Val Thr Asn Phe Pro Ile Val
            185                 190                 195

ctg atc ggc act gag ttc tgg gca ggt ttg gtg gat tgg atc cgt cac   739
Leu Ile Gly Thr Glu Phe Trp Ala Gly Leu Val Asp Trp Ile Arg His
        200                 205                 210

cgc ctg gta gag gaa ggc atg atc gat gag aag gat gtt gac cgg atg   787
Arg Leu Val Glu Glu Gly Met Ile Asp Glu Lys Asp Val Asp Arg Met
    215                 220                 225

ttg gtc act gat gac ctg gat cag gcc gtc aaa ttc atc gtc gat gca   835
Leu Val Thr Asp Asp Leu Asp Gln Ala Val Lys Phe Ile Val Asp Ala
230                 235                 240                 245

cac gct gga ttg gac gta gcg cgt ctc cac aat taagcagtgg ctacattagg 888
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His Ala Gly Leu Asp Val Ala Arg Leu His Asn
                250                 255

tgt                                                                    891


<210> 948
<211> 256
<212> PRT
<213> Corynebacterium glutamicum

<400> 948
Met Ala Pro Lys Gln Thr Pro Ser Pro Glu Lys Asn Arg Asn Leu Val
  1               5                  10                  15

Gly Pro Val Leu Gln Arg Arg Gln Thr Glu Gly Thr Phe Asp Gln Arg
             20                  25                  30

Leu Leu Glu Met Arg Ala Asp His Asn Trp Lys His Ala Asp Pro Trp
         35                  40                  45

Arg Val Leu Arg Ile Gln Ser Glu Phe Val Ala Gly Phe Asp Ala Leu
     50                  55                  60

His Glu Met Pro Lys Ala Val Thr Val Phe Gly Ser Ala Arg Ile Lys
 65                  70                  75                  80

Glu Asp His Pro Tyr Tyr Lys Ala Gly Val Glu Leu Gly Glu Lys Leu
                 85                  90                  95

Val Ala Ala Asp Tyr Ala Val Val Thr Gly Gly Gly Pro Gly Leu Met
            100                 105                 110

Glu Ala Pro Asn Lys Gly Ala Ser Glu Ala Asn Gly Leu Ser Val Gly
        115                 120                 125

Leu Gly Ile Glu Leu Pro His Glu Gln His Leu Asn Pro Tyr Val Asp
    130                 135                 140

Leu Gly Leu Asn Phe Arg Tyr Phe Phe Ala Arg Lys Thr Met Phe Leu
145                 150                 155                 160

Lys Tyr Ser Gln Ala Phe Val Cys Leu Pro Gly Gly Phe Gly Thr Leu
                165                 170                 175

Asp Glu Leu Phe Glu Val Leu Cys Met Val Gln Thr Gly Lys Val Thr
            180                 185                 190

Asn Phe Pro Ile Val Leu Ile Gly Thr Glu Phe Trp Ala Gly Leu Val
        195                 200                 205

Asp Trp Ile Arg His Arg Leu Val Glu Glu Gly Met Ile Asp Glu Lys
    210                 215                 220

Asp Val Asp Arg Met Leu Val Thr Asp Asp Leu Asp Gln Ala Val Lys
225                 230                 235                 240

Phe Ile Val Asp Ala His Ala Gly Leu Asp Val Ala Arg Leu His Asn
                245                 250                 255
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<210> 949
<211> 693
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(670)
<223> RXN02032

<400> 949
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ggtctatttt ttatgcccag gcacggctca taggagaacc atg ccc ttt cta caa 115
Met Pro Phe Leu Gln
1 5

atc tct ctg ctt tcc atc ggt gtc gcc gcc gat gcg ttt gct tgt tcc 163
Ile Ser Leu Leu Ser Ile Gly Val Ala Ala Asp Ala Phe Ala Cys Ser
10 15 20

gtt gtc cgc ggc acc gcc att caa gtc aac ctt ttc aaa cgc gca ctt 211
Val Val Arg Gly Thr Ala Ile Gln Val Asn Leu Phe Lys Arg Ala Leu
25 30 35

gtt ctc gcg ggc atc ttt ggt gtc ttc caa gcg gca atg cct tta atc 259
Val Leu Ala Gly Ile Phe Gly Val Phe Gln Ala Ala Met Pro Leu Ile
40 45 50

ggc tgg ttc att ggc cgt ttc ttt gct gga atc acc ttc atc gct gaa 307
Gly Trp Phe Ile Gly Arg Phe Phe Ala Gly Ile Thr Phe Ile Ala Glu
55 60 65

att gat cac tgg atc gct ttt gca cta ttg ggt att gtc ggc acc aaa 355
Ile Asp His Trp Ile Ala Phe Ala Leu Leu Gly Ile Val Gly Thr Lys
70 75 80 85

atg atc tgg gat gcc ttc caa cct gaa gat gat gaa acc att gtc gat 403
Met Ile Trp Asp Ala Phe Gln Pro Glu Asp Asp Glu Thr Ile Val Asp
90 95 100

gac ggc cgc gtt caa ttt aga cca gca att atc ctg ggg cta gcc acc 451
Asp Gly Arg Val Gln Phe Arg Pro Ala Ile Ile Leu Gly Leu Ala Thr
105 110 115

agc att gac gca tta gcc gta ggc atg ggc ctg gca ttc gtg gaa gtt 499
Ser Ile Asp Ala Leu Ala Val Gly Met Gly Leu Ala Phe Val Glu Val
120 125 130

tcc atc ctc aaa gtg gca ctg tcc atg ggc agc atc acc ttc gca ctt 547
Ser Ile Leu Lys Val Ala Leu Ser Met Gly Ser Ile Thr Phe Ala Leu
135 140 145

tcg ctt gct ggc gcc tgg atc gga cac cat ggt gga gga aag ttt ggc 595
Ser Leu Ala Gly Ala Trp Ile Gly His His Gly Gly Gly Lys Phe Gly
150 155 160 165

aag tgg gct acg att ctt ggc gga ata atc ttg atc gga atc ggc gca 643

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Lys Trp Ala Thr Ile Leu Gly Gly Ile Ile Leu Ile Gly Ile Gly Ala
                170                 175                 180

aac atc gtc tac gaa cac ctc agc gcg taaccctcgg cgcattatcc         690
Asn Ile Val Tyr Glu His Leu Ser Ala
            185                 190

tca                                                               693


<210> 950
<211> 190
<212> PRT
<213> Corynebacterium glutamicum

<400> 950
Met Pro Phe Leu Gln Ile Ser Leu Leu Ser Ile Gly Val Ala Ala Asp
  1               5                  10                  15

Ala Phe Ala Cys Ser Val Val Arg Gly Thr Ala Ile Gln Val Asn Leu
             20                  25                  30

Phe Lys Arg Ala Leu Val Leu Ala Gly Ile Phe Gly Val Phe Gln Ala
         35                  40                  45

Ala Met Pro Leu Ile Gly Trp Phe Ile Gly Arg Phe Phe Ala Gly Ile
     50                  55                  60

Thr Phe Ile Ala Glu Ile Asp His Trp Ile Ala Phe Ala Leu Leu Gly
 65                  70                  75                  80

Ile Val Gly Thr Lys Met Ile Trp Asp Ala Phe Gln Pro Glu Asp Asp
                 85                  90                  95

Glu Thr Ile Val Asp Asp Gly Arg Val Gln Phe Arg Pro Ala Ile Ile
            100                 105                 110

Leu Gly Leu Ala Thr Ser Ile Asp Ala Leu Ala Val Gly Met Gly Leu
        115                 120                 125

Ala Phe Val Glu Val Ser Ile Leu Lys Val Ala Leu Ser Met Gly Ser
    130                 135                 140

Ile Thr Phe Ala Leu Ser Leu Ala Gly Ala Trp Ile Gly His His Gly
145                 150                 155                 160

Gly Gly Lys Phe Gly Lys Trp Ala Thr Ile Leu Gly Gly Ile Ile Leu
                165                 170                 175

Ile Gly Ile Gly Ala Asn Ile Val Tyr Glu His Leu Ser Ala
            180                 185                 190


<210> 951
<211> 693
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(670)
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<223> FRXA02032

<400> 951

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cttaaaaagg ggctttatcg gttcaggcga gcgagacctt cggcgttcac acttcgccgg 60

ggtctatttt ttatgcccag gcacggctca taggagaacc atg ccc ttt cta caa   115
                                            Met Pro Phe Leu Gln
                                              1               5

atc tct ctg ctt tcc atc ggt gtc gcc gcc gat gcg ttt gct tgt tcc   163
Ile Ser Leu Leu Ser Ile Gly Val Ala Ala Asp Ala Phe Ala Cys Ser
                 10                  15                  20

gtt gtc cgc ggc acc gcc att caa gtc aac ctt ttc aaa cgc gca ctt   211
Val Val Arg Gly Thr Ala Ile Gln Val Asn Leu Phe Lys Arg Ala Leu
             25                  30                  35

gtt ctc gcg ggc atc ttt ggt gtc ttc caa gcg gca atg cct tta atc   259
Val Leu Ala Gly Ile Phe Gly Val Phe Gln Ala Ala Met Pro Leu Ile
         40                  45                  50

ggc tgg ttc att ggc cgt ttc ttt gct gga atc acc ttc atc gct gaa   307
Gly Trp Phe Ile Gly Arg Phe Phe Ala Gly Ile Thr Phe Ile Ala Glu
     55                  60                  65

att gat cac tgg atc gct ttt gca cta ttg ggt att gtc ggc acc aaa   355
Ile Asp His Trp Ile Ala Phe Ala Leu Leu Gly Ile Val Gly Thr Lys
 70                  75                  80                  85

atg atc tgg gat gcc ttc caa cct gaa gat gat gaa acc att gtc gat   403
Met Ile Trp Asp Ala Phe Gln Pro Glu Asp Asp Glu Thr Ile Val Asp
                 90                  95                 100

gac ggc cgc gtt caa ttt aga cca gca att atc ctg ggg cta gcc acc   451
Asp Gly Arg Val Gln Phe Arg Pro Ala Ile Ile Leu Gly Leu Ala Thr
            105                 110                 115

agc att gac gca tta gcc gta ggc atg ggc ctg gca ttc gtg gaa gtt   499
Ser Ile Asp Ala Leu Ala Val Gly Met Gly Leu Ala Phe Val Glu Val
        120                 125                 130

tcc atc ctc aaa gtg gca ctg tcc atg ggc agc atc acc ttc gca ctt   547
Ser Ile Leu Lys Val Ala Leu Ser Met Gly Ser Ile Thr Phe Ala Leu
    135                 140                 145

tcg ctt gct ggc gcc tgg atc gga cac cat ggt gga gga aag ttt ggc   595
Ser Leu Ala Gly Ala Trp Ile Gly His His Gly Gly Gly Lys Phe Gly
150                 155                 160                 165

aag tgg gct acg att ctt ggc gga ata atc ttg atc gga atc ggc gca   643
Lys Trp Ala Thr Ile Leu Gly Gly Ile Ile Leu Ile Gly Ile Gly Ala
                170                 175                 180

aac atc gtc tac gaa cac ctc agc gcg taaccctcgg cgcattatcc         690
Asn Ile Val Tyr Glu His Leu Ser Ala
            185                 190

tca                                                              693
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<210> 952

<211> 190
<212> PRT
<213> Corynebacterium glutamicum

<400> 952

Met	Pro	Phe	Leu	Gln	Ile	Ser	Leu	Leu	Ser	Ile	Gly	Val	Ala	Ala	Asp				
1				5					10						15				
Ala	Phe	Ala	Cys	Ser	Val	Val	Arg	Gly	Thr	Ala	Ile	Gln	Val	Asn	Leu				
			20					25						30					
Phe	Lys	Arg	Ala	Leu	Val	Leu	Ala	Gly	Ile	Phe	Gly	Val	Phe	Gln	Ala				
		35					40						45						
Ala	Met	Pro	Leu	Ile	Gly	Trp	Phe	Ile	Gly	Arg	Phe	Phe	Ala	Gly	Ile				
	50					55					60								
Thr	Phe	Ile	Ala	Glu	Ile	Asp	His	Trp	Ile	Ala	Phe	Ala	Leu	Leu	Gly				
65					70					75					80				
Ile	Val	Gly	Thr	Lys	Met	Ile	Trp	Asp	Ala	Phe	Gln	Pro	Glu	Asp	Asp				
				85					90						95				
Glu	Thr	Ile	Val	Asp	Asp	Gly	Arg	Val	Gln	Phe	Arg	Pro	Ala	Ile	Ile				
			100					105					110						
Leu	Gly	Leu	Ala	Thr	Ser	Ile	Asp	Ala	Leu	Ala	Val	Gly	Met	Gly	Leu				
		115					120					125							
Ala	Phe	Val	Glu	Val	Ser	Ile	Leu	Lys	Val	Ala	Leu	Ser	Met	Gly	Ser				
	130					135					140								
Ile	Thr	Phe	Ala	Leu	Ser	Leu	Ala	Gly	Ala	Trp	Ile	Gly	His	His	Gly				
145					150					155					160				
Gly	Gly	Lys	Phe	Gly	Lys	Trp	Ala	Thr	Ile	Leu	Gly	Gly	Ile	Ile	Leu				
				165					170					175					
Ile	Gly	Ile	Gly	Ala	Asn	Ile	Val	Tyr	Glu	His	Leu	Ser	Ala						
			180					185					190						

<210> 953
<211> 863
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(840)
<223> RXN02039

<400> 953

aag	gcg	tcg	ata	agc	aat	tta	agc	ttt	tgg	acg	tcc	acc	tcc	acc	acc				48
Lys	Ala	Ser	Ile	Ser	Asn	Leu	Ser	Phe	Trp	Thr	Ser	Thr	Ser	Thr	Thr				
1				5					10						15				
gca	ccc	ctt	tgg	ctc	gtg	ggc	acg	ctt	gtg	tgg	ctg	gcg	gtg	cag	gcg				96
Ala	Pro	Leu	Trp	Leu	Val	Gly	Thr	Leu	Val	Trp	Leu	Ala	Val	Gln	Ala				
			20					25						30					

```
gtg atg cat gac ggc gag ctt tac cat gtg gaa gtt ccc acg att gcg   144
Val Met His Asp Gly Glu Leu Tyr His Val Glu Val Pro Thr Ile Ala
         35                  40                  45

ctg gtc atc ggc ttt ggc gcg cag ctt ctg atc ggt gtg atg agt tat   192
Leu Val Ile Gly Phe Gly Ala Gln Leu Leu Ile Gly Val Met Ser Tyr
     50                  55                  60

cta ctg ccg tcg acg atg ggt ggc ggc gcg agc gcg gtg cgg act gga   240
Leu Leu Pro Ser Thr Met Gly Gly Gly Ala Ser Ala Val Arg Thr Gly
 65                  70                  75                  80

acg cac att tta aac act gcg ggg ctg ttt agg tgg acg ctg atc aac   288
Thr His Ile Leu Asn Thr Ala Gly Leu Phe Arg Trp Thr Leu Ile Asn
                 85                  90                  95

ggt ggc ctg gcg att tgg ctg ctc acc gac aat tcg tgg ctg cgc gtc   336
Gly Gly Leu Ala Ile Trp Leu Leu Thr Asp Asn Ser Trp Leu Arg Val
            100                 105                 110

gtg gtg tct ctg ctg agt atc gga gcg ttg gca gtt ttt gtc att ctg   384
Val Val Ser Leu Leu Ser Ile Gly Ala Leu Ala Val Phe Val Ile Leu
        115                 120                 125

ctg ccc aag gct gtg cgg gcg cag cgc gga gtg atc acc aaa aag cgc   432
Leu Pro Lys Ala Val Arg Ala Gln Arg Gly Val Ile Thr Lys Lys Arg
    130                 135                 140

gaa cca att act ccg ccg gag gag cct cga ctc aat caa att acc gcg   480
Glu Pro Ile Thr Pro Pro Glu Glu Pro Arg Leu Asn Gln Ile Thr Ala
145                 150                 155                 160

gga atc tct gtg ctt gcc ctg att ttg gca gca ttc ggt ggg ctc aac   528
Gly Ile Ser Val Leu Ala Leu Ile Leu Ala Ala Phe Gly Gly Leu Asn
                165                 170                 175

ccc ggt gtt gcg ccg gtg gca agc tca aat gaa gac gtc tat gct gtg   576
Pro Gly Val Ala Pro Val Ala Ser Ser Asn Glu Asp Val Tyr Ala Val
            180                 185                 190

acc att acc gca ggt gac atg gtg ttt atc cct gat gtg att gaa gtg   624
Thr Ile Thr Ala Gly Asp Met Val Phe Ile Pro Asp Val Ile Glu Val
        195                 200                 205

cct gct ggt aaa tca ctc gaa gtc acg atg ctc aac gaa gac gac atg   672
Pro Ala Gly Lys Ser Leu Glu Val Thr Met Leu Asn Glu Asp Asp Met
    210                 215                 220

gtg cac gat ctg aaa ttt gcc aac ggt gtg caa acc gga cgt gtg gcg   720
Val His Asp Leu Lys Phe Ala Asn Gly Val Gln Thr Gly Arg Val Ala
225                 230                 235                 240

cca ggt gat gaa att acg gtg acc gtc ggc gat att tcc gaa gac atg   768
Pro Gly Asp Glu Ile Thr Val Thr Val Gly Asp Ile Ser Glu Asp Met
                245                 250                 255

gac ggc tgg tgc acc atc gct ggg cac cgc gcg caa gga atg gat ctg   816
Asp Gly Trp Cys Thr Ile Ala Gly His Arg Ala Gln Gly Met Asp Leu
            260                 265                 270

gaa gta aag gtt gcg gct ccg aat taaccaaggg ctgctgaaaa act         863
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Glu Val Lys Val Ala Ala Pro Asn
        275                 280


<210> 954
<211> 280
<212> PRT
<213> Corynebacterium glutamicum

<400> 954
Lys Ala Ser Ile Ser Asn Leu Ser Phe Trp Thr Ser Thr Ser Thr Thr
  1               5                  10                  15

Ala Pro Leu Trp Leu Val Gly Thr Leu Val Trp Leu Ala Val Gln Ala
             20                  25                  30

Val Met His Asp Gly Glu Leu Tyr His Val Glu Val Pro Thr Ile Ala
         35                  40                  45

Leu Val Ile Gly Phe Gly Ala Gln Leu Leu Ile Gly Val Met Ser Tyr
     50                  55                  60

Leu Leu Pro Ser Thr Met Gly Gly Gly Ala Ser Ala Val Arg Thr Gly
 65                  70                  75                  80

Thr His Ile Leu Asn Thr Ala Gly Leu Phe Arg Trp Thr Leu Ile Asn
                 85                  90                  95

Gly Gly Leu Ala Ile Trp Leu Leu Thr Asp Asn Ser Trp Leu Arg Val
            100                 105                 110

Val Val Ser Leu Leu Ser Ile Gly Ala Leu Ala Val Phe Val Ile Leu
        115                 120                 125

Leu Pro Lys Ala Val Arg Ala Gln Arg Gly Val Ile Thr Lys Lys Arg
    130                 135                 140

Glu Pro Ile Thr Pro Pro Glu Glu Pro Arg Leu Asn Gln Ile Thr Ala
145                 150                 155                 160

Gly Ile Ser Val Leu Ala Leu Ile Leu Ala Ala Phe Gly Gly Leu Asn
                165                 170                 175

Pro Gly Val Ala Pro Val Ala Ser Ser Asn Glu Asp Val Tyr Ala Val
            180                 185                 190

Thr Ile Thr Ala Gly Asp Met Val Phe Ile Pro Asp Val Ile Glu Val
        195                 200                 205

Pro Ala Gly Lys Ser Leu Glu Val Thr Met Leu Asn Glu Asp Asp Met
    210                 215                 220

Val His Asp Leu Lys Phe Ala Asn Gly Val Gln Thr Gly Arg Val Ala
225                 230                 235                 240

Pro Gly Asp Glu Ile Thr Val Thr Val Gly Asp Ile Ser Glu Asp Met
                245                 250                 255

Asp Gly Trp Cys Thr Ile Ala Gly His Arg Ala Gln Gly Met Asp Leu
            260                 265                 270
```

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Glu Val Lys Val Ala Ala Pro Asn
        275                 280


<210> 955
<211> 833
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(810)
<223> FRXA02039

<400> 955
acg tcc acc tcc acc acc gca ccc ctt tgg ctc gtg ggc acg ctt gtg   48
Thr Ser Thr Ser Thr Thr Ala Pro Leu Trp Leu Val Gly Thr Leu Val
  1               5                  10                  15

tgg ctg gcg gtg cag gcg gtg atg cat gac ggc gag ctt tac cat gtg   96
Trp Leu Ala Val Gln Ala Val Met His Asp Gly Glu Leu Tyr His Val
             20                  25                  30

gaa gtt ccc acg att gcg ctg gtc atc ggc ttt ggc gcg cag ctt ctg   144
Glu Val Pro Thr Ile Ala Leu Val Ile Gly Phe Gly Ala Gln Leu Leu
         35                  40                  45

atc ggt gtg atg agt tat cta ctg ccg tcg acg atg ggt ggc ggc gcg   192
Ile Gly Val Met Ser Tyr Leu Leu Pro Ser Thr Met Gly Gly Gly Ala
     50                  55                  60

agc gcg gtg cgg act gga acg cac att tta aac act gcg ggg ctg ttt   240
Ser Ala Val Arg Thr Gly Thr His Ile Leu Asn Thr Ala Gly Leu Phe
 65                  70                  75                  80

agg tgg acg ctg atc aac ggt ggc ctg gcg att tgg ctg ctc acc gac   288
Arg Trp Thr Leu Ile Asn Gly Gly Leu Ala Ile Trp Leu Leu Thr Asp
                 85                  90                  95

aat tcg tgg ctg cgc gtc gtg gtg tct ctg ctg agt atc gga gcg ttg   336
Asn Ser Trp Leu Arg Val Val Val Ser Leu Leu Ser Ile Gly Ala Leu
            100                 105                 110

gca gtt ttt gtc att ctg ctg ccc aag gct gtg cgg gcg cag cgc gga   384
Ala Val Phe Val Ile Leu Leu Pro Lys Ala Val Arg Ala Gln Arg Gly
        115                 120                 125

gtg atc acc aaa aag cgc gaa cca att act ccg ccg gag gag cct cga   432
Val Ile Thr Lys Lys Arg Glu Pro Ile Thr Pro Pro Glu Glu Pro Arg
    130                 135                 140

ctc aat caa att acc gcg gga atc tct gtg ctt gcc ctg att ttg gca   480
Leu Asn Gln Ile Thr Ala Gly Ile Ser Val Leu Ala Leu Ile Leu Ala
145                 150                 155                 160

gca ttc ggt ggg ctc aac ccc ggt gtt gcg ccg gtg gca agc tca aat   528
Ala Phe Gly Gly Leu Asn Pro Gly Val Ala Pro Val Ala Ser Ser Asn
                165                 170                 175

gaa gac gtc tat gct gtg acc att acc gca ggt gac atg gtg ttt atc   576
Glu Asp Val Tyr Ala Val Thr Ile Thr Ala Gly Asp Met Val Phe Ile
```

```
            180                 185                 190

cct gat gtg att gaa gtg cct gct ggt aaa tca ctc gaa gtc acg atg   624
Pro Asp Val Ile Glu Val Pro Ala Gly Lys Ser Leu Glu Val Thr Met
        195                 200                 205

ctc aac gaa gac gac atg gtg cac gat ctg aaa ttt gcc aac ggt gtg   672
Leu Asn Glu Asp Asp Met Val His Asp Leu Lys Phe Ala Asn Gly Val
    210                 215                 220

caa acc gga cgt gtg gcg cca ggt gat gaa att acg gtg acc gtc ggc   720
Gln Thr Gly Arg Val Ala Pro Gly Asp Glu Ile Thr Val Thr Val Gly
225                 230                 235                 240

gat att tcc gaa gac atg gac ggc tgg tgc acc atc gct ggg cac cgc   768
Asp Ile Ser Glu Asp Met Asp Gly Trp Cys Thr Ile Ala Gly His Arg
                245                 250                 255

gcg caa gga atg gat ctg gaa gta aag gtt gcg gct ccg aat           810
Ala Gln Gly Met Asp Leu Glu Val Lys Val Ala Ala Pro Asn
            260                 265                 270

taaccaaggg ctgctgaaaa act                                        833


<210> 956
<211> 270
<212> PRT
<213> Corynebacterium glutamicum

<400> 956
Thr Ser Thr Ser Thr Thr Ala Pro Leu Trp Leu Val Gly Thr Leu Val
  1               5                  10                  15

Trp Leu Ala Val Gln Ala Val Met His Asp Gly Glu Leu Tyr His Val
             20                  25                  30

Glu Val Pro Thr Ile Ala Leu Val Ile Gly Phe Gly Ala Gln Leu Leu
         35                  40                  45

Ile Gly Val Met Ser Tyr Leu Leu Pro Ser Thr Met Gly Gly Gly Ala
     50                  55                  60

Ser Ala Val Arg Thr Gly Thr His Ile Leu Asn Thr Ala Gly Leu Phe
 65                  70                  75                  80

Arg Trp Thr Leu Ile Asn Gly Gly Leu Ala Ile Trp Leu Leu Thr Asp
                 85                  90                  95

Asn Ser Trp Leu Arg Val Val Val Ser Leu Leu Ser Ile Gly Ala Leu
            100                 105                 110

Ala Val Phe Val Ile Leu Leu Pro Lys Ala Val Arg Ala Gln Arg Gly
        115                 120                 125

Val Ile Thr Lys Lys Arg Glu Pro Ile Thr Pro Pro Glu Glu Pro Arg
    130                 135                 140

Leu Asn Gln Ile Thr Ala Gly Ile Ser Val Leu Ala Leu Ile Leu Ala
145                 150                 155                 160
```

```
Ala Phe Gly Gly Leu Asn Pro Gly Val Ala Pro Val Ala Ser Ser Asn
                165                 170                 175

Glu Asp Val Tyr Ala Val Thr Ile Thr Ala Gly Asp Met Val Phe Ile
            180                 185                 190

Pro Asp Val Ile Glu Val Pro Ala Gly Lys Ser Leu Glu Val Thr Met
        195                 200                 205

Leu Asn Glu Asp Asp Met Val His Asp Leu Lys Phe Ala Asn Gly Val
    210                 215                 220

Gln Thr Gly Arg Val Ala Pro Gly Asp Glu Ile Thr Val Thr Val Gly
225                 230                 235                 240

Asp Ile Ser Glu Asp Met Asp Gly Trp Cys Thr Ile Ala Gly His Arg
                245                 250                 255

Ala Gln Gly Met Asp Leu Glu Val Lys Val Ala Ala Pro Asn
            260                 265                 270


<210> 957
<211> 1506
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1483)
<223> RXN02044

<400> 957
ttactttctt aagtaattta acgaatttgg tctcgaaact gacctaaaac cccatgttgc 60

tagttggtgc aaaccaataa tagctatagc cccaatacaa atg gtc acc cca atc   115
                                              Met Val Thr Pro Ile
                                                1               5

atg ggg aat tcg aac tct atc ctg ggc att tac cgt cag aaa atc caa   163
Met Gly Asn Ser Asn Ser Ile Leu Gly Ile Tyr Arg Gln Lys Ile Gln
                10                  15                  20

aat cga cat ttg gtt tct acg ctt ttt agg gca tac ttc cca atc gtg   211
Asn Arg His Leu Val Ser Thr Leu Phe Arg Ala Tyr Phe Pro Ile Val
            25                  30                  35

acc gag ctg att att tta ttg att gtt atc gtg acg gcg ctc gcc ttc   259
Thr Glu Leu Ile Ile Leu Leu Ile Val Ile Val Thr Ala Leu Ala Phe
        40                  45                  50

gat ttc aca aac gga ttc cac gac acc ggc aat gcg atg gcc aca tcc   307
Asp Phe Thr Asn Gly Phe His Asp Thr Gly Asn Ala Met Ala Thr Ser
    55                  60                  65

att gcc aca ggc gct cta aaa cct aaa gtc gcc gtg gca cta tcc gcc   355
Ile Ala Thr Gly Ala Leu Lys Pro Lys Val Ala Val Ala Leu Ser Ala
70                  75                  80                  85

tca ctg aac ctt gtt ggc gca ttc ctc tct gta gaa gtt gcg aca act   403
Ser Leu Asn Leu Val Gly Ala Phe Leu Ser Val Glu Val Ala Thr Thr
```

```
                    90                  95                 100

gtt gcc aaa ggc gtt gtt gac ctc gac caa ttc gac cta agc aat gcc   451
Val Ala Lys Gly Val Val Asp Leu Asp Gln Phe Asp Leu Ser Asn Ala
            105                 110                 115

tgg gat tcc cac cag ctc ctg ctt gtc gtc ttc gcc ggc ctc att ggc   499
Trp Asp Ser His Gln Leu Leu Leu Val Val Phe Ala Gly Leu Ile Gly
        120                 125                 130

gcc atc gtc tgg aac ctt ctg acc tgg ctg cta ggc att cct tcc agc   547
Ala Ile Val Trp Asn Leu Leu Thr Trp Leu Leu Gly Ile Pro Ser Ser
    135                 140                 145

tcc tct cac gca ctt ttc ggt ggc ctc att ggc gcc gca att gct tca   595
Ser Ser His Ala Leu Phe Gly Gly Leu Ile Gly Ala Ala Ile Ala Ser
150                 155                 160                 165

ctc ggt ttc ggc gga gtg gtg tgg gaa ggt gtc ttg tcc aag atg atc   643
Leu Gly Phe Gly Gly Val Val Trp Glu Gly Val Leu Ser Lys Met Ile
                170                 175                 180

atc cca gca ttg gct gca cca gtt gtt gca ggt ctc gtg gcc gcc atc   691
Ile Pro Ala Leu Ala Ala Pro Val Val Ala Gly Leu Val Ala Ala Ile
            185                 190                 195

ggc act ttc gcc gtg tac agc atc aca aag gca gtt gga gac aac gag   739
Gly Thr Phe Ala Val Tyr Ser Ile Thr Lys Ala Val Gly Asp Asn Glu
        200                 205                 210

aag aac cgt tac ttc cgc tgg ggt cag atc ggc tcc gct tcc ttg gtt   787
Lys Asn Arg Tyr Phe Arg Trp Gly Gln Ile Gly Ser Ala Ser Leu Val
    215                 220                 225

tcc ctg gca cac ggc acc aac gat gcc cag aag acc atg ggc gtt atc   835
Ser Leu Ala His Gly Thr Asn Asp Ala Gln Lys Thr Met Gly Val Ile
230                 235                 240                 245

ttc ctt tcc ctg gtt gcc acc ggt cac ctg gga act gac gct gac atc   883
Phe Leu Ser Leu Val Ala Thr Gly His Leu Gly Thr Asp Ala Asp Ile
                250                 255                 260

cca ttc tgg gtc aag gct aca tgt gca ttg gca atc gca atc ggt acc   931
Pro Phe Trp Val Lys Ala Thr Cys Ala Leu Ala Ile Ala Ile Gly Thr
            265                 270                 275

tac ttg ggt ggt tgg cgc gtt atc cgc aca ctg ggc aaa ggc ttg gtt   979
Tyr Leu Gly Gly Trp Arg Val Ile Arg Thr Leu Gly Lys Gly Leu Val
        280                 285                 290

gag att gat tcc cct cag ggc atg gca gca gaa act tct tct gca gca   1027
Glu Ile Asp Ser Pro Gln Gly Met Ala Ala Glu Thr Ser Ser Ala Ala
    295                 300                 305

atc att ttg act tct tcc cac ttc ggt atg gca ctg tcc acc act cac   1075
Ile Ile Leu Thr Ser Ser His Phe Gly Met Ala Leu Ser Thr Thr His
310                 315                 320                 325

gtt gct act ggc tcc atc atg ggt acc ggc att gga cgt aaa ggg gcg   1123
Val Ala Thr Gly Ser Ile Met Gly Thr Gly Ile Gly Arg Lys Gly Ala
                330                 335                 340
```

```
aag gtt cgt tgg tcc gtc gca gga cgc atg gca atg gcc tgg gtt atc   1171
Lys Val Arg Trp Ser Val Ala Gly Arg Met Ala Met Ala Trp Val Ile
            345                 350                 355

acc ctc cct gcc tcc gcg atc gtt ggc gtt ttc tgc tgg tgg gta gct   1219
Thr Leu Pro Ala Ser Ala Ile Val Gly Val Phe Cys Trp Trp Val Ala
        360                 365                 370

cac gga att ggt ctt atc agc tca gac ctc ctc gga gtc ctc gtt gca   1267
His Gly Ile Gly Leu Ile Ser Ser Asp Leu Leu Gly Val Leu Val Ala
    375                 380                 385

ttc gcc att ctg gtc att ctg tct ggc tac att tac gcc cgt tcc cgt   1315
Phe Ala Ile Leu Val Ile Leu Ser Gly Tyr Ile Tyr Ala Arg Ser Arg
390                 395                 400                 405

cgc gtg cct gtt gat cca agc aac gtc aac gct gac tgg aat gaa gaa   1363
Arg Val Pro Val Asp Pro Ser Asn Val Asn Ala Asp Trp Asn Glu Glu
                410                 415                 420

tca aac agc gtg gaa cct gca aca cct tcc gcc ccg gct gct tct gag   1411
Ser Asn Ser Val Glu Pro Ala Thr Pro Ser Ala Pro Ala Ala Ser Glu
            425                 430                 435

att aca gaa gct cct gcc gct cca gcc gct caa gcc gtt caa gat ctc   1459
Ile Thr Glu Ala Pro Ala Ala Pro Ala Ala Gln Ala Val Gln Asp Leu
        440                 445                 450

aac aac gag aat gag gta acc aag taatgaactt cgctactatt ttc         1506
Asn Asn Glu Asn Glu Val Thr Lys
    455                 460
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<210> 958
<211> 461
<212> PRT
<213> Corynebacterium glutamicum

<400> 958

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Met Val Thr Pro Ile Met Gly Asn Ser Asn Ser Ile Leu Gly Ile Tyr
  1               5                  10                  15

Arg Gln Lys Ile Gln Asn Arg His Leu Val Ser Thr Leu Phe Arg Ala
             20                  25                  30

Tyr Phe Pro Ile Val Thr Glu Leu Ile Ile Leu Leu Ile Val Ile Val
         35                  40                  45

Thr Ala Leu Ala Phe Asp Phe Thr Asn Gly Phe His Asp Thr Gly Asn
     50                  55                  60

Ala Met Ala Thr Ser Ile Ala Thr Gly Ala Leu Lys Pro Lys Val Ala
 65                  70                  75                  80

Val Ala Leu Ser Ala Ser Leu Asn Leu Val Gly Ala Phe Leu Ser Val
                 85                  90                  95

Glu Val Ala Thr Thr Val Ala Lys Gly Val Val Asp Leu Asp Gln Phe
            100                 105                 110
```

```
Asp Leu Ser Asn Ala Trp Asp Ser His Gln Leu Leu Leu Val Val Phe
        115                 120                 125

Ala Gly Leu Ile Gly Ala Ile Val Trp Asn Leu Leu Thr Trp Leu Leu
    130                 135                 140

Gly Ile Pro Ser Ser Ser Ser His Ala Leu Phe Gly Gly Leu Ile Gly
145                 150                 155                 160

Ala Ala Ile Ala Ser Leu Gly Phe Gly Gly Val Val Trp Glu Gly Val
                165                 170                 175

Leu Ser Lys Met Ile Ile Pro Ala Leu Ala Ala Pro Val Val Ala Gly
            180                 185                 190

Leu Val Ala Ala Ile Gly Thr Phe Ala Val Tyr Ser Ile Thr Lys Ala
        195                 200                 205

Val Gly Asp Asn Glu Lys Asn Arg Tyr Phe Arg Trp Gly Gln Ile Gly
    210                 215                 220

Ser Ala Ser Leu Val Ser Leu Ala His Gly Thr Asn Asp Ala Gln Lys
225                 230                 235                 240

Thr Met Gly Val Ile Phe Leu Ser Leu Val Ala Thr Gly His Leu Gly
                245                 250                 255

Thr Asp Ala Asp Ile Pro Phe Trp Val Lys Ala Thr Cys Ala Leu Ala
            260                 265                 270

Ile Ala Ile Gly Thr Tyr Leu Gly Gly Trp Arg Val Ile Arg Thr Leu
        275                 280                 285

Gly Lys Gly Leu Val Glu Ile Asp Ser Pro Gln Gly Met Ala Ala Glu
    290                 295                 300

Thr Ser Ser Ala Ala Ile Ile Leu Thr Ser Ser His Phe Gly Met Ala
305                 310                 315                 320

Leu Ser Thr Thr His Val Ala Thr Gly Ser Ile Met Gly Thr Gly Ile
                325                 330                 335

Gly Arg Lys Gly Ala Lys Val Arg Trp Ser Val Ala Gly Arg Met Ala
            340                 345                 350

Met Ala Trp Val Ile Thr Leu Pro Ala Ser Ala Ile Val Gly Val Phe
        355                 360                 365

Cys Trp Trp Val Ala His Gly Ile Gly Leu Ile Ser Ser Asp Leu Leu
    370                 375                 380

Gly Val Leu Val Ala Phe Ala Ile Leu Val Ile Leu Ser Gly Tyr Ile
385                 390                 395                 400

Tyr Ala Arg Ser Arg Arg Val Pro Val Asp Pro Ser Asn Val Asn Ala
                405                 410                 415

Asp Trp Asn Glu Glu Ser Asn Ser Val Glu Pro Ala Thr Pro Ser Ala
            420                 425                 430

Pro Ala Ala Ser Glu Ile Thr Glu Ala Pro Ala Ala Pro Ala Ala Gln
```

```
        435                 440                 445

Ala Val Gln Asp Leu Asn Asn Glu Asn Glu Val Thr Lys
    450                 455                 460


<210> 959
<211> 384
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(361)
<223> RXN02045

<400> 959
caccttccgc cccggctgct tctgagatta cagaagctcc tgccgctcca gccgctcaag 60

ccgttcaaga tctcaacaac gagaatgagg taaccaagta atg aac ttc gct act   115
                                              Met Asn Phe Ala Thr
                                                1               5

att ttc gga agc atc ttt gag gtc acc ctc gtg ggc att ttg ctc ggc   163
Ile Phe Gly Ser Ile Phe Glu Val Thr Leu Val Gly Ile Leu Leu Gly
                10                  15                  20

gca ggc ctt cca gcc ctt ttt gca tta gga atc cgc ttt gct cac agc   211
Ala Gly Leu Pro Ala Leu Phe Ala Leu Gly Ile Arg Phe Ala His Ser
            25                  30                  35

cct tct tcc aac ggc acc aac gct ctt gga aaa att gct tca acc atc   259
Pro Ser Ser Asn Gly Thr Asn Ala Leu Gly Lys Ile Ala Ser Thr Ile
        40                  45                  50

tgc ttt gcc atc att gcg gtt gct atc atc gct ggc att ctc tgg gtc   307
Cys Phe Ala Ile Ile Ala Val Ala Ile Ile Ala Gly Ile Leu Trp Val
    55                  60                  65

acc aaa gca acg atc tac cag tac tct ggt ttc gac att ttc ggc act   355
Thr Lys Ala Thr Ile Tyr Gln Tyr Ser Gly Phe Asp Ile Phe Gly Thr
70                  75                  80                  85

gaa ggc taaaagcacc agctgcgaat aac                                 384
Glu Gly


<210> 960
<211> 87
<212> PRT
<213> Corynebacterium glutamicum

<400> 960
Met Asn Phe Ala Thr Ile Phe Gly Ser Ile Phe Glu Val Thr Leu Val
  1               5                  10                  15

Gly Ile Leu Leu Gly Ala Gly Leu Pro Ala Leu Phe Ala Leu Gly Ile
            20                  25                  30

Arg Phe Ala His Ser Pro Ser Ser Asn Gly Thr Asn Ala Leu Gly Lys
```

```
         35                  40                  45

Ile Ala Ser Thr Ile Cys Phe Ala Ile Ile Ala Val Ala Ile Ile Ala
     50                  55                  60

Gly Ile Leu Trp Val Thr Lys Ala Thr Ile Tyr Gln Tyr Ser Gly Phe
 65                  70                  75                  80

Asp Ile Phe Gly Thr Glu Gly
                 85


<210> 961
<211> 384
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(361)
<223> FRXA02045

<400> 961
caccttccgc cccggctgct tctgagatta cagaagctcc tgccgctcca gccgctcaag 60

ccgttcaaga tctcaacaac gagaatgagg taaccaagta atg aac ttc gct act   115
                                            Met Asn Phe Ala Thr
                                              1               5

att ttc gga agc atc ttt gag gtc acc ctc gtg ggc att ttg ctc ggc   163
Ile Phe Gly Ser Ile Phe Glu Val Thr Leu Val Gly Ile Leu Leu Gly
                10                  15                  20

gca ggc ctt cca gcc ctt ttt gca tta gga atc cgc ttt gct cac agc   211
Ala Gly Leu Pro Ala Leu Phe Ala Leu Gly Ile Arg Phe Ala His Ser
            25                  30                  35

cct tct tcc aac ggc acc aac gct ctt gga aaa att gct tca acc atc   259
Pro Ser Ser Asn Gly Thr Asn Ala Leu Gly Lys Ile Ala Ser Thr Ile
        40                  45                  50

tgc ttt gcc atc att gcg gtt gct atc atc gct ggc att ctc tgg gtc   307
Cys Phe Ala Ile Ile Ala Val Ala Ile Ile Ala Gly Ile Leu Trp Val
    55                  60                  65

acc aaa gca acg atc tac cag tac tct ggt ttc gac att ttc ggc act   355
Thr Lys Ala Thr Ile Tyr Gln Tyr Ser Gly Phe Asp Ile Phe Gly Thr
70                  75                  80                  85

gaa ggc taaaagcacc agctgcgaat aac                                 384
Glu Gly


<210> 962
<211> 87
<212> PRT
<213> Corynebacterium glutamicum

<400> 962
Met Asn Phe Ala Thr Ile Phe Gly Ser Ile Phe Glu Val Thr Leu Val
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  1               5                  10                  15

Gly Ile Leu Leu Gly Ala Gly Leu Pro Ala Leu Phe Ala Leu Gly Ile
            20                  25                  30

Arg Phe Ala His Ser Pro Ser Ser Asn Gly Thr Asn Ala Leu Gly Lys
        35                  40                  45

Ile Ala Ser Thr Ile Cys Phe Ala Ile Ile Ala Val Ala Ile Ile Ala
    50                  55                  60

Gly Ile Leu Trp Val Thr Lys Ala Thr Ile Tyr Gln Tyr Ser Gly Phe
65                  70                  75                  80

Asp Ile Phe Gly Thr Glu Gly
                85
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<210> 963
<211> 732
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(709)
<223> RXN02049

<400> 963

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atctggagtt gccggagttt ccttctggtg gtttggacta gtg cgc tat ctg acg   115
                                        Val Arg Tyr Leu Thr
                                          1               5

ctg gcc aca atc atc gca ggt ctc tcc ggg ttc gtc gtc atc atc atc   163
Leu Ala Thr Ile Ile Ala Gly Leu Ser Gly Phe Val Val Ile Ile Ile
                10                  15                  20

gct gcc tgg gcc ctt ggt gat tcc agc caa ctt tcc gaa gaa ttc acc   211
Ala Ala Trp Ala Leu Gly Asp Ser Ser Gln Leu Ser Glu Glu Phe Thr
            25                  30                  35

gcc tac tgg ggt ctg ttc ttt gca gga acc gga gtg ctg act ggg ttg   259
Ala Tyr Trp Gly Leu Phe Phe Ala Gly Thr Gly Val Leu Thr Gly Leu
        40                  45                  50

acg cag gag acg acc cgc gcg gtg acg gcc ggt tct cgt ggt ggt tct   307
Thr Gln Glu Thr Thr Arg Ala Val Thr Ala Gly Ser Arg Gly Gly Ser
    55                  60                  65

cgt ggt ggg cgt gct ggt tct gtt gtt gga ttt agg ccg ttt ttg ttt   355
Arg Gly Gly Arg Ala Gly Ser Val Val Gly Phe Arg Pro Phe Leu Phe
70                  75                  80                  85

agc ttc gtg gtt gcg gcg ata gtg ctc gtg gtg ctt ggc gct tcg gcg   403
Ser Phe Val Val Ala Ala Ile Val Leu Val Val Leu Gly Ala Ser Ala
                90                  95                  100

ccg ctg tgg atc ggc cag ctt tta agt aat ttg caa ggt gtt ggt gtt   451
Pro Leu Trp Ile Gly Gln Leu Leu Ser Asn Leu Gln Gly Val Gly Val
```

```
            105                 110                 115

ggg cta ctt gct gta ggt ctt gct agc tac gcg atc caa gcg aca atc   499
Gly Leu Leu Ala Val Gly Leu Ala Ser Tyr Ala Ile Gln Ala Thr Ile
        120                 125                 130

tcc ggc att ttt gtc cgg ctg cca att gtg gaa aga gta tgc ctc gct   547
Ser Gly Ile Phe Val Arg Leu Pro Ile Val Glu Arg Val Cys Leu Ala
    135                 140                 145

gat ttc ttt gga cac cgg cgt gcg cat ggt ttt aac tgt tgc cgc ctg   595
Asp Phe Phe Gly His Arg Arg Ala His Gly Phe Asn Cys Cys Arg Leu
150                 155                 160                 165

gtt gct ggg tta tca att gct ggc gtt ctt gat cat cac cgt tgt ggg   643
Val Ala Gly Leu Ser Ile Ala Gly Val Leu Asp His His Arg Cys Gly
                170                 175                 180

atc aat atc ctg gct ggt cat cgt gct gtg ctt cgg ttc ggt gcg ttc   691
Ile Asn Ile Leu Ala Gly His Arg Ala Val Leu Arg Phe Gly Ala Phe
            185                 190                 195

cgt ttt ggg atc ggt tgc tgatgtttca cggggcgttt tca                 732
Arg Phe Gly Ile Gly Cys
        200


<210> 964
<211> 203
<212> PRT
<213> Corynebacterium glutamicum

<400> 964
Val Arg Tyr Leu Thr Leu Ala Thr Ile Ile Ala Gly Leu Ser Gly Phe
  1               5                  10                  15

Val Val Ile Ile Ile Ala Ala Trp Ala Leu Gly Asp Ser Ser Gln Leu
             20                  25                  30

Ser Glu Glu Phe Thr Ala Tyr Trp Gly Leu Phe Phe Ala Gly Thr Gly
         35                  40                  45

Val Leu Thr Gly Leu Thr Gln Glu Thr Thr Arg Ala Val Thr Ala Gly
     50                  55                  60

Ser Arg Gly Gly Ser Arg Gly Gly Arg Ala Gly Ser Val Val Gly Phe
 65                  70                  75                  80

Arg Pro Phe Leu Phe Ser Phe Val Val Ala Ala Ile Val Leu Val Val
                 85                  90                  95

Leu Gly Ala Ser Ala Pro Leu Trp Ile Gly Gln Leu Leu Ser Asn Leu
            100                 105                 110

Gln Gly Val Gly Val Gly Leu Leu Ala Val Gly Leu Ala Ser Tyr Ala
        115                 120                 125

Ile Gln Ala Thr Ile Ser Gly Ile Phe Val Arg Leu Pro Ile Val Glu
    130                 135                 140

Arg Val Cys Leu Ala Asp Phe Phe Gly His Arg Arg Ala His Gly Phe
```

```
145                 150                 155                 160

Asn Cys Cys Arg Leu Val Ala Gly Leu Ser Ile Ala Gly Val Leu Asp
                165                 170                 175

His His Arg Cys Gly Ile Asn Ile Leu Ala Gly His Arg Ala Val Leu
            180                 185                 190

Arg Phe Gly Ala Phe Arg Phe Gly Ile Gly Cys
        195                 200
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<210> 965
<211> 570
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(547)
<223> FRXA02049

<400> 965

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tctacgcagt ctccacagac cacgcagctt tagatgcagt gtggcagtcc tggcttcgcg 60

atctggagtt gccggagttt ccttctggtg gtttggacta gtg cgc tat ctg acg   115
                                              Val Arg Tyr Leu Thr
                                                1               5

ctg gcc aca atc atc gca ggt ctc tcc ggg ttc gtc gtc atc atc atc   163
Leu Ala Thr Ile Ile Ala Gly Leu Ser Gly Phe Val Val Ile Ile Ile
                10                  15                  20

gct gcc tgg gcc ctt ggt gat tcc agc caa ctt tcc gaa gaa ttc acc   211
Ala Ala Trp Ala Leu Gly Asp Ser Ser Gln Leu Ser Glu Glu Phe Thr
            25                  30                  35

gcc tac tgg ggt ctg ttc ttt gca gga acc gga gtg ctg act ggg ttg   259
Ala Tyr Trp Gly Leu Phe Phe Ala Gly Thr Gly Val Leu Thr Gly Leu
        40                  45                  50

acg cag gag acg acc cgc gcg gtg acg gcc ggt tct cgt ggt ggt tct   307
Thr Gln Glu Thr Thr Arg Ala Val Thr Ala Gly Ser Arg Gly Gly Ser
    55                  60                  65

cgt ggt ggg cgt gct ggt tct gtt gtt gga ttt agg ccg ttt ttg ttt   355
Arg Gly Gly Arg Ala Gly Ser Val Val Gly Phe Arg Pro Phe Leu Phe
70                  75                  80                  85

agc ttc gtg gtt gcg gcg ata gtg ctc gtg gtg ctt ggc gct tcg gcg   403
Ser Phe Val Val Ala Ala Ile Val Leu Val Val Leu Gly Ala Ser Ala
                90                  95                  100

ccg ctg tgg atc ggc cag ctt tta agt aat ttg caa ggt gtt ggt gtt   451
Pro Leu Trp Ile Gly Gln Leu Leu Ser Asn Leu Gln Gly Val Gly Val
            105                 110                 115

ggg cta ctt gct gta ggt ctt gct agc tac gcg atc caa gcg aca atc   499
Gly Leu Leu Ala Val Gly Leu Ala Ser Tyr Ala Ile Gln Ala Thr Ile
        120                 125                 130
```

```
tcc ggc att ttt gtc cgg ctg cca att gtg gaa aag agt atg cct cgc   547
Ser Gly Ile Phe Val Arg Leu Pro Ile Val Glu Lys Ser Met Pro Arg
    135                 140                 145

tgatttcttt ggacaccggc gtg                                       570


<210> 966
<211> 149
<212> PRT
<213> Corynebacterium glutamicum

<400> 966
Val Arg Tyr Leu Thr Leu Ala Thr Ile Ile Ala Gly Leu Ser Gly Phe
  1               5                  10                  15

Val Val Ile Ile Ile Ala Ala Trp Ala Leu Gly Asp Ser Ser Gln Leu
             20                  25                  30

Ser Glu Glu Phe Thr Ala Tyr Trp Gly Leu Phe Phe Ala Gly Thr Gly
         35                  40                  45

Val Leu Thr Gly Leu Thr Gln Glu Thr Thr Arg Ala Val Thr Ala Gly
     50                  55                  60

Ser Arg Gly Gly Ser Arg Gly Gly Arg Ala Gly Ser Val Val Gly Phe
 65                  70                  75                  80

Arg Pro Phe Leu Phe Ser Phe Val Val Ala Ala Ile Val Leu Val Val
                 85                  90                  95

Leu Gly Ala Ser Ala Pro Leu Trp Ile Gly Gln Leu Leu Ser Asn Leu
            100                 105                 110

Gln Gly Val Gly Val Gly Leu Leu Ala Val Gly Leu Ala Ser Tyr Ala
        115                 120                 125

Ile Gln Ala Thr Ile Ser Gly Ile Phe Val Arg Leu Pro Ile Val Glu
    130                 135                 140

Lys Ser Met Pro Arg
145


<210> 967
<211> 918
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(895)
<223> RXN02050

<400> 967
ctacttgctg taggtcttgc tagctacgcg atccaagcga caatctccgg catttttgtc 60

cggctgccaa ttgtggaaag agtatgcctc gctgatttct ttg gac acc ggc gtg   115
                                                Leu Asp Thr Gly Val
                                                  1               5
```

```
cgc atg gtt tta act gtt gcc gcc tgg ttg ctg ggt tat caa ttg ctg   163
Arg Met Val Leu Thr Val Ala Ala Trp Leu Leu Gly Tyr Gln Leu Leu
                10                  15                  20

gcg ttc ttg atc atc acc gtt gtg gga tca ata tcc tgg ctg gtc atc   211
Ala Phe Leu Ile Ile Thr Val Val Gly Ser Ile Ser Trp Leu Val Ile
            25                  30                  35

gtg ctg tgc ttc ggt tcg gtg cgt tcc gtt ttg gga tcg gtt gct gat   259
Val Leu Cys Phe Gly Ser Val Arg Ser Val Leu Gly Ser Val Ala Asp
        40                  45                  50

gtt tca cgg ggc gtt ttc atc cga cag gct ctg ctt gcg atg gca gca   307
Val Ser Arg Gly Val Phe Ile Arg Gln Ala Leu Leu Ala Met Ala Ala
    55                  60                  65

tcc ggc gcc acg gca gtg ctg att act ggt ttc ccg acc ctg ctg aaa   355
Ser Gly Ala Thr Ala Val Leu Ile Thr Gly Phe Pro Thr Leu Leu Lys
70                  75                  80                  85

ttc acg aac cct tca gcg gtt gca gga ggg gtt tcg atg gcc gct gtt   403
Phe Thr Asn Pro Ser Ala Val Ala Gly Gly Val Ser Met Ala Ala Val
                90                  95                  100

tcc tac gcc gtc atc ctg acc cgc gct ccc ctg ctg gtt ccg ctg cag   451
Ser Tyr Ala Val Ile Leu Thr Arg Ala Pro Leu Leu Val Pro Leu Gln
            105                 110                 115

caa ttc caa tcg gcg atc atc gtt cgt ttt gtc aaa ggt acg tcc ggt   499
Gln Phe Gln Ser Ala Ile Ile Val Arg Phe Val Lys Gly Thr Ser Gly
        120                 125                 130

cca ttg aaa act ttg gcg ggt ccg ttg gca att gtg tgg gca gtc gga   547
Pro Leu Lys Thr Leu Ala Gly Pro Leu Ala Ile Val Trp Ala Val Gly
    135                 140                 145

ctt gtt gga gct ggt ctt gca tgg tta gtt ggc cca tgg atc ctg gac   595
Leu Val Gly Ala Gly Leu Ala Trp Leu Val Gly Pro Trp Ile Leu Asp
150                 155                 160                 165

gtt gta ctc caa aag gaa ctc ttc gcg gtc cct ggc tgg cta ctc gcg   643
Val Val Leu Gln Lys Glu Leu Phe Ala Val Pro Gly Trp Leu Leu Ala
                170                 175                 180

atg ctc acc tta ggc gcc acc acc acc gct tca ttg atg gtg tcc ggc   691
Met Leu Thr Leu Gly Ala Thr Thr Thr Ala Ser Leu Met Val Ser Gly
            185                 190                 195

tgc gcg gcg atc gcc ttt gaa cgt cac ggg atc tat ctc acc gga tgg   739
Cys Ala Ala Ile Ala Phe Glu Arg His Gly Ile Tyr Leu Thr Gly Trp
        200                 205                 210

gtt gtt gcc act gtt gtt gcc gtc gga ttc ttg ctg gga cct ttt gat   787
Val Val Ala Thr Val Val Ala Val Gly Phe Leu Leu Gly Pro Phe Asp
    215                 220                 225

ttg ggc gtc gct gct ggc ctt gcg ctc att gtt ggc cca ctc tgc ggt   835
Leu Gly Val Ala Ala Gly Leu Ala Leu Ile Val Gly Pro Leu Cys Gly
230                 235                 240                 245

ttg ctg gta cac atg gga gcg ttt gtt ggt ggg gat cgg aat cgg gtt   883
```

```
Leu Leu Val His Met Gly Ala Phe Val Gly Gly Asp Arg Asn Arg Val
                250                 255                 260

ttg act gcg gga tagtttggtt tgattggggg att                          918
Leu Thr Ala Gly
            265
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<210> 968
<211> 265
<212> PRT
<213> Corynebacterium glutamicum

<400> 968

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Leu Asp Thr Gly Val Arg Met Val Leu Thr Val Ala Ala Trp Leu Leu
  1               5                  10                  15

Gly Tyr Gln Leu Leu Ala Phe Leu Ile Ile Thr Val Val Gly Ser Ile
             20                  25                  30

Ser Trp Leu Val Ile Val Leu Cys Phe Gly Ser Val Arg Ser Val Leu
         35                  40                  45

Gly Ser Val Ala Asp Val Ser Arg Gly Val Phe Ile Arg Gln Ala Leu
     50                  55                  60

Leu Ala Met Ala Ala Ser Gly Ala Thr Ala Val Leu Ile Thr Gly Phe
 65                  70                  75                  80

Pro Thr Leu Leu Lys Phe Thr Asn Pro Ser Ala Val Ala Gly Gly Val
                 85                  90                  95

Ser Met Ala Ala Val Ser Tyr Ala Val Ile Leu Thr Arg Ala Pro Leu
            100                 105                 110

Leu Val Pro Leu Gln Gln Phe Gln Ser Ala Ile Ile Val Arg Phe Val
        115                 120                 125

Lys Gly Thr Ser Gly Pro Leu Lys Thr Leu Ala Gly Pro Leu Ala Ile
    130                 135                 140

Val Trp Ala Val Gly Leu Val Gly Ala Gly Leu Ala Trp Leu Val Gly
145                 150                 155                 160

Pro Trp Ile Leu Asp Val Val Leu Gln Lys Glu Leu Phe Ala Val Pro
                165                 170                 175

Gly Trp Leu Leu Ala Met Leu Thr Leu Gly Ala Thr Thr Thr Ala Ser
            180                 185                 190

Leu Met Val Ser Gly Cys Ala Ala Ile Ala Phe Glu Arg His Gly Ile
        195                 200                 205

Tyr Leu Thr Gly Trp Val Val Ala Thr Val Val Ala Val Gly Phe Leu
    210                 215                 220

Leu Gly Pro Phe Asp Leu Gly Val Ala Ala Gly Leu Ala Leu Ile Val
225                 230                 235                 240

Gly Pro Leu Cys Gly Leu Leu Val His Met Gly Ala Phe Val Gly Gly
                245                 250                 255
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Asp Arg Asn Arg Val Leu Thr Ala Gly
            260                 265


<210> 969
<211> 495
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(472)
<223> FRXA02050

<400> 969
cgcgctcccc tgctggttcc gctgcagcaa ttccaatcgg cgatcatcgt tcgttttgtc 60

aaaggtaccg tccggtccat tgaaaacttt ggcgggtccg ttg gca att gtg tgg   115
                                          Leu Ala Ile Val Trp
                                            1               5

gca gtc gga ctt gtt gga gct ggt ctt gca tgg tta gtt ggc cca tgg   163
Ala Val Gly Leu Val Gly Ala Gly Leu Ala Trp Leu Val Gly Pro Trp
                10                  15                  20

atc ctg gac gtt gta ctc caa aag gaa ctc ttc gcg gtc cct ggc tgg   211
Ile Leu Asp Val Val Leu Gln Lys Glu Leu Phe Ala Val Pro Gly Trp
            25                  30                  35

cta ctc gcg atg ctc acc tta ggc gcc acc acc acc gct tca ttg atg   259
Leu Leu Ala Met Leu Thr Leu Gly Ala Thr Thr Thr Ala Ser Leu Met
        40                  45                  50

gtg tcc ggc tgc gcg gcg atc gcc ttt gaa cgt cac ggg atc tat ctc   307
Val Ser Gly Cys Ala Ala Ile Ala Phe Glu Arg His Gly Ile Tyr Leu
    55                  60                  65

acc gga tgg gtt gtt gcc act gtt gtt gcc gtc gga ttc ttg ctg gga   355
Thr Gly Trp Val Val Ala Thr Val Val Ala Val Gly Phe Leu Leu Gly
70                  75                  80                  85

cct ttt gat ttg ggc gtc gct gct ggc ctt gcg ctc att gtt ggc cca   403
Pro Phe Asp Leu Gly Val Ala Ala Gly Leu Ala Leu Ile Val Gly Pro
                90                  95                  100

ctc tgc ggt ttg ctg gta cac atg gga gcg ttt gtt ggt ggg gat cgg   451
Leu Cys Gly Leu Leu Val His Met Gly Ala Phe Val Gly Gly Asp Arg
            105                 110                 115

aat cgg gtt ttg act gcg gga tagtttggtt tgattggggg att             495
Asn Arg Val Leu Thr Ala Gly
        120


<210> 970
<211> 124
<212> PRT
<213> Corynebacterium glutamicum

<400> 970
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```
Leu Ala Ile Val Trp Ala Val Gly Leu Val Gly Ala Gly Leu Ala Trp
  1               5                  10                  15

Leu Val Gly Pro Trp Ile Leu Asp Val Val Leu Gln Lys Glu Leu Phe
             20                  25                  30

Ala Val Pro Gly Trp Leu Leu Ala Met Leu Thr Leu Gly Ala Thr Thr
         35                  40                  45

Thr Ala Ser Leu Met Val Ser Gly Cys Ala Ala Ile Ala Phe Glu Arg
     50                  55                  60

His Gly Ile Tyr Leu Thr Gly Trp Val Val Ala Thr Val Val Ala Val
 65                  70                  75                  80

Gly Phe Leu Leu Gly Pro Phe Asp Leu Gly Val Ala Ala Gly Leu Ala
                 85                  90                  95

Leu Ile Val Gly Pro Leu Cys Gly Leu Leu Val His Met Gly Ala Phe
            100                 105                 110

Val Gly Gly Asp Arg Asn Arg Val Leu Thr Ala Gly
        115                 120


<210> 971
<211> 618
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(595)
<223> RXN02059

<400> 971
tcgggaaatt ccactcatga acgcctagtc tacgggaacc atttcaccag cgtgtacgtt 60

gtaaatgtga actgaaaaag tgaaaaggaa gatgataaag atg act caa cca cgg   115
                                            Met Thr Gln Pro Arg
                                              1               5

ccc gat gcc gca tct gtg tcg ctg gaa aag aag cgc cca gaa gga tgg   163
Pro Asp Ala Ala Ser Val Ser Leu Glu Lys Lys Arg Pro Glu Gly Trp
                 10                  15                  20

cca gtg gga agc ttt gaa aca tac cca gaa gcc caa gca gca gtg gat   211
Pro Val Gly Ser Phe Glu Thr Tyr Pro Glu Ala Gln Ala Ala Val Asp
             25                  30                  35

ttg ctc agt gat aat gca ttc ccc gtc acc gaa ttg acc att gtt ggt   259
Leu Leu Ser Asp Asn Ala Phe Pro Val Thr Glu Leu Thr Ile Val Gly
         40                  45                  50

gtg gac ctg att gaa gtg gaa cgc gtt aca ggt cgt ctc acg tgg ggt   307
Val Asp Leu Ile Glu Val Glu Arg Val Thr Gly Arg Leu Thr Trp Gly
     55                  60                  65

cgt gtg att gcc gga gga atg gca tct ggc gca tgg ttg ggt ctg ttc   355
Arg Val Ile Ala Gly Gly Met Ala Ser Gly Ala Trp Leu Gly Leu Phe
 70                  75                  80                  85
```

```
ttt ggc att gtc atg gcc ttg atg tct gga ttc tgg ttc tct tcc atc   403
Phe Gly Ile Val Met Ala Leu Met Ser Gly Phe Trp Phe Ser Ser Ile
                 90                  95                 100

gca gcg gga ata ggt atg ggt ttg gtg ttt ggc att gtc ggt gca gca   451
Ala Ala Gly Ile Gly Met Gly Leu Val Phe Gly Ile Val Gly Ala Ala
            105                 110                 115

gtt cct tat gct gct tcc aaa ggc aag cgg gac ttt acc tct tca act   499
Val Pro Tyr Ala Ala Ser Lys Gly Lys Arg Asp Phe Thr Ser Ser Thr
        120                 125                 130

caa att gtg gcg ggg cgc tat gat gtg att tgt tcc cca gaa cgt gct   547
Gln Ile Val Ala Gly Arg Tyr Asp Val Ile Cys Ser Pro Glu Arg Ala
    135                 140                 145

cgg gaa gct cga gac atg att gcc ctg aaa act cga gat ctc cgc caa   595
Arg Glu Ala Arg Asp Met Ile Ala Leu Lys Thr Arg Asp Leu Arg Gln
150                 155                 160                 165

taagttaaac taacgcctat gaa                                        618
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<210> 972
<211> 165
<212> PRT
<213> Corynebacterium glutamicum

<400> 972

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Met Thr Gln Pro Arg Pro Asp Ala Ala Ser Val Ser Leu Glu Lys Lys
  1               5                  10                  15

Arg Pro Glu Gly Trp Pro Val Gly Ser Phe Glu Thr Tyr Pro Glu Ala
             20                  25                  30

Gln Ala Ala Val Asp Leu Leu Ser Asp Asn Ala Phe Pro Val Thr Glu
         35                  40                  45

Leu Thr Ile Val Gly Val Asp Leu Ile Glu Val Glu Arg Val Thr Gly
     50                  55                  60

Arg Leu Thr Trp Gly Arg Val Ile Ala Gly Gly Met Ala Ser Gly Ala
 65                  70                  75                  80

Trp Leu Gly Leu Phe Phe Gly Ile Val Met Ala Leu Met Ser Gly Phe
                 85                  90                  95

Trp Phe Ser Ser Ile Ala Ala Gly Ile Gly Met Gly Leu Val Phe Gly
            100                 105                 110

Ile Val Gly Ala Ala Val Pro Tyr Ala Ala Ser Lys Gly Lys Arg Asp
        115                 120                 125

Phe Thr Ser Ser Thr Gln Ile Val Ala Gly Arg Tyr Asp Val Ile Cys
    130                 135                 140

Ser Pro Glu Arg Ala Arg Glu Ala Arg Asp Met Ile Ala Leu Lys Thr
145                 150                 155                 160

Arg Asp Leu Arg Gln
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165

<210> 973
<211> 618
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(595)
<223> FRXA02059

<400> 973
tcgggaaatt ccactcatga acgcctagtc tacgggaacc atttcaccag cgtgtacgtt 60

gtaaatgtga actgaaaaag tgaaaaggaa gatgataaag atg act caa cca cgg 115
Met Thr Gln Pro Arg
1 5

ccc gat gcc gca tct gtg tcg ctg gaa aag aag cgc cca gaa gga tgg 163
Pro Asp Ala Ala Ser Val Ser Leu Glu Lys Lys Arg Pro Glu Gly Trp
10 15 20

cca gtg gga agc ttt gaa aca tac cca gaa gcc caa gca gca gtg gat 211
Pro Val Gly Ser Phe Glu Thr Tyr Pro Glu Ala Gln Ala Ala Val Asp
25 30 35

ttg ctc agt gat aat gca ttc ccc gtc acc gaa ttg acc att gtt ggt 259
Leu Leu Ser Asp Asn Ala Phe Pro Val Thr Glu Leu Thr Ile Val Gly
40 45 50

gtg gac ctg att gaa gtg gaa cgc gtt aca ggt cgt ctc acg tgg ggt 307
Val Asp Leu Ile Glu Val Glu Arg Val Thr Gly Arg Leu Thr Trp Gly
55 60 65

cgt gtg att gcc gga gga atg gca tct ggc gca tgg ttg ggt ctg ttc 355
Arg Val Ile Ala Gly Gly Met Ala Ser Gly Ala Trp Leu Gly Leu Phe
70 75 80 85

ttt ggc att gtc atg gcc ttg atg tct gga ttc tgg ttc tct tcc atc 403
Phe Gly Ile Val Met Ala Leu Met Ser Gly Phe Trp Phe Ser Ser Ile
90 95 100

gca gcg gga ata ggt atg ggt ttg gtg ttt ggc att gtc ggt gca gca 451
Ala Ala Gly Ile Gly Met Gly Leu Val Phe Gly Ile Val Gly Ala Ala
105 110 115

gtt cct tat gct gct tcc aaa ggc aag cgg gac ttt acc tct tca act 499
Val Pro Tyr Ala Ala Ser Lys Gly Lys Arg Asp Phe Thr Ser Ser Thr
120 125 130

caa att gtg gcg ggg cgc tat gat gtg att tgt tcc cca gaa cgt gct 547
Gln Ile Val Ala Gly Arg Tyr Asp Val Ile Cys Ser Pro Glu Arg Ala
135 140 145

cgg gaa gct cga gac atg att gcc ctg aaa act cga gat ctc cgc caa 595
Arg Glu Ala Arg Asp Met Ile Ala Leu Lys Thr Arg Asp Leu Arg Gln
150 155 160 165

taagttaaac taacgcctat gaa 618

<210> 974
<211> 165
<212> PRT
<213> Corynebacterium glutamicum

<400> 974
Met Thr Gln Pro Arg Pro Asp Ala Ala Ser Val Ser Leu Glu Lys Lys
1 5 10 15

Arg Pro Glu Gly Trp Pro Val Gly Ser Phe Glu Thr Tyr Pro Glu Ala
20 25 30

Gln Ala Ala Val Asp Leu Leu Ser Asp Asn Ala Phe Pro Val Thr Glu
35 40 45

Leu Thr Ile Val Gly Val Asp Leu Ile Glu Val Glu Arg Val Thr Gly
50 55 60

Arg Leu Thr Trp Gly Arg Val Ile Ala Gly Gly Met Ala Ser Gly Ala
65 70 75 80

Trp Leu Gly Leu Phe Phe Gly Ile Val Met Ala Leu Met Ser Gly Phe
85 90 95

Trp Phe Ser Ser Ile Ala Ala Gly Ile Gly Met Gly Leu Val Phe Gly
100 105 110

Ile Val Gly Ala Ala Val Pro Tyr Ala Ala Ser Lys Gly Lys Arg Asp
115 120 125

Phe Thr Ser Ser Thr Gln Ile Val Ala Gly Arg Tyr Asp Val Ile Cys
130 135 140

Ser Pro Glu Arg Ala Arg Glu Ala Arg Asp Met Ile Ala Leu Lys Thr
145 150 155 160

Arg Asp Leu Arg Gln
165

<210> 975
<211> 615
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(592)
<223> RXN02066

<400> 975
ggaacttatc acaggcgaca tccgttttga gtagtaggta tcttggataa gaagttaccc 60

acatccttga aagtcgagac acaggaggtc atcggaagat atg ttc aat tcc gac 115
Met Phe Asn Ser Asp
1 5

acc acc gcg aat ctc caa gct aaa agt cga gat cgt gca gga tct aaa 163
Thr Thr Ala Asn Leu Gln Ala Lys Ser Arg Asp Arg Ala Gly Ser Lys

```
                10                  15                  20

gca aag cgc agc agg cca agt ttt gat tca gta gcg cgg gat gtt ttg   211
Ala Lys Arg Ser Arg Pro Ser Phe Asp Ser Val Ala Arg Asp Val Leu
            25                  30                  35

gat gtt cga aca aaa aca gca caa gtt aaa aac aag gct aaa gag ttt   259
Asp Val Arg Thr Lys Thr Ala Gln Val Lys Asn Lys Ala Lys Glu Phe
        40                  45                  50

tcc tct gtt gat cac ctt tca gca gac gcc gca gcc atg ttt gta gac   307
Ser Ser Val Asp His Leu Ser Ala Asp Ala Ala Ala Met Phe Val Asp
    55                  60                  65

aat gaa ctg tcc cgt ggc gcc atg cat cgc gcc agg ctg cac att gtg   355
Asn Glu Leu Ser Arg Gly Ala Met His Arg Ala Arg Leu His Ile Val
70                  75                  80                  85

cac tgc gct gaa tgt agg gaa gag att aac cgt cag cgg gaa acc gtt   403
His Cys Ala Glu Cys Arg Glu Glu Ile Asn Arg Gln Arg Glu Thr Val
                90                  95                  100

gat tat ctc cgc tca gag tgc aaa aac gaa gaa gtg tcc gcc cca atg   451
Asp Tyr Leu Arg Ser Glu Cys Lys Asn Glu Glu Val Ser Ala Pro Met
            105                 110                 115

gac ctc aaa gca cgg ctt gcc agc ctc gcc act gag tgc atg cct ggc   499
Asp Leu Lys Ala Arg Leu Ala Ser Leu Ala Thr Glu Cys Met Pro Gly
        120                 125                 130

cct ggc gca gag aat tta gca atg cag cgc cca gag tct ttt gtg gct   547
Pro Gly Ala Glu Asn Leu Ala Met Gln Arg Pro Glu Ser Phe Val Ala
    135                 140                 145

aaa gtt gag tcc gta gtg cgc gca gtt cgt aag aac caa ggc cgc       592
Lys Val Glu Ser Val Val Arg Ala Val Arg Lys Asn Gln Gly Arg
150                 155                 160

taatttttaa tccttattta cat                                        615
```

<210> 976
<211> 164
<212> PRT
<213> Corynebacterium glutamicum

<400> 976

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Met Phe Asn Ser Asp Thr Thr Ala Asn Leu Gln Ala Lys Ser Arg Asp
  1               5                  10                  15

Arg Ala Gly Ser Lys Ala Lys Arg Ser Arg Pro Ser Phe Asp Ser Val
            20                  25                  30

Ala Arg Asp Val Leu Asp Val Arg Thr Lys Thr Ala Gln Val Lys Asn
        35                  40                  45

Lys Ala Lys Glu Phe Ser Ser Val Asp His Leu Ser Ala Asp Ala Ala
    50                  55                  60

Ala Met Phe Val Asp Asn Glu Leu Ser Arg Gly Ala Met His Arg Ala
65                  70                  75                  80
```

```
Arg Leu His Ile Val His Cys Ala Glu Cys Arg Glu Glu Ile Asn Arg
                85                  90                  95

Gln Arg Glu Thr Val Asp Tyr Leu Arg Ser Glu Cys Lys Asn Glu Glu
            100                 105                 110

Val Ser Ala Pro Met Asp Leu Lys Ala Arg Leu Ala Ser Leu Ala Thr
        115                 120                 125

Glu Cys Met Pro Gly Pro Gly Ala Glu Asn Leu Ala Met Gln Arg Pro
    130                 135                 140

Glu Ser Phe Val Ala Lys Val Glu Ser Val Val Arg Ala Val Arg Lys
145                 150                 155                 160

Asn Gln Gly Arg
```

<210> 977
<211> 615
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(592)
<223> FRXA02066

<400> 977

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ggaacttatc acaggcgaca tccgttttga gtagtaggta tcttggataa gaagttaccc 60

acatccttga aagtcgagac acaggaggtc atcggaagat atg ttc aat tcc gac   115
                                            Met Phe Asn Ser Asp
                                              1               5

acc acc gcg aat ctc caa gct aaa agt cga gat cgt gca gga tct aaa   163
Thr Thr Ala Asn Leu Gln Ala Lys Ser Arg Asp Arg Ala Gly Ser Lys
                  10                  15                  20

gca aag cgc agc agg cca agt ttt gat tca gta gcg cgg gat gtt ttg   211
Ala Lys Arg Ser Arg Pro Ser Phe Asp Ser Val Ala Arg Asp Val Leu
              25                  30                  35

gat gtt cga aca aaa aca gca caa gtt aaa aac aag gct aaa gag ttt   259
Asp Val Arg Thr Lys Thr Ala Gln Val Lys Asn Lys Ala Lys Glu Phe
          40                  45                  50

tcc tct gtt gat cac ctt tca gca gac gcc gca gcc atg ttt gta gac   307
Ser Ser Val Asp His Leu Ser Ala Asp Ala Ala Ala Met Phe Val Asp
      55                  60                  65

aat gaa ctg tcc cgt ggc gcc atg cat cgc gcc agg ctg cac att gtg   355
Asn Glu Leu Ser Arg Gly Ala Met His Arg Ala Arg Leu His Ile Val
  70                  75                  80                  85

cac tgc gct gaa tgt agg gaa gag att aac cgt cag cgg gaa acc gtt   403
His Cys Ala Glu Cys Arg Glu Glu Ile Asn Arg Gln Arg Glu Thr Val
                  90                  95                 100
```

```
gat tat ctc cgc tca gag tgc aaa aac gaa gaa gtg tcc gcc cca atg   451
Asp Tyr Leu Arg Ser Glu Cys Lys Asn Glu Glu Val Ser Ala Pro Met
            105                 110                 115

gac ctc aaa gca cgg ctt gcc agc ctc gcc act gag tgc atg cct ggc   499
Asp Leu Lys Ala Arg Leu Ala Ser Leu Ala Thr Glu Cys Met Pro Gly
        120                 125                 130

cct ggc gca gag aat tta gca atg cag cgc cca gag tct ttt gtg gct   547
Pro Gly Ala Glu Asn Leu Ala Met Gln Arg Pro Glu Ser Phe Val Ala
    135                 140                 145

aaa gtt gag tcc gta gtg cgc gca gtt cgt aag aac caa ggc cgc       592
Lys Val Glu Ser Val Val Arg Ala Val Arg Lys Asn Gln Gly Arg
150                 155                 160

taatttttaa tccttattta cat                                        615
```

<210> 978
<211> 164
<212> PRT
<213> Corynebacterium glutamicum

<400> 978

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Met Phe Asn Ser Asp Thr Thr Ala Asn Leu Gln Ala Lys Ser Arg Asp
  1               5                  10                  15

Arg Ala Gly Ser Lys Ala Lys Arg Ser Arg Pro Ser Phe Asp Ser Val
             20                  25                  30

Ala Arg Asp Val Leu Asp Val Arg Thr Lys Thr Ala Gln Val Lys Asn
         35                  40                  45

Lys Ala Lys Glu Phe Ser Ser Val Asp His Leu Ser Ala Asp Ala Ala
     50                  55                  60

Ala Met Phe Val Asp Asn Glu Leu Ser Arg Gly Ala Met His Arg Ala
 65                  70                  75                  80

Arg Leu His Ile Val His Cys Ala Glu Cys Arg Glu Glu Ile Asn Arg
                 85                  90                  95

Gln Arg Glu Thr Val Asp Tyr Leu Arg Ser Glu Cys Lys Asn Glu Glu
            100                 105                 110

Val Ser Ala Pro Met Asp Leu Lys Ala Arg Leu Ala Ser Leu Ala Thr
        115                 120                 125

Glu Cys Met Pro Gly Pro Gly Ala Glu Asn Leu Ala Met Gln Arg Pro
    130                 135                 140

Glu Ser Phe Val Ala Lys Val Glu Ser Val Val Arg Ala Val Arg Lys
145                 150                 155                 160

Asn Gln Gly Arg
```

<210> 979
<211> 579

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> RXN02067

<400> 979
taaagttgag tccgtagtgc gcgcagttcg taagaaccaa ggccgctaat ttttaatcct 60

tatttacatt ttctgaaaga ccggtctgat gttttctagc gtg ggt tgg gga gag 115
Val Gly Trp Gly Glu
1 5

atc ttc ctc tta gtc gtt gtg ggc ctt gtt gtc atc ggc ccg gaa cgg 163
Ile Phe Leu Leu Val Val Val Gly Leu Val Val Ile Gly Pro Glu Arg
10 15 20

ttg cct cgt ttg atc cag gac gca cgc gct gcg ctg ctc gct gca cgt 211
Leu Pro Arg Leu Ile Gln Asp Ala Arg Ala Ala Leu Leu Ala Ala Arg
25 30 35

acc gct atc gac aat gca aag cag tcg ttg gac agt gat ttt ggt tcg 259
Thr Ala Ile Asp Asn Ala Lys Gln Ser Leu Asp Ser Asp Phe Gly Ser
40 45 50

gaa ttt gat gaa atc cga aag cca cta acc cag gtt gca cag tac agc 307
Glu Phe Asp Glu Ile Arg Lys Pro Leu Thr Gln Val Ala Gln Tyr Ser
55 60 65

cgg atg agc ccc aag acg gcc atc act aag gcg tta ttt gat aat gat 355
Arg Met Ser Pro Lys Thr Ala Ile Thr Lys Ala Leu Phe Asp Asn Asp
70 75 80 85

tcc tcg ttc ctg gat gac ttt gat cca aag aag atc atg gcc gaa gga 403
Ser Ser Phe Leu Asp Asp Phe Asp Pro Lys Lys Ile Met Ala Glu Gly
90 95 100

aca gaa ggc gaa gct cag cgc aac aag cag gca gct gac aac aat gcg 451
Thr Glu Gly Glu Ala Gln Arg Asn Lys Gln Ala Ala Asp Asn Asn Ala
105 110 115

aat gtg gtg gaa cgt cca gct gat ggt tcc acc gca cgc cca acg caa 499
Asn Val Val Glu Arg Pro Ala Asp Gly Ser Thr Ala Arg Pro Thr Gln
120 125 130

aac gat cca aaa gac ggc ccg aat tac tca ggt ggc gtc tct tgg acc 547
Asn Asp Pro Lys Asp Gly Pro Asn Tyr Ser Gly Gly Val Ser Trp Thr
135 140 145

gat att att tagcttttat ttaacgccaa gcc 579
Asp Ile Ile
150

<210> 980
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 980
Val Gly Trp Gly Glu Ile Phe Leu Leu Val Val Val Gly Leu Val Val
1 5 10 15

Ile Gly Pro Glu Arg Leu Pro Arg Leu Ile Gln Asp Ala Arg Ala Ala
20 25 30

Leu Leu Ala Ala Arg Thr Ala Ile Asp Asn Ala Lys Gln Ser Leu Asp
35 40 45

Ser Asp Phe Gly Ser Glu Phe Asp Glu Ile Arg Lys Pro Leu Thr Gln
50 55 60

Val Ala Gln Tyr Ser Arg Met Ser Pro Lys Thr Ala Ile Thr Lys Ala
65 70 75 80

Leu Phe Asp Asn Asp Ser Ser Phe Leu Asp Asp Phe Asp Pro Lys Lys
85 90 95

Ile Met Ala Glu Gly Thr Glu Gly Glu Ala Gln Arg Asn Lys Gln Ala
100 105 110

Ala Asp Asn Asn Ala Asn Val Val Glu Arg Pro Ala Asp Gly Ser Thr
115 120 125

Ala Arg Pro Thr Gln Asn Asp Pro Lys Asp Gly Pro Asn Tyr Ser Gly
130 135 140

Gly Val Ser Trp Thr Asp Ile Ile
145 150

<210> 981
<211> 579
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> FRXA02067

<400> 981
taaagttgag tccgtagtgc gcgcagttcg taagaaccaa ggccgctaat ttttaatcct 60

tatttacatt ttctgaaaga ccggtctgat gttttctagc gtg ggt tgg gga gag 115
Val Gly Trp Gly Glu
1 5

atc ttc ctc tta gtc gtt gtg ggc ctt gtt gtc atc ggc ccg gaa cgg 163
Ile Phe Leu Leu Val Val Val Gly Leu Val Val Ile Gly Pro Glu Arg
10 15 20

ttg cct cgt ttg atc cag gac gca cgc gct gcg ctg ctc gct gca cgt 211
Leu Pro Arg Leu Ile Gln Asp Ala Arg Ala Ala Leu Leu Ala Ala Arg
25 30 35

acc gct atc gac aat gca aag cag tcg ttg gac agt gat ttt ggt tcg 259
Thr Ala Ile Asp Asn Ala Lys Gln Ser Leu Asp Ser Asp Phe Gly Ser
40 45 50

```
gaa ttt gat gaa atc cga aag cca cta acc cag gtt gca cag tac agc   307
Glu Phe Asp Glu Ile Arg Lys Pro Leu Thr Gln Val Ala Gln Tyr Ser
     55                  60                  65

cgg atg agc ccc aag acg gcc atc act aag gcg tta ttt gat aat gat   355
Arg Met Ser Pro Lys Thr Ala Ile Thr Lys Ala Leu Phe Asp Asn Asp
 70                  75                  80                  85

tcc tcg ttc ctg gat gac ttt gat cca aag aag atc atg gcc gaa gga   403
Ser Ser Phe Leu Asp Asp Phe Asp Pro Lys Lys Ile Met Ala Glu Gly
                 90                  95                 100

aca gaa ggc gaa gct cag cgc aac aag cag gca gct gac aac aat gcg   451
Thr Glu Gly Glu Ala Gln Arg Asn Lys Gln Ala Ala Asp Asn Asn Ala
            105                 110                 115

aat gtg gtg gaa cgt cca gct gat ggt tcc acc gca cgc cca acg caa   499
Asn Val Val Glu Arg Pro Ala Asp Gly Ser Thr Ala Arg Pro Thr Gln
        120                 125                 130

aac gat cca aaa gac ggc ccg aat tac tca ggt ggc gtc tct tgg acc   547
Asn Asp Pro Lys Asp Gly Pro Asn Tyr Ser Gly Gly Val Ser Trp Thr
    135                 140                 145

gat att att tagcttttat ttaacgccaa gcc                            579
Asp Ile Ile
150
```

<210> 982
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 982

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Val Gly Trp Gly Glu Ile Phe Leu Leu Val Val Val Gly Leu Val Val
  1               5                  10                  15

Ile Gly Pro Glu Arg Leu Pro Arg Leu Ile Gln Asp Ala Arg Ala Ala
             20                  25                  30

Leu Leu Ala Ala Arg Thr Ala Ile Asp Asn Ala Lys Gln Ser Leu Asp
         35                  40                  45

Ser Asp Phe Gly Ser Glu Phe Asp Glu Ile Arg Lys Pro Leu Thr Gln
     50                  55                  60

Val Ala Gln Tyr Ser Arg Met Ser Pro Lys Thr Ala Ile Thr Lys Ala
 65                  70                  75                  80

Leu Phe Asp Asn Asp Ser Ser Phe Leu Asp Asp Phe Asp Pro Lys Lys
                 85                  90                  95

Ile Met Ala Glu Gly Thr Glu Gly Glu Ala Gln Arg Asn Lys Gln Ala
            100                 105                 110

Ala Asp Asn Asn Ala Asn Val Val Glu Arg Pro Ala Asp Gly Ser Thr
        115                 120                 125

Ala Arg Pro Thr Gln Asn Asp Pro Lys Asp Gly Pro Asn Tyr Ser Gly
    130                 135                 140
```

```
Gly Val Ser Trp Thr Asp Ile Ile
145                 150


<210> 983
<211> 912
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(889)
<223> RXN02075

<400> 983
agttttcgaa taccgtctac gtggagcttt gcggaaaata cgcaccgaga cctaggcgcg 60

ccatacgcat ggttcacagg atttcagtac gattaacccc atg tac aag gtc ttc   115
                                            Met Tyr Lys Val Phe
                                              1               5

gaa gca ctg gat gat tta gtt caa gcc gtt caa cgc gca tac ggc gtt   163
Glu Ala Leu Asp Asp Leu Val Gln Ala Val Gln Arg Ala Tyr Gly Val
                 10                  15                  20

ccc atg acc gga aat tgc gtg gtt ccc cgt cag gaa gtg ctt gcg ctt   211
Pro Met Thr Gly Asn Cys Val Val Pro Arg Gln Glu Val Leu Ala Leu
             25                  30                  35

ctc gat gat tta cgt gat gcg ctt cct gta gaa ctt gat gat gca caa   259
Leu Asp Asp Leu Arg Asp Ala Leu Pro Val Glu Leu Asp Asp Ala Gln
         40                  45                  50

gat gtg ctg gac cac cgt gat ggt gtg atc cgt gaa gct gaa gaa aag   307
Asp Val Leu Asp His Arg Asp Gly Val Ile Arg Glu Ala Glu Glu Lys
     55                  60                  65

gcc att gcc ttg gtc gac gat gca gaa aac gag gcc cga aac ctc ctt   355
Ala Ile Ala Leu Val Asp Asp Ala Glu Asn Glu Ala Arg Asn Leu Leu
 70                  75                  80                  85

gca cgc gca act gag gag tca gat gcc atg gtg gaa gac gcc acc aag   403
Ala Arg Ala Thr Glu Glu Ser Asp Ala Met Val Glu Asp Ala Thr Lys
                 90                  95                 100

cat gcg cat tct gtc gtt gct aag gct aat gac aca gcg gat cgc atc   451
His Ala His Ser Val Val Ala Lys Ala Asn Asp Thr Ala Asp Arg Ile
             105                 110                 115

gtg agt gac gct cgt cga gaa gca aac agc gtc acc gag cgc gcc cag   499
Val Ser Asp Ala Arg Arg Glu Ala Asn Ser Val Thr Glu Arg Ala Gln
         120                 125                 130

gct gaa tct gag cgc ctg gtc aac tcc ggc aat gat gcg tat cgc cgc   547
Ala Glu Ser Glu Arg Leu Val Asn Ser Gly Asn Asp Ala Tyr Arg Arg
     135                 140                 145

gcg gtt gct gaa ggc cag gcc gag cag gat cgc ctg gtc agc gag gca   595
Ala Val Ala Glu Gly Gln Ala Glu Gln Asp Arg Leu Val Ser Glu Ala
150                 155                 160                 165
```

```
gaa gtg gtg cgt cgc tcc acg gaa gaa gca cac cgc att gtg gat gca   643
Glu Val Val Arg Arg Ser Thr Glu Glu Ala His Arg Ile Val Asp Ala
                170                 175                 180

gcg cac gct gac tcc aac aag ctg cgc aat gaa tgc gat gac tac gtg   691
Ala His Ala Asp Ser Asn Lys Leu Arg Asn Glu Cys Asp Asp Tyr Val
            185                 190                 195

gat acc aag ttg gca gag ttt gaa acc tcg ctg tcc acc acg ttg cgt   739
Asp Thr Lys Leu Ala Glu Phe Glu Thr Ser Leu Ser Thr Thr Leu Arg
        200                 205                 210

tct gtc act gct gat cgt tcc gca cta cgc cga gga gct gga gct act   787
Ser Val Thr Ala Asp Arg Ser Ala Leu Arg Arg Gly Ala Gly Ala Thr
    215                 220                 225

ggc cgc gag ctg cgc gat gag caa ccg gca gcg cgt ggt gaa tat gag   835
Gly Arg Glu Leu Arg Asp Glu Gln Pro Ala Ala Arg Gly Glu Tyr Glu
230                 235                 240                 245

cgg gac tac gag cgt gat tat gaa cga ggc tac gaa cgc gac gat cga   883
Arg Asp Tyr Glu Arg Asp Tyr Glu Arg Gly Tyr Glu Arg Asp Asp Arg
                250                 255                 260

gac tac tagtttccaa gaaaccattt agg                                912
Asp Tyr
```

<210> 984
<211> 263
<212> PRT
<213> Corynebacterium glutamicum

<400> 984

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Met Tyr Lys Val Phe Glu Ala Leu Asp Asp Leu Val Gln Ala Val Gln
  1               5                  10                  15

Arg Ala Tyr Gly Val Pro Met Thr Gly Asn Cys Val Val Pro Arg Gln
             20                  25                  30

Glu Val Leu Ala Leu Leu Asp Asp Leu Arg Asp Ala Leu Pro Val Glu
         35                  40                  45

Leu Asp Asp Ala Gln Asp Val Leu Asp His Arg Asp Gly Val Ile Arg
     50                  55                  60

Glu Ala Glu Glu Lys Ala Ile Ala Leu Val Asp Asp Ala Glu Asn Glu
 65                  70                  75                  80

Ala Arg Asn Leu Leu Ala Arg Ala Thr Glu Glu Ser Asp Ala Met Val
                 85                  90                  95

Glu Asp Ala Thr Lys His Ala His Ser Val Val Ala Lys Ala Asn Asp
            100                 105                 110

Thr Ala Asp Arg Ile Val Ser Asp Ala Arg Arg Glu Ala Asn Ser Val
        115                 120                 125

Thr Glu Arg Ala Gln Ala Glu Ser Glu Arg Leu Val Asn Ser Gly Asn
```

```
    130                 135                 140

Asp Ala Tyr Arg Arg Ala Val Ala Glu Gly Gln Ala Glu Gln Asp Arg
145                 150                 155                 160

Leu Val Ser Glu Ala Glu Val Val Arg Arg Ser Thr Glu Glu Ala His
                165                 170                 175

Arg Ile Val Asp Ala Ala His Ala Asp Ser Asn Lys Leu Arg Asn Glu
            180                 185                 190

Cys Asp Asp Tyr Val Asp Thr Lys Leu Ala Glu Phe Glu Thr Ser Leu
        195                 200                 205

Ser Thr Thr Leu Arg Ser Val Thr Ala Asp Arg Ser Ala Leu Arg Arg
    210                 215                 220

Gly Ala Gly Ala Thr Gly Arg Glu Leu Arg Asp Glu Gln Pro Ala Ala
225                 230                 235                 240

Arg Gly Glu Tyr Glu Arg Asp Tyr Glu Arg Asp Tyr Glu Arg Gly Tyr
                245                 250                 255

Glu Arg Asp Asp Arg Asp Tyr
            260
```

<210> 985
<211> 657
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(634)
<223> RXN02076

<400> 985

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tagtttccaa gaaaccattt aggctttttc acctttccgt ctagcgatcc tcatctgatg 60

tatgtagtca cgatgaggta cgagtaggat cttcctggtc atg aaa tct cca ttt   115
                                            Met Lys Ser Pro Phe
                                              1               5

att ttt gat gtc gcc gca ctc ctt cgt gga agt gcc ctt ccg gaa cac   163
Ile Phe Asp Val Ala Ala Leu Leu Arg Gly Ser Ala Leu Pro Glu His
                 10                  15                  20

ctc acc caa tca ggt cca agc ccg acc cgc att ggt ccg gaa atg atc   211
Leu Thr Gln Ser Gly Pro Ser Pro Thr Arg Ile Gly Pro Glu Met Ile
             25                  30                  35

gcg atc ccc gag ggc gga aaa gtt atc gta gaa gcc cag atc att cca   259
Ala Ile Pro Glu Gly Gly Lys Val Ile Val Glu Ala Gln Ile Ile Pro
         40                  45                  50

ctc ggt gga ggc ctg gcc gtc gaa gca gat atc gaa gcg cag ctt ctg   307
Leu Gly Gly Gly Leu Ala Val Glu Ala Asp Ile Glu Ala Gln Leu Leu
     55                  60                  65

gga cag tgc tcc cgc tgc ctc cgc gaa ctc acc cca acc aag acg ctg   355
```

```
Gly Gln Cys Ser Arg Cys Leu Arg Glu Leu Thr Pro Thr Lys Thr Leu
 70                  75                  80                  85

cac gtc tct gag gtt ttt gct gcc gat cca gac ttt gtt act ggt gaa   403
His Val Ser Glu Val Phe Ala Ala Asp Pro Asp Phe Val Thr Gly Glu
                90                  95                 100

gat gca gca gat gac gaa gat gag ctg cca atg gtt aac caa gac cag   451
Asp Ala Ala Asp Asp Glu Asp Glu Leu Pro Met Val Asn Gln Asp Gln
            105                 110                 115

att gat ctg ctt cag tct gtc att gat gaa gct ggt ctg acc ttg ccg   499
Ile Asp Leu Leu Gln Ser Val Ile Asp Glu Ala Gly Leu Thr Leu Pro
        120                 125                 130

ttt aac cct gtc tgc gaa gaa ctt ggg tac ggc gca tgc cag gat gat   547
Phe Asn Pro Val Cys Glu Glu Leu Gly Tyr Gly Ala Cys Gln Asp Asp
    135                 140                 145

gaa acg cca gct cct gac ggt gtc tct gaa gaa gta gaa gac gag gaa   595
Glu Thr Pro Ala Pro Asp Gly Val Ser Glu Glu Val Glu Asp Glu Glu
150                 155                 160                 165

aag gtc gat ccg cgc tgg gct ggt ttg gag aag ttc ctg tgagcaggaa    644
Lys Val Asp Pro Arg Trp Ala Gly Leu Glu Lys Phe Leu
                170                 175

aaagaatcgc ctc                                                   657


<210> 986
<211> 178
<212> PRT
<213> Corynebacterium glutamicum

<400> 986
Met Lys Ser Pro Phe Ile Phe Asp Val Ala Ala Leu Leu Arg Gly Ser
  1               5                  10                  15

Ala Leu Pro Glu His Leu Thr Gln Ser Gly Pro Ser Pro Thr Arg Ile
             20                  25                  30

Gly Pro Glu Met Ile Ala Ile Pro Glu Gly Gly Lys Val Ile Val Glu
         35                  40                  45

Ala Gln Ile Ile Pro Leu Gly Gly Gly Leu Ala Val Glu Ala Asp Ile
     50                  55                  60

Glu Ala Gln Leu Leu Gly Gln Cys Ser Arg Cys Leu Arg Glu Leu Thr
 65                  70                  75                  80

Pro Thr Lys Thr Leu His Val Ser Glu Val Phe Ala Ala Asp Pro Asp
                85                  90                  95

Phe Val Thr Gly Glu Asp Ala Ala Asp Asp Glu Asp Glu Leu Pro Met
            100                 105                 110

Val Asn Gln Asp Gln Ile Asp Leu Leu Gln Ser Val Ile Asp Glu Ala
        115                 120                 125

Gly Leu Thr Leu Pro Phe Asn Pro Val Cys Glu Glu Leu Gly Tyr Gly
```

```
    130                 135                 140

Ala Cys Gln Asp Asp Glu Thr Pro Ala Pro Asp Gly Val Ser Glu Glu
145                 150                 155                 160

Val Glu Asp Glu Glu Lys Val Asp Pro Arg Trp Ala Gly Leu Glu Lys
                165                 170                 175

Phe Leu
```

<210> 987
<211> 657
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(634)
<223> FRXA02076

<400> 987

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tagtttccaa gaaaccattt aggctttttc acctttccgt ctagcgatcc tcatctgatg 60

tatgtagtca cgatgaggta cgagtaggat cttcctggtc atg aaa tct cca ttt   115
                                            Met Lys Ser Pro Phe
                                              1               5

att ttt gat gtc gcc gca ctc ctt cgt gga agt gcc ctt ccg gaa cac   163
Ile Phe Asp Val Ala Ala Leu Leu Arg Gly Ser Ala Leu Pro Glu His
                10                  15                  20

ctc acc caa tca ggt cca agc ccg acc cgc att ggt ccg gaa atg atc   211
Leu Thr Gln Ser Gly Pro Ser Pro Thr Arg Ile Gly Pro Glu Met Ile
            25                  30                  35

gcg atc ccc gag ggc gga aaa gtt atc gta gaa gcc cag atc att cca   259
Ala Ile Pro Glu Gly Gly Lys Val Ile Val Glu Ala Gln Ile Ile Pro
        40                  45                  50

ctc ggt gga ggc ctg gcc gtc gaa gca gat atc gaa gcg cag ctt ctg   307
Leu Gly Gly Gly Leu Ala Val Glu Ala Asp Ile Glu Ala Gln Leu Leu
    55                  60                  65

gga cag tgc tcc cgc tgc ctc cgc gaa ctc acc cca acc aag acg ctg   355
Gly Gln Cys Ser Arg Cys Leu Arg Glu Leu Thr Pro Thr Lys Thr Leu
70                  75                  80                  85

cac gtc tct gag gtt ttt gct gcc gat cca gac ttt gtt act ggt gaa   403
His Val Ser Glu Val Phe Ala Ala Asp Pro Asp Phe Val Thr Gly Glu
                90                  95                  100

gat gca gca gat gac gaa gat gag ctg cca atg gtt aac caa gac cag   451
Asp Ala Ala Asp Asp Glu Asp Glu Leu Pro Met Val Asn Gln Asp Gln
            105                 110                 115

att gat ctg ctt cag tct gtc att gat gaa gct ggt ctg acc ttg ccg   499
Ile Asp Leu Leu Gln Ser Val Ile Asp Glu Ala Gly Leu Thr Leu Pro
        120                 125                 130
```

```
ttt aac cct gtc tgc gaa gaa ctt ggg tac ggc gca tgc cag gat gat   547
Phe Asn Pro Val Cys Glu Glu Leu Gly Tyr Gly Ala Cys Gln Asp Asp
    135                 140                 145

gaa acg cca gct cct gac ggt gtc tct gaa gaa gta gaa gac gag gaa   595
Glu Thr Pro Ala Pro Asp Gly Val Ser Glu Glu Val Glu Asp Glu Glu
150                 155                 160                 165

aag gtc gat ccg cgc tgg gct ggt ttg gag aag ttc ctg tgagcaggaa    644
Lys Val Asp Pro Arg Trp Ala Gly Leu Glu Lys Phe Leu
                170                 175

aaagaatcgc ctc                                                   657
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<210> 988
<211> 178
<212> PRT
<213> Corynebacterium glutamicum

<400> 988

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Met Lys Ser Pro Phe Ile Phe Asp Val Ala Ala Leu Leu Arg Gly Ser
  1               5                  10                  15

Ala Leu Pro Glu His Leu Thr Gln Ser Gly Pro Ser Pro Thr Arg Ile
             20                  25                  30

Gly Pro Glu Met Ile Ala Ile Pro Glu Gly Gly Lys Val Ile Val Glu
         35                  40                  45

Ala Gln Ile Ile Pro Leu Gly Gly Gly Leu Ala Val Glu Ala Asp Ile
     50                  55                  60

Glu Ala Gln Leu Leu Gly Gln Cys Ser Arg Cys Leu Arg Glu Leu Thr
 65                  70                  75                  80

Pro Thr Lys Thr Leu His Val Ser Glu Val Phe Ala Ala Asp Pro Asp
                 85                  90                  95

Phe Val Thr Gly Glu Asp Ala Ala Asp Asp Glu Asp Glu Leu Pro Met
            100                 105                 110

Val Asn Gln Asp Gln Ile Asp Leu Leu Gln Ser Val Ile Asp Glu Ala
        115                 120                 125

Gly Leu Thr Leu Pro Phe Asn Pro Val Cys Glu Glu Leu Gly Tyr Gly
    130                 135                 140

Ala Cys Gln Asp Asp Glu Thr Pro Ala Pro Asp Gly Val Ser Glu Glu
145                 150                 155                 160

Val Glu Asp Glu Glu Lys Val Asp Pro Arg Trp Ala Gly Leu Glu Lys
                165                 170                 175

Phe Leu
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<210> 989
<211> 840
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(817)
<223> RXN02094

<400> 989
ttccacctct acaccggagt tcttccaacc aacgaccaga tcattgctgc ggaggagttc 60

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tccaagtaaa tttctctccc ctatttttag gaggcaccac atg gct gaa cac aac   115
                                             Met Ala Glu His Asn
                                               1               5

gcc atc atc acg gat gca gta cat tcc gac ccc gct gtt tta gaa gac   163
Ala Ile Ile Thr Asp Ala Val His Ser Asp Pro Ala Val Leu Glu Asp
                 10                  15                  20

aac gcc ggg ttc agc gga aag tac cta atc cgt gcc ctg gac aag gca   211
Asn Ala Gly Phe Ser Gly Lys Tyr Leu Ile Arg Ala Leu Asp Lys Ala
             25                  30                  35

gct cat atg caa aca ggt gcc atc gag gga tac att tct tgg ctt cgg   259
Ala His Met Gln Thr Gly Ala Ile Glu Gly Tyr Ile Ser Trp Leu Arg
         40                  45                  50

aag cac aat cct gag aaa aca ccg gcg cag ctg cag gta ctc gtc gac   307
Lys His Asn Pro Glu Lys Thr Pro Ala Gln Leu Gln Val Leu Val Asp
     55                  60                  65

aag cat ttt atg cgc ctt gcc acc ggc tct ggc gct ggt gtg ggc atg   355
Lys His Phe Met Arg Leu Ala Thr Gly Ser Gly Ala Gly Val Gly Met
 70                  75                  80                  85

gct gcg gcc gtg cca ggc att ggc ttt gtc acg ggt gct ctt gcc gtt   403
Ala Ala Ala Val Pro Gly Ile Gly Phe Val Thr Gly Ala Leu Ala Val
                 90                  95                 100

ggt gct gaa tcg ttg gtg ttt ttg gat gct gct gcg ttt tac acc atg   451
Gly Ala Glu Ser Leu Val Phe Leu Asp Ala Ala Ala Phe Tyr Thr Met
            105                 110                 115

gca tcc gcg cac ctg cgt ggc atc gac atc cgc cat cct gaa cgc cga   499
Ala Ser Ala His Leu Arg Gly Ile Asp Ile Arg His Pro Glu Arg Arg
        120                 125                 130

cgt ggt ttg att ttg gtg gtt ctg ctg ggc acc gca ggc aaa gcc att   547
Arg Gly Leu Ile Leu Val Val Leu Leu Gly Thr Ala Gly Lys Ala Ile
    135                 140                 145

gtt gac gca ggc gtc ggt gat tta tcc aag aaa aac cac gcg ccg ggc   595
Val Asp Ala Gly Val Gly Asp Leu Ser Lys Lys Asn His Ala Pro Gly
150                 155                 160                 165

att gcg att tcc cgg ttt aat atc ggt ggc ttg atg gaa gtc aac ggc   643
Ile Ala Ile Ser Arg Phe Asn Ile Gly Gly Leu Met Glu Val Asn Gly
                170                 175                 180

cga ctg atg cgc tac gca gtg aag gaa gta agc aag cgt ttc cgt tcg   691
Arg Leu Met Arg Tyr Ala Val Lys Glu Val Ser Lys Arg Phe Arg Ser
            185                 190                 195
```

```
gca ttg att ggc aaa att ctg ccg ttt ggt atc ggt gcg gtg ctg ggc   739
Ala Leu Ile Gly Lys Ile Leu Pro Phe Gly Ile Gly Ala Val Leu Gly
        200                 205                 210

acg atg gcc aac cgc aaa att gcc aag agg act gtc gga aac gca tac   787
Thr Met Ala Asn Arg Lys Ile Ala Lys Arg Thr Val Gly Asn Ala Tyr
    215                 220                 225

gac tct ctt ggt cct ctc ccc acc cat ttt taagtactca agacccttcc     837
Asp Ser Leu Gly Pro Leu Pro Thr His Phe
230                 235

aac                                                               840
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<210> 990
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

<400> 990

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Met Ala Glu His Asn Ala Ile Ile Thr Asp Ala Val His Ser Asp Pro
  1               5                  10                  15

Ala Val Leu Glu Asp Asn Ala Gly Phe Ser Gly Lys Tyr Leu Ile Arg
             20                  25                  30

Ala Leu Asp Lys Ala Ala His Met Gln Thr Gly Ala Ile Glu Gly Tyr
         35                  40                  45

Ile Ser Trp Leu Arg Lys His Asn Pro Glu Lys Thr Pro Ala Gln Leu
     50                  55                  60

Gln Val Leu Val Asp Lys His Phe Met Arg Leu Ala Thr Gly Ser Gly
 65                  70                  75                  80

Ala Gly Val Gly Met Ala Ala Ala Val Pro Gly Ile Gly Phe Val Thr
                 85                  90                  95

Gly Ala Leu Ala Val Gly Ala Glu Ser Leu Val Phe Leu Asp Ala Ala
            100                 105                 110

Ala Phe Tyr Thr Met Ala Ser Ala His Leu Arg Gly Ile Asp Ile Arg
        115                 120                 125

His Pro Glu Arg Arg Arg Gly Leu Ile Leu Val Val Leu Leu Gly Thr
    130                 135                 140

Ala Gly Lys Ala Ile Val Asp Ala Gly Val Gly Asp Leu Ser Lys Lys
145                 150                 155                 160

Asn His Ala Pro Gly Ile Ala Ile Ser Arg Phe Asn Ile Gly Gly Leu
                165                 170                 175

Met Glu Val Asn Gly Arg Leu Met Arg Tyr Ala Val Lys Glu Val Ser
            180                 185                 190

Lys Arg Phe Arg Ser Ala Leu Ile Gly Lys Ile Leu Pro Phe Gly Ile
        195                 200                 205
```

```
Gly Ala Val Leu Gly Thr Met Ala Asn Arg Lys Ile Ala Lys Arg Thr
    210                 215                 220

Val Gly Asn Ala Tyr Asp Ser Leu Gly Pro Leu Pro Thr His Phe
225                 230                 235


<210> 991
<211> 840
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(817)
<223> FRXA02094

<400> 991
ttccacctct acaccggagt tcttccaacc aacgaccaga tcattgctgc ggaggagttc 60

tccaagtaaa tttctctccc ctatttttag gaggcaccac atg gct gaa cac aac   115
                                            Met Ala Glu His Asn
                                              1               5

gcc atc atc acg gat gca gta cat tcc gac ccc gct gtt tta gaa gac   163
Ala Ile Ile Thr Asp Ala Val His Ser Asp Pro Ala Val Leu Glu Asp
                10                  15                  20

aac gcc ggg ttc agc gga aag tac cta atc cgt gcc ctg gac aag gca   211
Asn Ala Gly Phe Ser Gly Lys Tyr Leu Ile Arg Ala Leu Asp Lys Ala
            25                  30                  35

gct cat atg caa aca ggt gcc atc gag gga tac att tct tgg ctt cgg   259
Ala His Met Gln Thr Gly Ala Ile Glu Gly Tyr Ile Ser Trp Leu Arg
        40                  45                  50

aag cac aat cct gag aaa aca ccg gcg cag ctg cag gta ctc gtc gac   307
Lys His Asn Pro Glu Lys Thr Pro Ala Gln Leu Gln Val Leu Val Asp
    55                  60                  65

aag cat ttt atg cgc ctt gcc acc ggc tct ggc gct ggt gtg ggc atg   355
Lys His Phe Met Arg Leu Ala Thr Gly Ser Gly Ala Gly Val Gly Met
70                  75                  80                  85

gct gcg gcc gtg cca ggc att ggc ttt gtc acg ggt gct ctt gcc gtt   403
Ala Ala Ala Val Pro Gly Ile Gly Phe Val Thr Gly Ala Leu Ala Val
                90                  95                  100

ggt gct gaa tcg ttg gtg ttt ttg gat gct gct gcg ttt tac acc atg   451
Gly Ala Glu Ser Leu Val Phe Leu Asp Ala Ala Ala Phe Tyr Thr Met
            105                 110                 115

gca tcc gcg cac ctg cgt ggc atc gac atc cgc cat cct gaa cgc cga   499
Ala Ser Ala His Leu Arg Gly Ile Asp Ile Arg His Pro Glu Arg Arg
        120                 125                 130

cgt ggt ttg att ttg gtg gtt ctg ctg ggc acc gca ggc aaa gcc att   547
Arg Gly Leu Ile Leu Val Val Leu Leu Gly Thr Ala Gly Lys Ala Ile
    135                 140                 145

gtt gac gca ggc gtc ggt gat tta tcc aag aaa aac cac gcg ccg ggc   595
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```
Val Asp Ala Gly Val Gly Asp Leu Ser Lys Lys Asn His Ala Pro Gly
150                 155                 160                 165

att gcg att tcc cgg ttt aat atc ggt ggc ttg atg gaa gtc aac ggc   643
Ile Ala Ile Ser Arg Phe Asn Ile Gly Gly Leu Met Glu Val Asn Gly
                170                 175                 180

cga ctg atg cgc tac gca gtg aag gaa gta agc aag cgt ttc cgt tcg   691
Arg Leu Met Arg Tyr Ala Val Lys Glu Val Ser Lys Arg Phe Arg Ser
            185                 190                 195

gca ttg att ggc aaa att ctg ccg ttt ggt atc ggt gcg gtg ctg ggc   739
Ala Leu Ile Gly Lys Ile Leu Pro Phe Gly Ile Gly Ala Val Leu Gly
        200                 205                 210

acg atg gcc aac cgc aaa att gcc aag agg act gtc gga aac gca tac   787
Thr Met Ala Asn Arg Lys Ile Ala Lys Arg Thr Val Gly Asn Ala Tyr
    215                 220                 225

gac tct ctt ggt cct ctc ccc acc cat ttt taagtactca agacccttcc     837
Asp Ser Leu Gly Pro Leu Pro Thr His Phe
230                 235

aac                                                               840


<210> 992
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

<400> 992
Met Ala Glu His Asn Ala Ile Ile Thr Asp Ala Val His Ser Asp Pro
  1               5                  10                  15

Ala Val Leu Glu Asp Asn Ala Gly Phe Ser Gly Lys Tyr Leu Ile Arg
             20                  25                  30

Ala Leu Asp Lys Ala Ala His Met Gln Thr Gly Ala Ile Glu Gly Tyr
         35                  40                  45

Ile Ser Trp Leu Arg Lys His Asn Pro Glu Lys Thr Pro Ala Gln Leu
     50                  55                  60

Gln Val Leu Val Asp Lys His Phe Met Arg Leu Ala Thr Gly Ser Gly
 65                  70                  75                  80

Ala Gly Val Gly Met Ala Ala Ala Val Pro Gly Ile Gly Phe Val Thr
                 85                  90                  95

Gly Ala Leu Ala Val Gly Ala Glu Ser Leu Val Phe Leu Asp Ala Ala
            100                 105                 110

Ala Phe Tyr Thr Met Ala Ser Ala His Leu Arg Gly Ile Asp Ile Arg
        115                 120                 125

His Pro Glu Arg Arg Arg Gly Leu Ile Leu Val Val Leu Leu Gly Thr
    130                 135                 140

Ala Gly Lys Ala Ile Val Asp Ala Gly Val Gly Asp Leu Ser Lys Lys
145                 150                 155                 160
```

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Asn His Ala Pro Gly Ile Ala Ile Ser Arg Phe Asn Ile Gly Gly Leu
               165                 170                 175

Met Glu Val Asn Gly Arg Leu Met Arg Tyr Ala Val Lys Glu Val Ser
            180                 185                 190

Lys Arg Phe Arg Ser Ala Leu Ile Gly Lys Ile Leu Pro Phe Gly Ile
        195                 200                 205

Gly Ala Val Leu Gly Thr Met Ala Asn Arg Lys Ile Ala Lys Arg Thr
    210                 215                 220

Val Gly Asn Ala Tyr Asp Ser Leu Gly Pro Leu Pro Thr His Phe
225                 230                 235


<210> 993
<211> 1245
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1222)
<223> RXN02104

<400> 993
catggattcc catttggagc cttatttaca caggccacct ggcttgtttc ccaccgcgat 60

gtgccacaat aacgccataa cagaaaggca tactgacaca atg tcc aac tcc ccc   115
                                              Met Ser Asn Ser Pro
                                                1               5

acc gac gtt tca acg agc gca cct cga att atg atc gcg cca gat tcc   163
Thr Asp Val Ser Thr Ser Ala Pro Arg Ile Met Ile Ala Pro Asp Ser
                10                  15                  20

tac aaa gga acc gct acc gca tca gaa gct gcg caa tac tta ggc gaa   211
Tyr Lys Gly Thr Ala Thr Ala Ser Glu Ala Ala Gln Tyr Leu Gly Glu
            25                  30                  35

ggc gtg ttg gaa att ttg ccc aac gcc tcc att acg ttg gca ccc atg   259
Gly Val Leu Glu Ile Leu Pro Asn Ala Ser Ile Thr Leu Ala Pro Met
        40                  45                  50

gcc gac ggt ggc gaa gga aca tcc tca gtt ttc ggc ggg cag gtc ata   307
Ala Asp Gly Gly Glu Gly Thr Ser Ser Val Phe Gly Gly Gln Val Ile
    55                  60                  65

aca tta ccc acg aca aat gcc gcg gga cgc ctc acc gaa gcc agc tac   355
Thr Leu Pro Thr Thr Asn Ala Ala Gly Arg Leu Thr Glu Ala Ser Tyr
70                  75                  80                  85

acc tta gat tcc gaa aca aac act gcc tac att gac atc gcc gca gcc   403
Thr Leu Asp Ser Glu Thr Asn Thr Ala Tyr Ile Asp Ile Ala Ala Ala
                90                  95                  100

tcc ggt ttg ccc gcc gtt gca gac gat cta gtc ccc acc acc ggc gat   451
Ser Gly Leu Pro Ala Val Ala Asp Asp Leu Val Pro Thr Thr Gly Asp
            105                 110                 115
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acc tac ggc acc ggc gtt ttg atc gca gac gcg gtc acc cgt ggc gca   499
Thr Tyr Gly Thr Gly Val Leu Ile Ala Asp Ala Val Thr Arg Gly Ala
        120                 125                 130

act cgc att gct tta ggc ctt ggc gga tca gcc aca act gac gcc ggc   547
Thr Arg Ile Ala Leu Gly Leu Gly Gly Ser Ala Thr Thr Asp Ala Gly
    135                 140                 145

tca gga att ctc atc gcc ctc ggc gcc gtc cca cgc aac aaa gag ggc   595
Ser Gly Ile Leu Ile Ala Leu Gly Ala Val Pro Arg Asn Lys Glu Gly
150                 155                 160                 165

tac gca cta cga acc ggt ggc gcc gac ctc atc aac ctc gat tac atc   643
Tyr Ala Leu Arg Thr Gly Gly Ala Asp Leu Ile Asn Leu Asp Tyr Ile
                170                 175                 180

gat acc gcc gaa ctc aac atc ccc gca gcc gcc gtc gaa tgg atc ctg   691
Asp Thr Ala Glu Leu Asn Ile Pro Ala Ala Ala Val Glu Trp Ile Leu
            185                 190                 195

ctc acc gat gtc gac gcc ccc gcc acc ggc ccg cag ggc gcg gcc acc   739
Leu Thr Asp Val Asp Ala Pro Ala Thr Gly Pro Gln Gly Ala Ala Thr
        200                 205                 210

gta ttc ggg ccc caa aaa ggt gcc acc gaa aaa gac att tcg ctt ctc   787
Val Phe Gly Pro Gln Lys Gly Ala Thr Glu Lys Asp Ile Ser Leu Leu
    215                 220                 225

gac gcc gcc ctc cac cac gcc tgc gcc caa ctg gaa gtt gat ggc aca   835
Asp Ala Ala Leu His His Ala Cys Ala Gln Leu Glu Val Asp Gly Thr
230                 235                 240                 245

aag cca ggt atg ggc gca gcc ggg ggc att gca atc gga ctg acg tgg   883
Lys Pro Gly Met Gly Ala Ala Gly Gly Ile Ala Ile Gly Leu Thr Trp
                250                 255                 260

ctg tcc acc ctc atg cac ggc aac gac caa cag atc cat atc ctc ccc   931
Leu Ser Thr Leu Met His Gly Asn Asp Gln Gln Ile His Ile Leu Pro
            265                 270                 275

ggc gcg cca ctg att gcc cgc tcc aac gga atc gag gat gcg ctg cca   979
Gly Ala Pro Leu Ile Ala Arg Ser Asn Gly Ile Glu Asp Ala Leu Pro
        280                 285                 290

gaa act gac ttg ttg atc acc ggt gaa ggc cga cta gat tcc caa tcg   1027
Glu Thr Asp Leu Leu Ile Thr Gly Glu Gly Arg Leu Asp Ser Gln Ser
    295                 300                 305

ttc acc gga aag gtt gtg ggc acc ctc cac ggt tta gct aaa gcc cac   1075
Phe Thr Gly Lys Val Val Gly Thr Leu His Gly Leu Ala Lys Ala His
310                 315                 320                 325

gat gtg gat ctc gct gtt gcg gcc ggc atc gtg gaa ggc ggt att ccc   1123
Asp Val Asp Leu Ala Val Ala Ala Gly Ile Val Glu Gly Gly Ile Pro
                330                 335                 340

gat gat ttc cta gcg gta gaa atg att aaa tcc tcc gac gtt gca gca   1171
Asp Asp Phe Leu Ala Val Glu Met Ile Lys Ser Ser Asp Val Ala Ala
            345                 350                 355
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caa tta cgt gat gca ggc cga agg atc gct caa gaa tac gta gct caa 1219
Gln Leu Arg Asp Ala Gly Arg Arg Ile Ala Gln Glu Tyr Val Ala Gln
360 365 370

aac tagcgaagga tctccacagt cca 1245
Asn

<210> 994
<211> 374
<212> PRT
<213> Corynebacterium glutamicum

<400> 994
Met Ser Asn Ser Pro Thr Asp Val Ser Thr Ser Ala Pro Arg Ile Met
1 5 10 15

Ile Ala Pro Asp Ser Tyr Lys Gly Thr Ala Thr Ala Ser Glu Ala Ala
20 25 30

Gln Tyr Leu Gly Glu Gly Val Leu Glu Ile Leu Pro Asn Ala Ser Ile
35 40 45

Thr Leu Ala Pro Met Ala Asp Gly Gly Glu Gly Thr Ser Ser Val Phe
50 55 60

Gly Gly Gln Val Ile Thr Leu Pro Thr Thr Asn Ala Ala Gly Arg Leu
65 70 75 80

Thr Glu Ala Ser Tyr Thr Leu Asp Ser Glu Thr Asn Thr Ala Tyr Ile
85 90 95

Asp Ile Ala Ala Ala Ser Gly Leu Pro Ala Val Ala Asp Asp Leu Val
100 105 110

Pro Thr Thr Gly Asp Thr Tyr Gly Thr Gly Val Leu Ile Ala Asp Ala
115 120 125

Val Thr Arg Gly Ala Thr Arg Ile Ala Leu Gly Leu Gly Gly Ser Ala
130 135 140

Thr Thr Asp Ala Gly Ser Gly Ile Leu Ile Ala Leu Gly Ala Val Pro
145 150 155 160

Arg Asn Lys Glu Gly Tyr Ala Leu Arg Thr Gly Gly Ala Asp Leu Ile
165 170 175

Asn Leu Asp Tyr Ile Asp Thr Ala Glu Leu Asn Ile Pro Ala Ala Ala
180 185 190

Val Glu Trp Ile Leu Leu Thr Asp Val Asp Ala Pro Ala Thr Gly Pro
195 200 205

Gln Gly Ala Ala Thr Val Phe Gly Pro Gln Lys Gly Ala Thr Glu Lys
210 215 220

Asp Ile Ser Leu Leu Asp Ala Ala Leu His His Ala Cys Ala Gln Leu
225 230 235 240

Glu Val Asp Gly Thr Lys Pro Gly Met Gly Ala Ala Gly Gly Ile Ala

```
                245                 250                 255

Ile Gly Leu Thr Trp Leu Ser Thr Leu Met His Gly Asn Asp Gln Gln
            260                 265                 270

Ile His Ile Leu Pro Gly Ala Pro Leu Ile Ala Arg Ser Asn Gly Ile
        275                 280                 285

Glu Asp Ala Leu Pro Glu Thr Asp Leu Leu Ile Thr Gly Glu Gly Arg
    290                 295                 300

Leu Asp Ser Gln Ser Phe Thr Gly Lys Val Val Gly Thr Leu His Gly
305                 310                 315                 320

Leu Ala Lys Ala His Asp Val Asp Leu Ala Val Ala Ala Gly Ile Val
                325                 330                 335

Glu Gly Gly Ile Pro Asp Asp Phe Leu Ala Val Glu Met Ile Lys Ser
            340                 345                 350

Ser Asp Val Ala Ala Gln Leu Arg Asp Ala Gly Arg Arg Ile Ala Gln
        355                 360                 365

Glu Tyr Val Ala Gln Asn
    370


<210> 995
<211> 443
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(420)
<223> FRXA02104

<400> 995
cac gcc tgc gcc caa ctg gaa gtt gat ggc aca aag cca ggt atg ggc   48
His Ala Cys Ala Gln Leu Glu Val Asp Gly Thr Lys Pro Gly Met Gly
  1               5                  10                  15

gca gcc ggg ggc att gca atc gga ctg acg tgg ctg tcc acc ctc atg   96
Ala Ala Gly Gly Ile Ala Ile Gly Leu Thr Trp Leu Ser Thr Leu Met
             20                  25                  30

cac ggc aac gac caa cag atc cat atc ctc ccc ggc gcg cca ctg att   144
His Gly Asn Asp Gln Gln Ile His Ile Leu Pro Gly Ala Pro Leu Ile
         35                  40                  45

gcc cgc tcc aac gga atc gag gat gcg ctg cca gaa act gac ttg ttg   192
Ala Arg Ser Asn Gly Ile Glu Asp Ala Leu Pro Glu Thr Asp Leu Leu
     50                  55                  60

atc acc ggt gaa ggc cga cta gat tcc caa tcg ttc acc gga aag gtt   240
Ile Thr Gly Glu Gly Arg Leu Asp Ser Gln Ser Phe Thr Gly Lys Val
 65                  70                  75                  80

gtg ggc acc ctc cac ggt tta gct aaa gcc cac gat gtg gat ctc gct   288
Val Gly Thr Leu His Gly Leu Ala Lys Ala His Asp Val Asp Leu Ala
                 85                  90                  95
```

```
gtt gcg gcc ggc atc gtg gaa ggc ggt att ccc gat gat ttc cta gcg   336
Val Ala Ala Gly Ile Val Glu Gly Gly Ile Pro Asp Asp Phe Leu Ala
            100                 105                 110

gta gaa atg att aaa tcc tcc gac gtt gca gca caa tta cgt gat gca   384
Val Glu Met Ile Lys Ser Ser Asp Val Ala Ala Gln Leu Arg Asp Ala
        115                 120                 125

ggc cga agg atc gct caa gaa tac gta gct caa aac tagcgaagga        430
Gly Arg Arg Ile Ala Gln Glu Tyr Val Ala Gln Asn
    130                 135                 140

tctccacagt cca                                                   443
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<210> 996
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

<400> 996

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His Ala Cys Ala Gln Leu Glu Val Asp Gly Thr Lys Pro Gly Met Gly
  1               5                  10                  15

Ala Ala Gly Gly Ile Ala Ile Gly Leu Thr Trp Leu Ser Thr Leu Met
             20                  25                  30

His Gly Asn Asp Gln Gln Ile His Ile Leu Pro Gly Ala Pro Leu Ile
         35                  40                  45

Ala Arg Ser Asn Gly Ile Glu Asp Ala Leu Pro Glu Thr Asp Leu Leu
     50                  55                  60

Ile Thr Gly Glu Gly Arg Leu Asp Ser Gln Ser Phe Thr Gly Lys Val
 65                  70                  75                  80

Val Gly Thr Leu His Gly Leu Ala Lys Ala His Asp Val Asp Leu Ala
                 85                  90                  95

Val Ala Ala Gly Ile Val Glu Gly Gly Ile Pro Asp Asp Phe Leu Ala
            100                 105                 110

Val Glu Met Ile Lys Ser Ser Asp Val Ala Ala Gln Leu Arg Asp Ala
        115                 120                 125

Gly Arg Arg Ile Ala Gln Glu Tyr Val Ala Gln Asn
    130                 135                 140
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<210> 997
<211> 553
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(553)
<223> FRXA02071

<400> 997

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catggattcc catttggagc cttatttaca caggccacct ggcttgtttc ccaccgcgat 60

gtgccacaat aacgccataa cagaaaggca tactgacaca atg tcc aac tcc ccc   115
                                            Met Ser Asn Ser Pro
                                              1               5

acc gac gtt tca acg agc gca cct cga att atg atc gcg cca gat tcc   163
Thr Asp Val Ser Thr Ser Ala Pro Arg Ile Met Ile Ala Pro Asp Ser
                 10                  15                  20

tac aaa gga acc gct acc gca tca gaa gct gcg caa tac tta ggc gaa   211
Tyr Lys Gly Thr Ala Thr Ala Ser Glu Ala Ala Gln Tyr Leu Gly Glu
             25                  30                  35

ggc gtg ttg gaa att ttg ccc aac gcc tcc att acg ttg gca ccc atg   259
Gly Val Leu Glu Ile Leu Pro Asn Ala Ser Ile Thr Leu Ala Pro Met
         40                  45                  50

gcc gac ggt ggc gaa gga aca tcc tca gtt ttc ggc ggg cag gtc ata   307
Ala Asp Gly Gly Glu Gly Thr Ser Ser Val Phe Gly Gly Gln Val Ile
     55                  60                  65

aca tta ccc acg aca aat gcc gcg gga cgc ctc acc gaa gcc agc tac   355
Thr Leu Pro Thr Thr Asn Ala Ala Gly Arg Leu Thr Glu Ala Ser Tyr
 70                  75                  80                  85

acc tta gat tcc gaa aca aac act gcc tac att gac atc gcc gca gcc   403
Thr Leu Asp Ser Glu Thr Asn Thr Ala Tyr Ile Asp Ile Ala Ala Ala
                 90                  95                 100

tcc ggt ttg ccc gcc gtt gca gac gat cta gtc ccc acc acc ggc gat   451
Ser Gly Leu Pro Ala Val Ala Asp Asp Leu Val Pro Thr Thr Gly Asp
             105                 110                 115

acc tac ggc acc ggc gtt ttg atc gca gac gcg gtc acc cgt ggc gca   499
Thr Tyr Gly Thr Gly Val Leu Ile Ala Asp Ala Val Thr Arg Gly Ala
         120                 125                 130

act cgc att gct tta ggc ctt ggc gga tca gcc aca act gac gcc ggc   547
Thr Arg Ile Ala Leu Gly Leu Gly Gly Ser Ala Thr Thr Asp Ala Gly
     135                 140                 145

tca gga                                                          553
Ser Gly
150


<210> 998
<211> 151
<212> PRT
<213> Corynebacterium glutamicum

<400> 998
Met Ser Asn Ser Pro Thr Asp Val Ser Thr Ser Ala Pro Arg Ile Met
  1               5                  10                  15

Ile Ala Pro Asp Ser Tyr Lys Gly Thr Ala Thr Ala Ser Glu Ala Ala
             20                  25                  30

Gln Tyr Leu Gly Glu Gly Val Leu Glu Ile Leu Pro Asn Ala Ser Ile
         35                  40                  45
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```
Thr Leu Ala Pro Met Ala Asp Gly Gly Glu Gly Thr Ser Ser Val Phe
     50                  55                  60

Gly Gly Gln Val Ile Thr Leu Pro Thr Thr Asn Ala Ala Gly Arg Leu
 65                  70                  75                  80

Thr Glu Ala Ser Tyr Thr Leu Asp Ser Glu Thr Asn Thr Ala Tyr Ile
                 85                  90                  95

Asp Ile Ala Ala Ala Ser Gly Leu Pro Ala Val Ala Asp Asp Leu Val
            100                 105                 110

Pro Thr Thr Gly Asp Thr Tyr Gly Thr Gly Val Leu Ile Ala Asp Ala
        115                 120                 125

Val Thr Arg Gly Ala Thr Arg Ile Ala Leu Gly Leu Gly Gly Ser Ala
    130                 135                 140

Thr Thr Asp Ala Gly Ser Gly
145                 150
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Sequence Listing

<210> 999
<211> 465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(442)
<223> RXN02107

<400> 999
aagaagtaga gctcagcgat gaagatttcg cggcaggcca cgacctagta aaaaccaaat 60

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acgccaccga ggagtggact aagcgagttc aatagtttct atg gat ctg cac aag   115
                                               Met Asp Leu His Lys
                                                 1               5

gta gct gca gcg cac gcg gcg act ctt ccc ctg agc acc aaa gag ttt   163
Val Ala Ala Ala His Ala Ala Thr Leu Pro Leu Ser Thr Lys Glu Phe
                10                  15                  20

cct ttc gga ccc gag cac gaa gtg tac aaa gtg cgg ggc aag gta ttt   211
Pro Phe Gly Pro Glu His Glu Val Tyr Lys Val Arg Gly Lys Val Phe
            25                  30                  35

ttg ctg ctc acg ata cta aat gat gag ccg att atc acg ctg aaa tca   259
Leu Leu Leu Thr Ile Leu Asn Asp Glu Pro Ile Ile Thr Leu Lys Ser
        40                  45                  50

gac ccc gag att ggc gct tca cta cgc agt ggc ttc ccc acc atc cag   307
Asp Pro Glu Ile Gly Ala Ser Leu Arg Ser Gly Phe Pro Thr Ile Gln
    55                  60                  65

gct gga tat cac atg aac aaa gtg cac tgg ctg agc att agc gat ggt   355
Ala Gly Tyr His Met Asn Lys Val His Trp Leu Ser Ile Ser Asp Gly
70                  75                  80                  85

gaa cgg atc acg aaa gac ttc atc gaa ggt ctc gtg gaa gag tcc tat   403
```

```
Glu Arg Ile Thr Lys Asp Phe Ile Glu Gly Leu Val Glu Glu Ser Tyr
                 90                  95                 100

gaa ctg gta att tcc acc ttg ccg aag tat aaa agg cct taacttggtt    452
Glu Leu Val Ile Ser Thr Leu Pro Lys Tyr Lys Arg Pro
            105                 110

gcttgcgggt ggc                                                   465


<210> 1000
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 1000
Met Asp Leu His Lys Val Ala Ala Ala His Ala Ala Thr Leu Pro Leu
  1               5                  10                  15

Ser Thr Lys Glu Phe Pro Phe Gly Pro Glu His Glu Val Tyr Lys Val
             20                  25                  30

Arg Gly Lys Val Phe Leu Leu Leu Thr Ile Leu Asn Asp Glu Pro Ile
         35                  40                  45

Ile Thr Leu Lys Ser Asp Pro Glu Ile Gly Ala Ser Leu Arg Ser Gly
     50                  55                  60

Phe Pro Thr Ile Gln Ala Gly Tyr His Met Asn Lys Val His Trp Leu
 65                  70                  75                  80

Ser Ile Ser Asp Gly Glu Arg Ile Thr Lys Asp Phe Ile Glu Gly Leu
                 85                  90                  95

Val Glu Glu Ser Tyr Glu Leu Val Ile Ser Thr Leu Pro Lys Tyr Lys
            100                 105                 110

Arg Pro


<210> 1001
<211> 465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(442)
<223> FRXA02107

<400> 1001
aagaagtaga gctcagcgat gaagatttcg cggcaggcca cgacctagta aaaaccaaat 60

acgccaccga ggagtggact aagcgagttc aatagtttct atg gat ctg cac aag   115
                                               Met Asp Leu His Lys
                                                 1               5

gta gct gca gcg cac gcg gcg act ctt ccc ctg agc acc aaa gag ttt   163
Val Ala Ala Ala His Ala Ala Thr Leu Pro Leu Ser Thr Lys Glu Phe
                 10                  15                  20
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```
cct ttc gga ccc gag cac gaa gtg tac aaa gtg cgg ggc aag gta ttt   211
Pro Phe Gly Pro Glu His Glu Val Tyr Lys Val Arg Gly Lys Val Phe
            25                  30                  35

ttg ctg ctc acg ata cta aat gat gag ccg att atc acg ctg aaa tca   259
Leu Leu Leu Thr Ile Leu Asn Asp Glu Pro Ile Ile Thr Leu Lys Ser
        40                  45                  50

gac ccc gag att ggc gct tca cta cgc agt ggc ttc ccc acc atc cag   307
Asp Pro Glu Ile Gly Ala Ser Leu Arg Ser Gly Phe Pro Thr Ile Gln
    55                  60                  65

gct gga tat cac atg aac aaa gtg cac tgg ctg agc att agc gat ggt   355
Ala Gly Tyr His Met Asn Lys Val His Trp Leu Ser Ile Ser Asp Gly
70                  75                  80                  85

gaa cgg atc acg aaa gac ttc atc gaa ggt ctc gtg gaa gag tcc tat   403
Glu Arg Ile Thr Lys Asp Phe Ile Glu Gly Leu Val Glu Glu Ser Tyr
                90                  95                  100

gaa ctg gta att tcc acc ttg ccg aag tat aaa agg cct taacttggtt    452
Glu Leu Val Ile Ser Thr Leu Pro Lys Tyr Lys Arg Pro
            105                 110

gcttgcgggt ggc                                                   465


<210> 1002
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 1002
Met Asp Leu His Lys Val Ala Ala Ala His Ala Ala Thr Leu Pro Leu
  1               5                  10                  15

Ser Thr Lys Glu Phe Pro Phe Gly Pro Glu His Glu Val Tyr Lys Val
            20                  25                  30

Arg Gly Lys Val Phe Leu Leu Leu Thr Ile Leu Asn Asp Glu Pro Ile
        35                  40                  45

Ile Thr Leu Lys Ser Asp Pro Glu Ile Gly Ala Ser Leu Arg Ser Gly
    50                  55                  60

Phe Pro Thr Ile Gln Ala Gly Tyr His Met Asn Lys Val His Trp Leu
65                  70                  75                  80

Ser Ile Ser Asp Gly Glu Arg Ile Thr Lys Asp Phe Ile Glu Gly Leu
                85                  90                  95

Val Glu Glu Ser Tyr Glu Leu Val Ile Ser Thr Leu Pro Lys Tyr Lys
            100                 105                 110

Arg Pro


<210> 1003
<211> 732
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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(709)
<223> RXN02108

<400> 1003
aagacttcat cgaaggtctc gtggaagagt cctatgaact ggtaatttcc accttgccga 60

agtataaaag gccttaactt ggttgcttgc gggtggcaag atg ggt gat atg aaa 115
Met Gly Asp Met Lys
1 5

att acc cgc cac atc cat gca tgc gtt gag atc tca cag gga aac gat 163
Ile Thr Arg His Ile His Ala Cys Val Glu Ile Ser Gln Gly Asn Asp
10 15 20

cga atc att att gat ccc ggt act ttt ggc gcc cca gat tta tgt ggc 211
Arg Ile Ile Ile Asp Pro Gly Thr Phe Gly Ala Pro Asp Leu Cys Gly
25 30 35

gcg acc atc ctg gtc acc cac aat cat gcc gat cac gtt gat ccc gag 259
Ala Thr Ile Leu Val Thr His Asn His Ala Asp His Val Asp Pro Glu
40 45 50

ttg ctc aag ccc ggc atg acg att tac gcg cct cga tca gta gca cat 307
Leu Leu Lys Pro Gly Met Thr Ile Tyr Ala Pro Arg Ser Val Ala His
55 60 65

tca att cca gta gaa tgc cac atc gtg gaa cac ggc cga aac ttt acc 355
Ser Ile Pro Val Glu Cys His Ile Val Glu His Gly Arg Asn Phe Thr
70 75 80 85

gtt ggg tcc cta tcc gtt gag gtt ctt ggt tct gaa cat gcg atg ctc 403
Val Gly Ser Leu Ser Val Glu Val Leu Gly Ser Glu His Ala Met Leu
90 95 100

acc cat tcc atg ccg atc gcg gaa aac gtt gga tac tta atc aac ggc 451
Thr His Ser Met Pro Ile Ala Glu Asn Val Gly Tyr Leu Ile Asn Gly
105 110 115

cga gtg ctc cac ccc ggc gat acc ttc caa ccc att aaa gat gtc gaa 499
Arg Val Leu His Pro Gly Asp Thr Phe Gln Pro Ile Lys Asp Val Glu
120 125 130

ctc gcc ctg gtt cct gtc aac ggc ccc tgg gtg aaa atg ctg gat gtg 547
Leu Ala Leu Val Pro Val Asn Gly Pro Trp Val Lys Met Leu Asp Val
135 140 145

gaa ggc tat ttg aag aaa ttt cca cca aag cgt ttc atc ggc att cac 595
Glu Gly Tyr Leu Lys Lys Phe Pro Pro Lys Arg Phe Ile Gly Ile His
150 155 160 165

gat ggc att gtt aat gat cgc ggt ttg gcg atc aac aag aag ttc tta 643
Asp Gly Ile Val Asn Asp Arg Gly Leu Ala Ile Asn Lys Lys Phe Leu
170 175 180

acg cat ctt ggt gaa acc tat ggc tcg gaa tac tcg ccg ctt gaa gag 691
Thr His Leu Gly Glu Thr Tyr Gly Ser Glu Tyr Ser Pro Leu Glu Glu

185 190 195

gga gag tcg ttg gaa att tagattcttg gtttagattc ttg 732
Gly Glu Ser Leu Glu Ile
200

<210> 1004
<211> 203
<212> PRT
<213> Corynebacterium glutamicum

<400> 1004
Met Gly Asp Met Lys Ile Thr Arg His Ile His Ala Cys Val Glu Ile
1 5 10 15

Ser Gln Gly Asn Asp Arg Ile Ile Ile Asp Pro Gly Thr Phe Gly Ala
20 25 30

Pro Asp Leu Cys Gly Ala Thr Ile Leu Val Thr His Asn His Ala Asp
35 40 45

His Val Asp Pro Glu Leu Leu Lys Pro Gly Met Thr Ile Tyr Ala Pro
50 55 60

Arg Ser Val Ala His Ser Ile Pro Val Glu Cys His Ile Val Glu His
65 70 75 80

Gly Arg Asn Phe Thr Val Gly Ser Leu Ser Val Glu Val Leu Gly Ser
85 90 95

Glu His Ala Met Leu Thr His Ser Met Pro Ile Ala Glu Asn Val Gly
100 105 110

Tyr Leu Ile Asn Gly Arg Val Leu His Pro Gly Asp Thr Phe Gln Pro
115 120 125

Ile Lys Asp Val Glu Leu Ala Leu Val Pro Val Asn Gly Pro Trp Val
130 135 140

Lys Met Leu Asp Val Glu Gly Tyr Leu Lys Lys Phe Pro Pro Lys Arg
145 150 155 160

Phe Ile Gly Ile His Asp Gly Ile Val Asn Asp Arg Gly Leu Ala Ile
165 170 175

Asn Lys Lys Phe Leu Thr His Leu Gly Glu Thr Tyr Gly Ser Glu Tyr
180 185 190

Ser Pro Leu Glu Glu Gly Glu Ser Leu Glu Ile
195 200

<210> 1005
<211> 558
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(535)

<223> FRXA02108

<400> 1005
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tcatgccgat cacgttgatc ccgagttgct caagcccggc atg acg att tac gcg 115
Met Thr Ile Tyr Ala
1 5

cct cga tca gta gca cat tca att cca gta gaa tgc cac atc gtg gaa 163
Pro Arg Ser Val Ala His Ser Ile Pro Val Glu Cys His Ile Val Glu
10 15 20

cac ggc cga aac ttt acc gtt ggg tcc cta tcc gtt gag gtt ctt ggt 211
His Gly Arg Asn Phe Thr Val Gly Ser Leu Ser Val Glu Val Leu Gly
25 30 35

tct gaa cat gcg atg ctc acc cat tcc atg ccg atc gcg gaa aac gtt 259
Ser Glu His Ala Met Leu Thr His Ser Met Pro Ile Ala Glu Asn Val
40 45 50

gga tac tta atc aac ggc cga gtg ctc cac ccc ggc gat acc ttc caa 307
Gly Tyr Leu Ile Asn Gly Arg Val Leu His Pro Gly Asp Thr Phe Gln
55 60 65

ccc att aaa gat gtc gaa ctc gcc ctg gtt cct gtc aac ggc ccc tgg 355
Pro Ile Lys Asp Val Glu Leu Ala Leu Val Pro Val Asn Gly Pro Trp
70 75 80 85

gtg aaa atg ctg gat gtg gaa ggc tat ttg aag aaa ttt cca cca aag 403
Val Lys Met Leu Asp Val Glu Gly Tyr Leu Lys Lys Phe Pro Pro Lys
90 95 100

cgt ttc atc ggc att cac gat ggc att gtt aat gat cgc ggt ttg gcg 451
Arg Phe Ile Gly Ile His Asp Gly Ile Val Asn Asp Arg Gly Leu Ala
105 110 115

atc aac aag aag ttc tta acg cat ctt ggt gaa acc tat ggc tcg gaa 499
Ile Asn Lys Lys Phe Leu Thr His Leu Gly Glu Thr Tyr Gly Ser Glu
120 125 130

tac tcg ccg ctt gaa gag gga gag tcg ttg gaa att tagattcttg 545
Tyr Ser Pro Leu Glu Glu Gly Glu Ser Leu Glu Ile
135 140 145

gtttagattc ttg 558

<210> 1006
<211> 145
<212> PRT
<213> Corynebacterium glutamicum

<400> 1006
Met Thr Ile Tyr Ala Pro Arg Ser Val Ala His Ser Ile Pro Val Glu
1 5 10 15

Cys His Ile Val Glu His Gly Arg Asn Phe Thr Val Gly Ser Leu Ser
20 25 30

Val Glu Val Leu Gly Ser Glu His Ala Met Leu Thr His Ser Met Pro

```
         35                  40                  45

Ile Ala Glu Asn Val Gly Tyr Leu Ile Asn Gly Arg Val Leu His Pro
     50                  55                  60

Gly Asp Thr Phe Gln Pro Ile Lys Asp Val Glu Leu Ala Leu Val Pro
 65                  70                  75                  80

Val Asn Gly Pro Trp Val Lys Met Leu Asp Val Glu Gly Tyr Leu Lys
                 85                  90                  95

Lys Phe Pro Pro Lys Arg Phe Ile Gly Ile His Asp Gly Ile Val Asn
            100                 105                 110

Asp Arg Gly Leu Ala Ile Asn Lys Lys Phe Leu Thr His Leu Gly Glu
        115                 120                 125

Thr Tyr Gly Ser Glu Tyr Ser Pro Leu Glu Glu Gly Glu Ser Leu Glu
    130                 135                 140

Ile
145
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<210> 1007
<211> 509
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(486)
<223> RXN02114

<400> 1007

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tcc atc ggc tac gcc tgg acc acc gca ttt cac gca ctc aca cca ggc   48
Ser Ile Gly Tyr Ala Trp Thr Thr Ala Phe His Ala Leu Thr Pro Gly
  1               5                  10                  15

ctt ggc ggc atc gcc att ggt att tgg ctg ctc ggt ggt gtg ctc ggt   96
Leu Gly Gly Ile Ala Ile Gly Ile Trp Leu Leu Gly Gly Val Leu Gly
             20                  25                  30

ggg ttg gtt atc cgc aag ccg ggt gcc gca att ttc gtt gaa gta gtg   144
Gly Leu Val Ile Arg Lys Pro Gly Ala Ala Ile Phe Val Glu Val Val
         35                  40                  45

gcc gca tgt gtc tct gca gcg ctt gct tca cag ttt ggt atc tcc acc   192
Ala Ala Cys Val Ser Ala Ala Leu Ala Ser Gln Phe Gly Ile Ser Thr
     50                  55                  60

att tac tcc ggc ttg gcg cag gga atc ggc gct gaa atc atc ttc gcg   240
Ile Tyr Ser Gly Leu Ala Gln Gly Ile Gly Ala Glu Ile Ile Phe Ala
 65                  70                  75                  80

ctg ttc ctc tac cgt cgc tac agc ctg ccc acc acc atg ctt gca ggt   288
Leu Phe Leu Tyr Arg Arg Tyr Ser Leu Pro Thr Thr Met Leu Ala Gly
                 85                  90                  95

atg ggc gca ggt ggc ggc gca att ttc ctg gaa atg ttc ttc tac gga   336
Met Gly Ala Gly Gly Gly Ala Ile Phe Leu Glu Met Phe Phe Tyr Gly
```

```
            100                 105                 110

aac ctc gca aag acg atg tcc ttc aac atc atc tat tcc acc act gtc   384
Asn Leu Ala Lys Thr Met Ser Phe Asn Ile Ile Tyr Ser Thr Thr Val
        115                 120                 125

ctt att tcc ggt gcg atc ctt gcc ggc ctg ctc agc tgg tac ctg gtc   432
Leu Ile Ser Gly Ala Ile Leu Ala Gly Leu Leu Ser Trp Tyr Leu Val
    130                 135                 140

cgc gcg ttg gcg agg act ggt gca ctt gat cgt ttc gcc gct ggc cgc   480
Arg Ala Leu Ala Arg Thr Gly Ala Leu Asp Arg Phe Ala Ala Gly Arg
145                 150                 155                 160

gag gta taaatgacca ccgcacttgg aac                                 509
Glu Val
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<210> 1008
<211> 162
<212> PRT
<213> Corynebacterium glutamicum

<400> 1008

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Ser Ile Gly Tyr Ala Trp Thr Thr Ala Phe His Ala Leu Thr Pro Gly
  1               5                  10                  15

Leu Gly Gly Ile Ala Ile Gly Ile Trp Leu Leu Gly Gly Val Leu Gly
             20                  25                  30

Gly Leu Val Ile Arg Lys Pro Gly Ala Ala Ile Phe Val Glu Val Val
         35                  40                  45

Ala Ala Cys Val Ser Ala Ala Leu Ala Ser Gln Phe Gly Ile Ser Thr
     50                  55                  60

Ile Tyr Ser Gly Leu Ala Gln Gly Ile Gly Ala Glu Ile Ile Phe Ala
 65                  70                  75                  80

Leu Phe Leu Tyr Arg Arg Tyr Ser Leu Pro Thr Thr Met Leu Ala Gly
                 85                  90                  95

Met Gly Ala Gly Gly Gly Ala Ile Phe Leu Glu Met Phe Phe Tyr Gly
            100                 105                 110

Asn Leu Ala Lys Thr Met Ser Phe Asn Ile Ile Tyr Ser Thr Thr Val
        115                 120                 125

Leu Ile Ser Gly Ala Ile Leu Ala Gly Leu Leu Ser Trp Tyr Leu Val
    130                 135                 140

Arg Ala Leu Ala Arg Thr Gly Ala Leu Asp Arg Phe Ala Ala Gly Arg
145                 150                 155                 160

Glu Val
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<210> 1009
<211> 509

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(486)
<223> FRXA02114

<400> 1009

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tcc atc ggc tac gcc tgg acc acc gca ttt cac gca ctc aca cca ggc   48
Ser Ile Gly Tyr Ala Trp Thr Thr Ala Phe His Ala Leu Thr Pro Gly
  1               5                  10                  15

ctt ggc ggc atc gcc att ggt att tgg ctg ctc ggt ggt gtg ctc ggt   96
Leu Gly Gly Ile Ala Ile Gly Ile Trp Leu Leu Gly Gly Val Leu Gly
             20                  25                  30

ggg ttg gtt atc cgc aag ccg ggt gcc gca att ttc gtt gaa gta gtg   144
Gly Leu Val Ile Arg Lys Pro Gly Ala Ala Ile Phe Val Glu Val Val
         35                  40                  45

gcc gca tgt gtc tct gca gcg ctt gct tca cag ttt ggt atc tcc acc   192
Ala Ala Cys Val Ser Ala Ala Leu Ala Ser Gln Phe Gly Ile Ser Thr
     50                  55                  60

att tac tcc ggc ttg gcg cag gga atc ggc gct gaa atc atc ttc gcg   240
Ile Tyr Ser Gly Leu Ala Gln Gly Ile Gly Ala Glu Ile Ile Phe Ala
 65                  70                  75                  80

ctg ttc ctc tac cgt cgc tac agc ctg ccc acc acc atg ctt gca ggt   288
Leu Phe Leu Tyr Arg Arg Tyr Ser Leu Pro Thr Thr Met Leu Ala Gly
                 85                  90                  95

atg ggc gca ggt ggc ggc gca att ttc ctg gaa atg ttc ttc tac gga   336
Met Gly Ala Gly Gly Gly Ala Ile Phe Leu Glu Met Phe Phe Tyr Gly
            100                 105                 110

aac ctc gca aag acg atg tcc ttc aac atc atc tat tcc acc act gtc   384
Asn Leu Ala Lys Thr Met Ser Phe Asn Ile Ile Tyr Ser Thr Thr Val
        115                 120                 125

ctt att tcc ggt gcg atc ctt gcc ggc ctg ctc agc tgg tac ctg gtc   432
Leu Ile Ser Gly Ala Ile Leu Ala Gly Leu Leu Ser Trp Tyr Leu Val
    130                 135                 140

cgc gcg ttg gcg agg act ggt gca ctt gat cgt ttc gcc gct ggc cgc   480
Arg Ala Leu Ala Arg Thr Gly Ala Leu Asp Arg Phe Ala Ala Gly Arg
145                 150                 155                 160

gag gta taaatgacca ccgcacttgg aac                                 509
Glu Val
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<210> 1010
<211> 162
<212> PRT
<213> Corynebacterium glutamicum

<400> 1010

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Ser Ile Gly Tyr Ala Trp Thr Thr Ala Phe His Ala Leu Thr Pro Gly
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  1               5                  10                  15

Leu Gly Gly Ile Ala Ile Gly Ile Trp Leu Leu Gly Gly Val Leu Gly
             20                  25                  30

Gly Leu Val Ile Arg Lys Pro Gly Ala Ala Ile Phe Val Glu Val Val
         35                  40                  45

Ala Ala Cys Val Ser Ala Ala Leu Ala Ser Gln Phe Gly Ile Ser Thr
     50                  55                  60

Ile Tyr Ser Gly Leu Ala Gln Gly Ile Gly Ala Glu Ile Ile Phe Ala
 65                  70                  75                  80

Leu Phe Leu Tyr Arg Arg Tyr Ser Leu Pro Thr Thr Met Leu Ala Gly
                 85                  90                  95

Met Gly Ala Gly Gly Gly Ala Ile Phe Leu Glu Met Phe Phe Tyr Gly
            100                 105                 110

Asn Leu Ala Lys Thr Met Ser Phe Asn Ile Ile Tyr Ser Thr Thr Val
        115                 120                 125

Leu Ile Ser Gly Ala Ile Leu Ala Gly Leu Leu Ser Trp Tyr Leu Val
    130                 135                 140

Arg Ala Leu Ala Arg Thr Gly Ala Leu Asp Arg Phe Ala Ala Gly Arg
145                 150                 155                 160

Glu Val
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<210> 1011
<211> 828
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(805)
<223> RXN02121

<400> 1011
ccgggaaatc ttcaggcgtc tcctcccata tgctgctgac aaattccaga acaggatcgt 60

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tgggatacct tcgagacaaa cttccgaaag ctccgcaacc atg atc acc tca cca   115
                                             Met Ile Thr Ser Pro
                                               1               5

ttt gag cgc gag ctg aag ctg ctc aac gag ggg gaa ctg ggt att gtc   163
Phe Glu Arg Glu Leu Lys Leu Leu Asn Glu Gly Glu Leu Gly Ile Val
                 10                  15                  20

cag cag ttg gtg gaa tca agc aac atc gga ttc atc gtc gat ctt gaa   211
Gln Gln Leu Val Glu Ser Ser Asn Ile Gly Phe Ile Val Asp Leu Glu
             25                  30                  35

tta gat ggc gat tat ggg tgg gcg gtc tac aaa ccg gaa ttg ggg gag   259
Leu Asp Gly Asp Tyr Gly Trp Ala Val Tyr Lys Pro Glu Leu Gly Glu
         40                  45                  50
```

```
caa ccc ctg tgg gat ttc cct cct ggc ctg tac aaa cgt gaa cgt gca   307
Gln Pro Leu Trp Asp Phe Pro Pro Gly Leu Tyr Lys Arg Glu Arg Ala
     55                  60                  65

gcc ttt gtg atc agt gag ttt ttg ggt tgg aac atc gtg cct cca acg   355
Ala Phe Val Ile Ser Glu Phe Leu Gly Trp Asn Ile Val Pro Pro Thr
 70                  75                  80                  85

gtg atc atg cac gat gcc ccg gct ggt gtg ggc tcg gtg cag tgg ttt   403
Val Ile Met His Asp Ala Pro Ala Gly Val Gly Ser Val Gln Trp Phe
                 90                  95                 100

att gaa aac aat ggc gaa cac tat ttt cca ctg ttt gac acc cgc gct   451
Ile Glu Asn Asn Gly Glu His Tyr Phe Pro Leu Phe Asp Thr Arg Ala
            105                 110                 115

gac ctg cat ccg cag ttt gtc cgc atg gct gtg ttt gat ctg ttg tgc   499
Asp Leu His Pro Gln Phe Val Arg Met Ala Val Phe Asp Leu Leu Cys
        120                 125                 130

aac aac act gac cgg aaa gcg ggc cat gtg ttg tta gac ggc gat cat   547
Asn Asn Thr Asp Arg Lys Ala Gly His Val Leu Leu Asp Gly Asp His
    135                 140                 145

att tgg ggc atc gat cac ggg ttg tgt ttt tcc gtc gaa ccg aag ctg   595
Ile Trp Gly Ile Asp His Gly Leu Cys Phe Ser Val Glu Pro Lys Leu
150                 155                 160                 165

cgc acg gtg att tgg gat ttc gca ggc tgc acc att cca gat gac ttg   643
Arg Thr Val Ile Trp Asp Phe Ala Gly Cys Thr Ile Pro Asp Asp Leu
                170                 175                 180

gtg aca gat gtt gag cag ctt ttg gag gac gtc ccg gaa gaa ctt cat   691
Val Thr Asp Val Glu Gln Leu Leu Glu Asp Val Pro Glu Glu Leu His
            185                 190                 195

cag ctt ctt cat ccc gca gaa att gat gcg ctg cag cgc cgt gcc tca   739
Gln Leu Leu His Pro Ala Glu Ile Asp Ala Leu Gln Arg Arg Ala Ser
        200                 205                 210

aga atc agc agg tta ccg ttc ctt ccg cag gcg aaa tcg cat cgt caa   787
Arg Ile Ser Arg Leu Pro Phe Leu Pro Gln Ala Lys Ser His Arg Gln
    215                 220                 225

ttc cct tgg cca ctt gtt tgagtaggct ggcgggcagg tgc                828
Phe Pro Trp Pro Leu Val
230                 235
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<210> 1012
<211> 235
<212> PRT
<213> Corynebacterium glutamicum

<400> 1012

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Met Ile Thr Ser Pro Phe Glu Arg Glu Leu Lys Leu Leu Asn Glu Gly
  1               5                  10                  15

Glu Leu Gly Ile Val Gln Gln Leu Val Glu Ser Ser Asn Ile Gly Phe
             20                  25                  30
```

```
Ile Val Asp Leu Glu Leu Asp Gly Asp Tyr Gly Trp Ala Val Tyr Lys
         35                  40                  45

Pro Glu Leu Gly Glu Gln Pro Leu Trp Asp Phe Pro Pro Gly Leu Tyr
     50                  55                  60

Lys Arg Glu Arg Ala Ala Phe Val Ile Ser Glu Phe Leu Gly Trp Asn
 65                  70                  75                  80

Ile Val Pro Pro Thr Val Ile Met His Asp Ala Pro Ala Gly Val Gly
                 85                  90                  95

Ser Val Gln Trp Phe Ile Glu Asn Asn Gly Glu His Tyr Phe Pro Leu
            100                 105                 110

Phe Asp Thr Arg Ala Asp Leu His Pro Gln Phe Val Arg Met Ala Val
        115                 120                 125

Phe Asp Leu Leu Cys Asn Asn Thr Asp Arg Lys Ala Gly His Val Leu
    130                 135                 140

Leu Asp Gly Asp His Ile Trp Gly Ile Asp His Gly Leu Cys Phe Ser
145                 150                 155                 160

Val Glu Pro Lys Leu Arg Thr Val Ile Trp Asp Phe Ala Gly Cys Thr
                165                 170                 175

Ile Pro Asp Asp Leu Val Thr Asp Val Glu Gln Leu Leu Glu Asp Val
            180                 185                 190

Pro Glu Glu Leu His Gln Leu Leu His Pro Ala Glu Ile Asp Ala Leu
        195                 200                 205

Gln Arg Arg Ala Ser Arg Ile Ser Arg Leu Pro Phe Leu Pro Gln Ala
    210                 215                 220

Lys Ser His Arg Gln Phe Pro Trp Pro Leu Val
225                 230                 235
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<210> 1013
<211> 828
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(805)
<223> FRXA02121

<400> 1013
ccgggaaatc ttcaggcgtc tcctcccata tgctgctgac aaattccaga acaggatcgt 60

tgggatacct tcgagacaaa cttccgaaag ctccgcaacc atg atc acc tca cca 115
                                               Met Ile Thr Ser Pro
                                                 1   5

ttt gag cgc gag ctg aag ctg ctc aac gag ggg gaa ctg ggt att gtc 163
Phe Glu Arg Glu Leu Lys Leu Leu Asn Glu Gly Glu Leu Gly Ile Val
                10   15   20

```
cag cag ttg gtg gaa tca agc aac atc gga ttc atc gtc gat ctt gaa   211
Gln Gln Leu Val Glu Ser Ser Asn Ile Gly Phe Ile Val Asp Leu Glu
            25                  30                  35

tta gat ggc gat tat ggg tgg gcg gtc tac aaa ccg gaa ttg ggg gag   259
Leu Asp Gly Asp Tyr Gly Trp Ala Val Tyr Lys Pro Glu Leu Gly Glu
        40                  45                  50

caa ccc ctg tgg gat ttc cct cct ggc ctg tac aaa cgt gaa cgt gca   307
Gln Pro Leu Trp Asp Phe Pro Pro Gly Leu Tyr Lys Arg Glu Arg Ala
    55                  60                  65

gcc ttt gtg atc agt gag ttt ttg ggt tgg aac atc gtg cct cca acg   355
Ala Phe Val Ile Ser Glu Phe Leu Gly Trp Asn Ile Val Pro Pro Thr
70                  75                  80                  85

gtg atc atg cac gat gcc ccg gct ggt gtg ggc tcg gtg cag tgg ttt   403
Val Ile Met His Asp Ala Pro Ala Gly Val Gly Ser Val Gln Trp Phe
                90                  95                  100

att gaa aac aat ggc gaa cac tat ttt cca ctg ttt gac acc cgc gct   451
Ile Glu Asn Asn Gly Glu His Tyr Phe Pro Leu Phe Asp Thr Arg Ala
            105                 110                 115

gac ctg cat ccg cag ttt gtc cgc atg gct gtg ttt gat ctg ttg tgc   499
Asp Leu His Pro Gln Phe Val Arg Met Ala Val Phe Asp Leu Leu Cys
        120                 125                 130

aac aac act gac cgg aaa tcg ggc cat gtg ttg cta gac ggc gat cat   547
Asn Asn Thr Asp Arg Lys Ser Gly His Val Leu Leu Asp Gly Asp His
    135                 140                 145

att tgg ggc atc gat cac ggg ttg tgt ttt tcc gtc gaa ccg aag ctg   595
Ile Trp Gly Ile Asp His Gly Leu Cys Phe Ser Val Glu Pro Lys Leu
150                 155                 160                 165

cgc acg gtg att tgg gat ttc gca ggc tgc acc att cca gat gac ttg   643
Arg Thr Val Ile Trp Asp Phe Ala Gly Cys Thr Ile Pro Asp Asp Leu
                170                 175                 180

gtg aca gat gtt gag cag ctt ttg gag gac gtc ccg gaa gaa ctt cat   691
Val Thr Asp Val Glu Gln Leu Leu Glu Asp Val Pro Glu Glu Leu His
            185                 190                 195

cag ctt ctt cat ccc gca gaa att gat gcg ctg cag cgc cgt gcc tca   739
Gln Leu Leu His Pro Ala Glu Ile Asp Ala Leu Gln Arg Arg Ala Ser
        200                 205                 210

aga atc agc agg tta ccg ttc ctt ccg cag gcg aaa tcg cat cgt caa   787
Arg Ile Ser Arg Leu Pro Phe Leu Pro Gln Ala Lys Ser His Arg Gln
    215                 220                 225

ttc cct tgg cca ctt gtt tgagtaggct ggcgggcagg tgc                828
Phe Pro Trp Pro Leu Val
230                 235
```

<210> 1014
<211> 235
<212> PRT

<213> Corynebacterium glutamicum

<400> 1014

```
Met Ile Thr Ser Pro Phe Glu Arg Glu Leu Lys Leu Leu Asn Glu Gly
  1               5                  10                  15

Glu Leu Gly Ile Val Gln Gln Leu Val Glu Ser Ser Asn Ile Gly Phe
             20                  25                  30

Ile Val Asp Leu Glu Leu Asp Gly Asp Tyr Gly Trp Ala Val Tyr Lys
         35                  40                  45

Pro Glu Leu Gly Glu Gln Pro Leu Trp Asp Phe Pro Pro Gly Leu Tyr
     50                  55                  60

Lys Arg Glu Arg Ala Ala Phe Val Ile Ser Glu Phe Leu Gly Trp Asn
 65                  70                  75                  80

Ile Val Pro Pro Thr Val Ile Met His Asp Ala Pro Ala Gly Val Gly
                 85                  90                  95

Ser Val Gln Trp Phe Ile Glu Asn Asn Gly Glu His Tyr Phe Pro Leu
            100                 105                 110

Phe Asp Thr Arg Ala Asp Leu His Pro Gln Phe Val Arg Met Ala Val
        115                 120                 125

Phe Asp Leu Leu Cys Asn Asn Thr Asp Arg Lys Ser Gly His Val Leu
    130                 135                 140

Leu Asp Gly Asp His Ile Trp Gly Ile Asp His Gly Leu Cys Phe Ser
145                 150                 155                 160

Val Glu Pro Lys Leu Arg Thr Val Ile Trp Asp Phe Ala Gly Cys Thr
                165                 170                 175

Ile Pro Asp Asp Leu Val Thr Asp Val Glu Gln Leu Leu Glu Asp Val
            180                 185                 190

Pro Glu Glu Leu His Gln Leu Leu His Pro Ala Glu Ile Asp Ala Leu
        195                 200                 205

Gln Arg Arg Ala Ser Arg Ile Ser Arg Leu Pro Phe Leu Pro Gln Ala
    210                 215                 220

Lys Ser His Arg Gln Phe Pro Trp Pro Leu Val
225                 230                 235
```

<210> 1015
<211> 465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(442)
<223> RXN02138

<400> 1015
tcactcgccg gagatccgta aaaaggggag tacactgcaa gcctatgatg tcccggccta 60

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aaagtaattc aaagggccaa cagttaagga gactaaagcg atg acc gct cca tca   115
                                            Met Thr Ala Pro Ser
                                              1               5

acc aac acc ggt gtt atc ttg acc gag tcc gca gcg tcc aaa gct aag   163
Thr Asn Thr Gly Val Ile Leu Thr Glu Ser Ala Ala Ser Lys Ala Lys
                 10                  15                  20

gca ctc atc gat cag gaa ggc cgc gac gac ctc tct ctg cgt atc gcc   211
Ala Leu Ile Asp Gln Glu Gly Arg Asp Asp Leu Ser Leu Arg Ile Ala
             25                  30                  35

gtt cag cct ggc ggc tgc tct ggc ctt cgt tac cag ctt tac ttc gac   259
Val Gln Pro Gly Gly Cys Ser Gly Leu Arg Tyr Gln Leu Tyr Phe Asp
         40                  45                  50

gac cgc acc ctt gat ggc gat aag gaa gac atc gtc ggt ggc gtt cgc   307
Asp Arg Thr Leu Asp Gly Asp Lys Glu Asp Ile Val Gly Gly Val Arg
     55                  60                  65

ctt gtc gtt gac aag atg agc acc cca tac ttg ctc ggc gct cag atc   355
Leu Val Val Asp Lys Met Ser Thr Pro Tyr Leu Leu Gly Ala Gln Ile
 70                  75                  80                  85

gac ttc gct gac acc atc gag cag cag ggc ttc acc atc gac aac cca   403
Asp Phe Ala Asp Thr Ile Glu Gln Gln Gly Phe Thr Ile Asp Asn Pro
                 90                  95                 100

aac gca ggc agc tct tgc gct tgt ggt gac tcc ttc aac taaagagatt    452
Asn Ala Gly Ser Ser Cys Ala Cys Gly Asp Ser Phe Asn
             105                 110

ccgttatgta gga                                                   465


<210> 1016
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 1016
Met Thr Ala Pro Ser Thr Asn Thr Gly Val Ile Leu Thr Glu Ser Ala
  1               5                  10                  15

Ala Ser Lys Ala Lys Ala Leu Ile Asp Gln Glu Gly Arg Asp Asp Leu
             20                  25                  30

Ser Leu Arg Ile Ala Val Gln Pro Gly Gly Cys Ser Gly Leu Arg Tyr
         35                  40                  45

Gln Leu Tyr Phe Asp Asp Arg Thr Leu Asp Gly Asp Lys Glu Asp Ile
     50                  55                  60

Val Gly Gly Val Arg Leu Val Val Asp Lys Met Ser Thr Pro Tyr Leu
 65                  70                  75                  80

Leu Gly Ala Gln Ile Asp Phe Ala Asp Thr Ile Glu Gln Gln Gly Phe
                 85                  90                  95

Thr Ile Asp Asn Pro Asn Ala Gly Ser Ser Cys Ala Cys Gly Asp Ser
```

```
            100                 105                 110

Phe Asn



<210> 1017
<211> 465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(442)
<223> FRXA02138

<400> 1017
tcactcgccg gagatccgta aaaaggggag tacactgcaa gcctatgatg tcccggccta 60

aaagtaattc aaagggccaa cagttaagga gactaaagcg atg acc gct cca tca   115
                                            Met Thr Ala Pro Ser
                                              1               5

acc aac acc ggt gtt atc ttg acc gag tcc gca gcg tcc aaa gct aag   163
Thr Asn Thr Gly Val Ile Leu Thr Glu Ser Ala Ala Ser Lys Ala Lys
                 10                  15                  20

gca ctc atc gat cag gaa ggc cgc gac gac ctc tct ctg cgt atc gcc   211
Ala Leu Ile Asp Gln Glu Gly Arg Asp Asp Leu Ser Leu Arg Ile Ala
             25                  30                  35

gtt cag cct ggc ggc tgc tct ggc ctt cgt tac cag ctt tac ttc gac   259
Val Gln Pro Gly Gly Cys Ser Gly Leu Arg Tyr Gln Leu Tyr Phe Asp
         40                  45                  50

gac cgc acc ctt gat ggc gat aag gaa gac atc gtc ggt ggc gtt cgc   307
Asp Arg Thr Leu Asp Gly Asp Lys Glu Asp Ile Val Gly Gly Val Arg
     55                  60                  65

ctt gtc gtt gac aag atg agc acc cca tac ttg ctc ggc gct cag atc   355
Leu Val Val Asp Lys Met Ser Thr Pro Tyr Leu Leu Gly Ala Gln Ile
 70                  75                  80                  85

gac ttc gct gac acc atc gag cag cag ggc ttc acc atc gac aac cca   403
Asp Phe Ala Asp Thr Ile Glu Gln Gln Gly Phe Thr Ile Asp Asn Pro
                 90                  95                 100

aac gca ggc agc tct tgc gct tgt ggt gac tcc ttc aac taaagagatt    452
Asn Ala Gly Ser Ser Cys Ala Cys Gly Asp Ser Phe Asn
            105                 110

ccgttatgta gga                                                   465


<210> 1018
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 1018
Met Thr Ala Pro Ser Thr Asn Thr Gly Val Ile Leu Thr Glu Ser Ala
```

```
  1               5                  10                  15

Ala Ser Lys Ala Lys Ala Leu Ile Asp Gln Glu Gly Arg Asp Asp Leu
            20                  25                  30

Ser Leu Arg Ile Ala Val Gln Pro Gly Gly Cys Ser Gly Leu Arg Tyr
        35                  40                  45

Gln Leu Tyr Phe Asp Asp Arg Thr Leu Asp Gly Asp Lys Glu Asp Ile
    50                  55                  60

Val Gly Gly Val Arg Leu Val Val Asp Lys Met Ser Thr Pro Tyr Leu
65                  70                  75                  80

Leu Gly Ala Gln Ile Asp Phe Ala Asp Thr Ile Glu Gln Gln Gly Phe
                85                  90                  95

Thr Ile Asp Asn Pro Asn Ala Gly Ser Ser Cys Ala Cys Gly Asp Ser
            100                 105                 110

Phe Asn
```

US 20040265956A1

<210> 1019
<211> 1311
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1288)
<223> RXN02151

<400> 1019

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atgagcgcat cgtctttttt aggagttgtc cgccaccgtg aaaactggaa acttaaaccc 60

agccccacag caggtgacgg ctccccagaa caaggctcgt atg gat tgg cca gac   115
                                            Met Asp Trp Pro Asp
                                              1               5

atc gcc aag gga ata tcc atc cta ggt gtc gtg tta cta cac gtg tcg   163
Ile Ala Lys Gly Ile Ser Ile Leu Gly Val Val Leu Leu His Val Ser
                10                  15                  20

ttg gca att cca ggt ggc cag gac acc atg atg tcc cac ctg aac gca   211
Leu Ala Ile Pro Gly Gly Gln Asp Thr Met Met Ser His Leu Asn Ala
            25                  30                  35

ctg ctt gat cca ctt cgg atg cca tta ttt ttt atg gtg agt gga ttt   259
Leu Leu Asp Pro Leu Arg Met Pro Leu Phe Phe Met Val Ser Gly Phe
        40                  45                  50

ttt gca gtt aaa gtt ctg aat caa agc ttt ggt gaa ctt ttc cgc ggg   307
Phe Ala Val Lys Val Leu Asn Gln Ser Phe Gly Glu Leu Phe Arg Gly
    55                  60                  65

cga ctg tgg ttc tac ctg gtt cca tat ttg ctg tgg act cca gtg aat   355
Arg Leu Trp Phe Tyr Leu Val Pro Tyr Leu Leu Trp Thr Pro Val Asn
70                  75                  80                  85
```

```
ctt tat cta cac cgc ctc gag ggc aca gtt ttt acc ggt aga gca ccg   403
Leu Tyr Leu His Arg Leu Glu Gly Thr Val Phe Thr Gly Arg Ala Pro
                 90                  95                 100

gga aca tgg gaa tgg tac agc ggc tcg atg ctc tcg gcc acc aat atg   451
Gly Thr Trp Glu Trp Tyr Ser Gly Ser Met Leu Ser Ala Thr Asn Met
            105                 110                 115

tac tgg ttc ctc tac ttc ttg gtc atc ttc aac cta ttt tta tgg gca   499
Tyr Trp Phe Leu Tyr Phe Leu Val Ile Phe Asn Leu Phe Leu Trp Ala
        120                 125                 130

acg aga aaa ctc cca gct tgg gca att gtg gcg ttg gtg gcc tca ctg   547
Thr Arg Lys Leu Pro Ala Trp Ala Ile Val Ala Leu Val Ala Ser Leu
    135                 140                 145

tgg cta ctt atg ccg gct tat agc gag att gag att cta cgc aag tcc   595
Trp Leu Leu Met Pro Ala Tyr Ser Glu Ile Glu Ile Leu Arg Lys Ser
150                 155                 160                 165

att att tac ttg cct aca ttc ctc att ggc gct tac ttc cgc cca ctg   643
Ile Ile Tyr Leu Pro Thr Phe Leu Ile Gly Ala Tyr Phe Arg Pro Leu
                170                 175                 180

att tcg cgt ttt gca gaa gcc gca aca agg cca aaa gca ata gtg ttt   691
Ile Ser Arg Phe Ala Glu Ala Ala Thr Arg Pro Lys Ala Ile Val Phe
            185                 190                 195

gca gcg gtc ctt tat gtc tcg gga ctt gct ttg ggc gtg atc tca aat   739
Ala Ala Val Leu Tyr Val Ser Gly Leu Ala Leu Gly Val Ile Ser Asn
        200                 205                 210

ggg ctg cgc gac agc gaa aac cat ggc gca agc gtg ctg tgg ctg atg   787
Gly Leu Arg Asp Ser Glu Asn His Gly Ala Ser Val Leu Trp Leu Met
    215                 220                 225

aac ctc cgc gat act ttt gct cat gca ctc ggc ggc aac ctc act gga   835
Asn Leu Arg Asp Thr Phe Ala His Ala Leu Gly Gly Asn Leu Thr Gly
230                 235                 240                 245

ttc gat atg gat cac ctt cct gga atg atc att cgg att gtt tcc ctg   883
Phe Asp Met Asp His Leu Pro Gly Met Ile Ile Arg Ile Val Ser Leu
                250                 255                 260

cct gca gga att gtg ttg tgc gta tgg ctt ggc cga ata aag cca gta   931
Pro Ala Gly Ile Val Leu Cys Val Trp Leu Gly Arg Ile Lys Pro Val
            265                 270                 275

ggg gag ttt ttg aaa ctt att ggt agg cac acc ctt ccc atc tac att   979
Gly Glu Phe Leu Lys Leu Ile Gly Arg His Thr Leu Pro Ile Tyr Ile
        280                 285                 290

ggg cat gca aca gga cta tcg ctg att ttt ggt ttc ggc ttg cgc tgg   1027
Gly His Ala Thr Gly Leu Ser Leu Ile Phe Gly Phe Gly Leu Arg Trp
    295                 300                 305

aat ttc atg gag att gat aac ttc tct gac agt ttg tgg cac cac acc   1075
Asn Phe Met Glu Ile Asp Asn Phe Ser Asp Ser Leu Trp His His Thr
310                 315                 320                 325

aat acg tgg atg gtc atc gcg ttt gcc tgc gcg atg ctc ggc ggg tac   1123
```

```
Asn Thr Trp Met Val Ile Ala Phe Ala Cys Ala Met Leu Gly Gly Tyr
                330                 335                 340

ctg acc tat ctg atc tcg cga gtt cca gtg ctg gga tgg act ctt gtt   1171
Leu Thr Tyr Leu Ile Ser Arg Val Pro Val Leu Gly Trp Thr Leu Val
            345                 350                 355

ccc cct aaa ctg cca gaa cca gat aaa act cca gct aaa gca caa gct   1219
Pro Pro Lys Leu Pro Glu Pro Asp Lys Thr Pro Ala Lys Ala Gln Ala
        360                 365                 370

gat tct cac gtt aaa gct cag tct gcg aag cct atg aat gct tct acc   1267
Asp Ser His Val Lys Ala Gln Ser Ala Lys Pro Met Asn Ala Ser Thr
    375                 380                 385

tct tct aag acg tac ggt ata taactgaagc ataacctgtg tga            1311
Ser Ser Lys Thr Tyr Gly Ile
390                 395


<210> 1020
<211> 396
<212> PRT
<213> Corynebacterium glutamicum

<400> 1020
Met Asp Trp Pro Asp Ile Ala Lys Gly Ile Ser Ile Leu Gly Val Val
  1               5                  10                  15

Leu Leu His Val Ser Leu Ala Ile Pro Gly Gly Gln Asp Thr Met Met
             20                  25                  30

Ser His Leu Asn Ala Leu Leu Asp Pro Leu Arg Met Pro Leu Phe Phe
         35                  40                  45

Met Val Ser Gly Phe Phe Ala Val Lys Val Leu Asn Gln Ser Phe Gly
     50                  55                  60

Glu Leu Phe Arg Gly Arg Leu Trp Phe Tyr Leu Val Pro Tyr Leu Leu
 65                  70                  75                  80

Trp Thr Pro Val Asn Leu Tyr Leu His Arg Leu Glu Gly Thr Val Phe
                 85                  90                  95

Thr Gly Arg Ala Pro Gly Thr Trp Glu Trp Tyr Ser Gly Ser Met Leu
            100                 105                 110

Ser Ala Thr Asn Met Tyr Trp Phe Leu Tyr Phe Leu Val Ile Phe Asn
        115                 120                 125

Leu Phe Leu Trp Ala Thr Arg Lys Leu Pro Ala Trp Ala Ile Val Ala
    130                 135                 140

Leu Val Ala Ser Leu Trp Leu Leu Met Pro Ala Tyr Ser Glu Ile Glu
145                 150                 155                 160

Ile Leu Arg Lys Ser Ile Ile Tyr Leu Pro Thr Phe Leu Ile Gly Ala
                165                 170                 175

Tyr Phe Arg Pro Leu Ile Ser Arg Phe Ala Glu Ala Ala Thr Arg Pro
            180                 185                 190
```

```
Lys Ala Ile Val Phe Ala Ala Val Leu Tyr Val Ser Gly Leu Ala Leu
        195                 200                 205

Gly Val Ile Ser Asn Gly Leu Arg Asp Ser Glu Asn His Gly Ala Ser
    210                 215                 220

Val Leu Trp Leu Met Asn Leu Arg Asp Thr Phe Ala His Ala Leu Gly
225                 230                 235                 240

Gly Asn Leu Thr Gly Phe Asp Met Asp His Leu Pro Gly Met Ile Ile
                245                 250                 255

Arg Ile Val Ser Leu Pro Ala Gly Ile Val Leu Cys Val Trp Leu Gly
            260                 265                 270

Arg Ile Lys Pro Val Gly Glu Phe Leu Lys Leu Ile Gly Arg His Thr
        275                 280                 285

Leu Pro Ile Tyr Ile Gly His Ala Thr Gly Leu Ser Leu Ile Phe Gly
    290                 295                 300

Phe Gly Leu Arg Trp Asn Phe Met Glu Ile Asp Asn Phe Ser Asp Ser
305                 310                 315                 320

Leu Trp His His Thr Asn Thr Trp Met Val Ile Ala Phe Ala Cys Ala
                325                 330                 335

Met Leu Gly Gly Tyr Leu Thr Tyr Leu Ile Ser Arg Val Pro Val Leu
            340                 345                 350

Gly Trp Thr Leu Val Pro Pro Lys Leu Pro Glu Pro Asp Lys Thr Pro
        355                 360                 365

Ala Lys Ala Gln Ala Asp Ser His Val Lys Ala Gln Ser Ala Lys Pro
    370                 375                 380

Met Asn Ala Ser Thr Ser Ser Lys Thr Tyr Gly Ile
385                 390                 395
```

<210> 1021
<211> 1311
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1288)
<223> FRXA02151

<400> 1021

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atgagcgcat cgtctttttt aggagttgtc cgccaccgtg aaaactggaa acttaaaccc 60

agccccacag caggtgacgg ctccccagaa caaggctcgt atg gat tgg cca gac   115
                                            Met Asp Trp Pro Asp
                                              1               5

atc gcc aag gga ata tcc atc cta ggt gtc gtg tta cta cac gtg tcg   163
Ile Ala Lys Gly Ile Ser Ile Leu Gly Val Val Leu Leu His Val Ser
                 10                  15                  20
```

```
ttg gca att cca ggt ggc cag gac acc atg atg tcc cac ctg aac gca   211
Leu Ala Ile Pro Gly Gly Gln Asp Thr Met Met Ser His Leu Asn Ala
            25                  30                  35

ctg ctt gat cca ctt cgg atg cca tta ttt ttt atg gtg agt gga ttt   259
Leu Leu Asp Pro Leu Arg Met Pro Leu Phe Phe Met Val Ser Gly Phe
        40                  45                  50

ttt gca gtt aaa gtt ctg aat caa agc ttt ggt gaa ctt ttc cgc ggg   307
Phe Ala Val Lys Val Leu Asn Gln Ser Phe Gly Glu Leu Phe Arg Gly
    55                  60                  65

cga ctg tgg ttc tac ctg gtt cca tat ttg ctg tgg act cca gtg aat   355
Arg Leu Trp Phe Tyr Leu Val Pro Tyr Leu Leu Trp Thr Pro Val Asn
70                  75                  80                  85

ctt tat cta cac cgc ctc gag ggc aca gtt ttt acc ggt aga gca ccg   403
Leu Tyr Leu His Arg Leu Glu Gly Thr Val Phe Thr Gly Arg Ala Pro
                90                  95                  100

gga aca tgg gaa tgg tac agc ggc tcg atg ctc tcg gcc acc aat atg   451
Gly Thr Trp Glu Trp Tyr Ser Gly Ser Met Leu Ser Ala Thr Asn Met
            105                 110                 115

tac tgg ttc ctc tac ttc ttg gtc atc ttc aac cta ttt tta tgg gca   499
Tyr Trp Phe Leu Tyr Phe Leu Val Ile Phe Asn Leu Phe Leu Trp Ala
        120                 125                 130

acg aga aaa ctc cca gct tgg gca att gtg gcg ttg gtg gcc tca ctg   547
Thr Arg Lys Leu Pro Ala Trp Ala Ile Val Ala Leu Val Ala Ser Leu
    135                 140                 145

tgg cta ctt atg ccg gct tat agc gag att gag att cta cgc aag tcc   595
Trp Leu Leu Met Pro Ala Tyr Ser Glu Ile Glu Ile Leu Arg Lys Ser
150                 155                 160                 165

att att tac ttg cct aca ttc ctc att ggc gct tac ttc cgc cca ctg   643
Ile Ile Tyr Leu Pro Thr Phe Leu Ile Gly Ala Tyr Phe Arg Pro Leu
                170                 175                 180

att tcg cgt ttt gca gaa gcc gca aca agg cca aaa gca ata gtg ttt   691
Ile Ser Arg Phe Ala Glu Ala Ala Thr Arg Pro Lys Ala Ile Val Phe
            185                 190                 195

gca gcg gtc ctt tat gtc tcg gga ctt gct ttg ggc gtg atc tca aat   739
Ala Ala Val Leu Tyr Val Ser Gly Leu Ala Leu Gly Val Ile Ser Asn
        200                 205                 210

ggg ctg cgc gac agc gaa aac cat ggc gca agc gtg ctg tgg ctg atg   787
Gly Leu Arg Asp Ser Glu Asn His Gly Ala Ser Val Leu Trp Leu Met
    215                 220                 225

aac ctc cgc gat act ttt gct cat gca ctc ggc ggc aac ctc act gga   835
Asn Leu Arg Asp Thr Phe Ala His Ala Leu Gly Gly Asn Leu Thr Gly
230                 235                 240                 245

ttc gat atg gat cac ctt cct gga atg atc att cgg att gtt tcc ctg   883
Phe Asp Met Asp His Leu Pro Gly Met Ile Ile Arg Ile Val Ser Leu
                250                 255                 260
```

```
cct gca gga att gtg ttg tgc gta tgg ctt ggc cga ata aag cca gta   931
Pro Ala Gly Ile Val Leu Cys Val Trp Leu Gly Arg Ile Lys Pro Val
            265                 270                 275

ggg gag ttt ttg aaa ctt att ggt agg cac acc ctt ccc atc tac att   979
Gly Glu Phe Leu Lys Leu Ile Gly Arg His Thr Leu Pro Ile Tyr Ile
        280                 285                 290

ggg cat gca aca gga cta tcg ctg att ttt ggt ttc ggc ttg cgc tgg   1027
Gly His Ala Thr Gly Leu Ser Leu Ile Phe Gly Phe Gly Leu Arg Trp
    295                 300                 305

aat ttc atg gag att gat aac ttc tct gac agt ttg tgg cac cac acc   1075
Asn Phe Met Glu Ile Asp Asn Phe Ser Asp Ser Leu Trp His His Thr
310                 315                 320                 325

aat acg tgg atg gtc atc gcg ttt gcc tgc gcg atg ctc ggc ggg tac   1123
Asn Thr Trp Met Val Ile Ala Phe Ala Cys Ala Met Leu Gly Gly Tyr
                330                 335                 340

ctg acc tat ctg atc tcg cga gtt cca gtg ctg gga tgg act ctt gtt   1171
Leu Thr Tyr Leu Ile Ser Arg Val Pro Val Leu Gly Trp Thr Leu Val
            345                 350                 355

ccc cct aaa ctg cca gaa cca gat aaa act cca gct aaa gca caa gct   1219
Pro Pro Lys Leu Pro Glu Pro Asp Lys Thr Pro Ala Lys Ala Gln Ala
        360                 365                 370

gat tct cac gtt aaa gct cag tct gcg aag cct atg aat gct tct acc   1267
Asp Ser His Val Lys Ala Gln Ser Ala Lys Pro Met Asn Ala Ser Thr
    375                 380                 385

tct tct aag acg tac ggt ata taactgaagc ataacctgtg tga            1311
Ser Ser Lys Thr Tyr Gly Ile
390                 395
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<210> 1022
<211> 396
<212> PRT
<213> Corynebacterium glutamicum

<400> 1022

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Met Asp Trp Pro Asp Ile Ala Lys Gly Ile Ser Ile Leu Gly Val Val
  1               5                  10                  15

Leu Leu His Val Ser Leu Ala Ile Pro Gly Gly Gln Asp Thr Met Met
             20                  25                  30

Ser His Leu Asn Ala Leu Leu Asp Pro Leu Arg Met Pro Leu Phe Phe
         35                  40                  45

Met Val Ser Gly Phe Phe Ala Val Lys Val Leu Asn Gln Ser Phe Gly
     50                  55                  60

Glu Leu Phe Arg Gly Arg Leu Trp Phe Tyr Leu Val Pro Tyr Leu Leu
 65                  70                  75                  80

Trp Thr Pro Val Asn Leu Tyr Leu His Arg Leu Glu Gly Thr Val Phe
                 85                  90                  95
```

```
Thr Gly Arg Ala Pro Gly Thr Trp Glu Trp Tyr Ser Gly Ser Met Leu
            100                 105                 110

Ser Ala Thr Asn Met Tyr Trp Phe Leu Tyr Phe Leu Val Ile Phe Asn
        115                 120                 125

Leu Phe Leu Trp Ala Thr Arg Lys Leu Pro Ala Trp Ala Ile Val Ala
    130                 135                 140

Leu Val Ala Ser Leu Trp Leu Leu Met Pro Ala Tyr Ser Glu Ile Glu
145                 150                 155                 160

Ile Leu Arg Lys Ser Ile Ile Tyr Leu Pro Thr Phe Leu Ile Gly Ala
                165                 170                 175

Tyr Phe Arg Pro Leu Ile Ser Arg Phe Ala Glu Ala Ala Thr Arg Pro
            180                 185                 190

Lys Ala Ile Val Phe Ala Ala Val Leu Tyr Val Ser Gly Leu Ala Leu
        195                 200                 205

Gly Val Ile Ser Asn Gly Leu Arg Asp Ser Glu Asn His Gly Ala Ser
    210                 215                 220

Val Leu Trp Leu Met Asn Leu Arg Asp Thr Phe Ala His Ala Leu Gly
225                 230                 235                 240

Gly Asn Leu Thr Gly Phe Asp Met Asp His Leu Pro Gly Met Ile Ile
                245                 250                 255

Arg Ile Val Ser Leu Pro Ala Gly Ile Val Leu Cys Val Trp Leu Gly
            260                 265                 270

Arg Ile Lys Pro Val Gly Glu Phe Leu Lys Leu Ile Gly Arg His Thr
        275                 280                 285

Leu Pro Ile Tyr Ile Gly His Ala Thr Gly Leu Ser Leu Ile Phe Gly
    290                 295                 300

Phe Gly Leu Arg Trp Asn Phe Met Glu Ile Asp Asn Phe Ser Asp Ser
305                 310                 315                 320

Leu Trp His His Thr Asn Thr Trp Met Val Ile Ala Phe Ala Cys Ala
                325                 330                 335

Met Leu Gly Gly Tyr Leu Thr Tyr Leu Ile Ser Arg Val Pro Val Leu
            340                 345                 350

Gly Trp Thr Leu Val Pro Pro Lys Leu Pro Glu Pro Asp Lys Thr Pro
        355                 360                 365

Ala Lys Ala Gln Ala Asp Ser His Val Lys Ala Gln Ser Ala Lys Pro
    370                 375                 380

Met Asn Ala Ser Thr Ser Ser Lys Thr Tyr Gly Ile
385                 390                 395
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<210> 1023
<211> 969
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(946)
<223> RXN02169

<400> 1023
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ctgttactgg tgggattaat acttattttt gggagaactt ttg gac atg caa ata 115
Leu Asp Met Gln Ile
1 5

aac cgc cga ggc ttc tta aaa gcc acc aca gga ctt gcc act atc ggc 163
Asn Arg Arg Gly Phe Leu Lys Ala Thr Thr Gly Leu Ala Thr Ile Gly
10 15 20

gct gcc agc atg ttt atg cca aag gcc aac gcc ctt gga gca atc aag 211
Ala Ala Ser Met Phe Met Pro Lys Ala Asn Ala Leu Gly Ala Ile Lys
25 30 35

ggc acc gtc atc gac tac gca gca ggc gtc ccc agc gca gca tcc att 259
Gly Thr Val Ile Asp Tyr Ala Ala Gly Val Pro Ser Ala Ala Ser Ile
40 45 50

aaa aat gca ggg cac ctt gga gct gtc cgt tac gtg tca cag cga cgc 307
Lys Asn Ala Gly His Leu Gly Ala Val Arg Tyr Val Ser Gln Arg Arg
55 60 65

ccc ggc act gaa tcc tgg atg atc ggc aag cca gtc aca ctg gca gaa 355
Pro Gly Thr Glu Ser Trp Met Ile Gly Lys Pro Val Thr Leu Ala Glu
70 75 80 85

acc cga gct ttt gaa caa aac ggc ctc aaa acc gca tcc gtc tat caa 403
Thr Arg Ala Phe Glu Gln Asn Gly Leu Lys Thr Ala Ser Val Tyr Gln
90 95 100

tac gga aag gca gag acc gcc gat tgg aag aac ggc gcc gca gga gcg 451
Tyr Gly Lys Ala Glu Thr Ala Asp Trp Lys Asn Gly Ala Ala Gly Ala
105 110 115

gca acc cac gct cca cag gca att gcg ctt cac gtg gca gct ggt ggc 499
Ala Thr His Ala Pro Gln Ala Ile Ala Leu His Val Ala Ala Gly Gly
120 125 130

cct aaa aat cgc ccc atc tac gtg gcg atc gac gac aac cca agc tgg 547
Pro Lys Asn Arg Pro Ile Tyr Val Ala Ile Asp Asp Asn Pro Ser Trp
135 140 145

tct gaa tac acc aat cag att cgc ccc tac ctc cag gca ttc aat gtt 595
Ser Glu Tyr Thr Asn Gln Ile Arg Pro Tyr Leu Gln Ala Phe Asn Val
150 155 160 165

gcg ctg tcc gct gcc ggc tac cag tta ggt gtc tac ggc aac tac aac 643
Ala Leu Ser Ala Ala Gly Tyr Gln Leu Gly Val Tyr Gly Asn Tyr Asn
170 175 180

gtc att aat tgg gct atc gcc gac ggc ctt gga gaa ttc ttc tgg atg 691
Val Ile Asn Trp Ala Ile Ala Asp Gly Leu Gly Glu Phe Phe Trp Met
185 190 195

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cac aac tgg gga tca gaa gga aag atc cac cca cgc acc acc atc cac   739
His Asn Trp Gly Ser Glu Gly Lys Ile His Pro Arg Thr Thr Ile His
        200                 205                 210

cag atc cgc att gat aag gac acc ctc gac gga gtc ggc atc gac atg   787
Gln Ile Arg Ile Asp Lys Asp Thr Leu Asp Gly Val Gly Ile Asp Met
    215                 220                 225

aac aat gtc tat gca gac gac tgg ggt cag tgg acc cca ggc aac gcg   835
Asn Asn Val Tyr Ala Asp Asp Trp Gly Gln Trp Thr Pro Gly Asn Ala
230                 235                 240                 245

gtt gac gat gcc atc ccc acc att cct gga aac tcc aac acg gga aca   883
Val Asp Asp Ala Ile Pro Thr Ile Pro Gly Asn Ser Asn Thr Gly Thr
                250                 255                 260

ggt act gga att gat gct gac acc atc aac caa gta atc aag att ctt   931
Gly Thr Gly Ile Asp Ala Asp Thr Ile Asn Gln Val Ile Lys Ile Leu
            265                 270                 275

ggc acc cta tct agc taaactagcc gtgctgactc aca                    969
Gly Thr Leu Ser Ser
        280
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<210> 1024
<211> 282
<212> PRT
<213> Corynebacterium glutamicum

<400> 1024

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Leu Asp Met Gln Ile Asn Arg Arg Gly Phe Leu Lys Ala Thr Thr Gly
  1               5                  10                  15

Leu Ala Thr Ile Gly Ala Ala Ser Met Phe Met Pro Lys Ala Asn Ala
             20                  25                  30

Leu Gly Ala Ile Lys Gly Thr Val Ile Asp Tyr Ala Ala Gly Val Pro
         35                  40                  45

Ser Ala Ala Ser Ile Lys Asn Ala Gly His Leu Gly Ala Val Arg Tyr
     50                  55                  60

Val Ser Gln Arg Arg Pro Gly Thr Glu Ser Trp Met Ile Gly Lys Pro
 65                  70                  75                  80

Val Thr Leu Ala Glu Thr Arg Ala Phe Glu Gln Asn Gly Leu Lys Thr
                 85                  90                  95

Ala Ser Val Tyr Gln Tyr Gly Lys Ala Glu Thr Ala Asp Trp Lys Asn
            100                 105                 110

Gly Ala Ala Gly Ala Ala Thr His Ala Pro Gln Ala Ile Ala Leu His
        115                 120                 125

Val Ala Ala Gly Gly Pro Lys Asn Arg Pro Ile Tyr Val Ala Ile Asp
    130                 135                 140

Asp Asn Pro Ser Trp Ser Glu Tyr Thr Asn Gln Ile Arg Pro Tyr Leu
145                 150                 155                 160
```

```
Gln Ala Phe Asn Val Ala Leu Ser Ala Ala Gly Tyr Gln Leu Gly Val
                165                 170                 175

Tyr Gly Asn Tyr Asn Val Ile Asn Trp Ala Ile Ala Asp Gly Leu Gly
            180                 185                 190

Glu Phe Phe Trp Met His Asn Trp Gly Ser Glu Gly Lys Ile His Pro
        195                 200                 205

Arg Thr Thr Ile His Gln Ile Arg Ile Asp Lys Asp Thr Leu Asp Gly
    210                 215                 220

Val Gly Ile Asp Met Asn Asn Val Tyr Ala Asp Asp Trp Gly Gln Trp
225                 230                 235                 240

Thr Pro Gly Asn Ala Val Asp Asp Ala Ile Pro Thr Ile Pro Gly Asn
                245                 250                 255

Ser Asn Thr Gly Thr Gly Thr Gly Ile Asp Ala Asp Thr Ile Asn Gln
            260                 265                 270

Val Ile Lys Ile Leu Gly Thr Leu Ser Ser
        275                 280
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<210> 1025
<211> 969
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(946)
<223> FRXA02169

<400> 1025

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gttaaaggtc gaaaaatccc acccctagcc cttttaaatg agtgttgtta ttgttaacca 60

ctgttactgg tgggattaat acttattttt gggagaactt ttg gac atg caa ata   115
                                              Leu Asp Met Gln Ile
                                                1               5

aac cgc cga ggc ttc tta aaa gcc acc aca gga ctt gcc act atc ggc   163
Asn Arg Arg Gly Phe Leu Lys Ala Thr Thr Gly Leu Ala Thr Ile Gly
                10                  15                  20

gct gcc agc atg ttt atg cca aag gcc aac gcc ctt gga gca atc aag   211
Ala Ala Ser Met Phe Met Pro Lys Ala Asn Ala Leu Gly Ala Ile Lys
            25                  30                  35

ggc acc gtc atc gac tac gca gca ggc gtc ccc agc gca gca tcc att   259
Gly Thr Val Ile Asp Tyr Ala Ala Gly Val Pro Ser Ala Ala Ser Ile
        40                  45                  50

aaa aat gca ggg cac ctt gga gct gtc cgt tac gtg tca cag cga cgc   307
Lys Asn Ala Gly His Leu Gly Ala Val Arg Tyr Val Ser Gln Arg Arg
    55                  60                  65

ccc ggc act gaa tcc tgg atg atc ggc aag cca gtc aca ctg gca gaa   355
Pro Gly Thr Glu Ser Trp Met Ile Gly Lys Pro Val Thr Leu Ala Glu
```

```
 70                  75                  80                  85

acc cga gct ttt gaa caa aac ggc ctc aaa acc gca tcc gtc tat caa   403
Thr Arg Ala Phe Glu Gln Asn Gly Leu Lys Thr Ala Ser Val Tyr Gln
                90                  95                 100

tac gga aag gca gag acc gcc gat tgg aag aac ggc gcc gca gga gcg   451
Tyr Gly Lys Ala Glu Thr Ala Asp Trp Lys Asn Gly Ala Ala Gly Ala
            105                 110                 115

gca acc cac gct cca cag gca att gcg ctt cac gtg gca gct ggt ggc   499
Ala Thr His Ala Pro Gln Ala Ile Ala Leu His Val Ala Ala Gly Gly
        120                 125                 130

cct aaa aat cgc ccc atc tac gtg gcg atc gac gac aac cca agc tgg   547
Pro Lys Asn Arg Pro Ile Tyr Val Ala Ile Asp Asp Asn Pro Ser Trp
    135                 140                 145

tct gaa tac acc aat cag att cgc ccc tac ctc cag gca ttc aat gtt   595
Ser Glu Tyr Thr Asn Gln Ile Arg Pro Tyr Leu Gln Ala Phe Asn Val
150                 155                 160                 165

gcg ctg tcc gct gcc ggc tac cag tta ggt gtc tac ggc aac tac aac   643
Ala Leu Ser Ala Ala Gly Tyr Gln Leu Gly Val Tyr Gly Asn Tyr Asn
                170                 175                 180

gtc att aat tgg gct atc gcc gac ggc ctt gga gaa ttc ttc tgg atg   691
Val Ile Asn Trp Ala Ile Ala Asp Gly Leu Gly Glu Phe Phe Trp Met
            185                 190                 195

cac aac tgg gga tca gaa gga aag atc cac cca cgc acc acc atc cac   739
His Asn Trp Gly Ser Glu Gly Lys Ile His Pro Arg Thr Thr Ile His
        200                 205                 210

cag atc cgc att gat aag gac acc ctc gac gga gtc ggc atc gac atg   787
Gln Ile Arg Ile Asp Lys Asp Thr Leu Asp Gly Val Gly Ile Asp Met
    215                 220                 225

aac aat gtc tat gca gac gac tgg ggt cag tgg acc cca ggc aac gcg   835
Asn Asn Val Tyr Ala Asp Asp Trp Gly Gln Trp Thr Pro Gly Asn Ala
230                 235                 240                 245

gtt gac gat gcc atc ccc acc att cct gga aac tcc aac acg gga aca   883
Val Asp Asp Ala Ile Pro Thr Ile Pro Gly Asn Ser Asn Thr Gly Thr
                250                 255                 260

ggt act gga att gat gct gac acc atc aac caa gta atc aag att ctt   931
Gly Thr Gly Ile Asp Ala Asp Thr Ile Asn Gln Val Ile Lys Ile Leu
            265                 270                 275

ggc acc cta tct agc taaactagcc gtgctgactc aca                    969
Gly Thr Leu Ser Ser
        280
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<210> 1026
<211> 282
<212> PRT
<213> Corynebacterium glutamicum

<400> 1026

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Leu Asp Met Gln Ile Asn Arg Arg Gly Phe Leu Lys Ala Thr Thr Gly
  1               5                  10                  15

Leu Ala Thr Ile Gly Ala Ala Ser Met Phe Met Pro Lys Ala Asn Ala
            20                  25                  30

Leu Gly Ala Ile Lys Gly Thr Val Ile Asp Tyr Ala Ala Gly Val Pro
         35                  40                  45

Ser Ala Ala Ser Ile Lys Asn Ala Gly His Leu Gly Ala Val Arg Tyr
     50                  55                  60

Val Ser Gln Arg Arg Pro Gly Thr Glu Ser Trp Met Ile Gly Lys Pro
 65                  70                  75                  80

Val Thr Leu Ala Glu Thr Arg Ala Phe Glu Gln Asn Gly Leu Lys Thr
                85                  90                  95

Ala Ser Val Tyr Gln Tyr Gly Lys Ala Glu Thr Ala Asp Trp Lys Asn
            100                 105                 110

Gly Ala Ala Gly Ala Ala Thr His Ala Pro Gln Ala Ile Ala Leu His
        115                 120                 125

Val Ala Ala Gly Gly Pro Lys Asn Arg Pro Ile Tyr Val Ala Ile Asp
    130                 135                 140

Asp Asn Pro Ser Trp Ser Glu Tyr Thr Asn Gln Ile Arg Pro Tyr Leu
145                 150                 155                 160

Gln Ala Phe Asn Val Ala Leu Ser Ala Ala Gly Tyr Gln Leu Gly Val
                165                 170                 175

Tyr Gly Asn Tyr Asn Val Ile Asn Trp Ala Ile Ala Asp Gly Leu Gly
            180                 185                 190

Glu Phe Phe Trp Met His Asn Trp Gly Ser Glu Gly Lys Ile His Pro
        195                 200                 205

Arg Thr Thr Ile His Gln Ile Arg Ile Asp Lys Asp Thr Leu Asp Gly
    210                 215                 220

Val Gly Ile Asp Met Asn Asn Val Tyr Ala Asp Asp Trp Gly Gln Trp
225                 230                 235                 240

Thr Pro Gly Asn Ala Val Asp Asp Ala Ile Pro Thr Ile Pro Gly Asn
                245                 250                 255

Ser Asn Thr Gly Thr Gly Thr Gly Ile Asp Ala Asp Thr Ile Asn Gln
            260                 265                 270

Val Ile Lys Ile Leu Gly Thr Leu Ser Ser
        275                 280
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<210> 1027
<211> 1581
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(1558)
<223> RXN02180

<400> 1027
gtttcagcta aaagaagaat ccttgctagt ggaatcagct gagttttcca cgagttttcc 60

agctttctca caacttgaat agaaattgag gtatccggca atg acg tca ggg aaa 115
Met Thr Ser Gly Lys
1 5

tca acg agt act agg gga gcc cta gac cgg tat ttc aaa atc tcg gag 163
Ser Thr Ser Thr Arg Gly Ala Leu Asp Arg Tyr Phe Lys Ile Ser Glu
10 15 20

cga gga tca agc att ggc acg gaa atc cgt gca ggt gtg gtc aca ttc 211
Arg Gly Ser Ser Ile Gly Thr Glu Ile Arg Ala Gly Val Val Thr Phe
25 30 35

ttc gcg atg gcc tac atc atc atc ctc aac ccc ttg atc ctt ggc acc 259
Phe Ala Met Ala Tyr Ile Ile Ile Leu Asn Pro Leu Ile Leu Gly Thr
40 45 50

acc cct gac gta gag ggc aac acc cta ggc atc gca cag gtt gca gcg 307
Thr Pro Asp Val Glu Gly Asn Thr Leu Gly Ile Ala Gln Val Ala Ala
55 60 65

gca aca gcg ctt gcc gct ggt gtc atg acc atc gcg ttt ggt ttg att 355
Ala Thr Ala Leu Ala Ala Gly Val Met Thr Ile Ala Phe Gly Leu Ile
70 75 80 85

gcg cgt tat cca ttc ggc att gct gct ggc ctg gga att aac acc atg 403
Ala Arg Tyr Pro Phe Gly Ile Ala Ala Gly Leu Gly Ile Asn Thr Met
90 95 100

gtc gcc gtg aca ctg gtt tca ggt gag ggc ctg acc tgg ccg gaa gca 451
Val Ala Val Thr Leu Val Ser Gly Glu Gly Leu Thr Trp Pro Glu Ala
105 110 115

atg gga ctt gtg gtc ctt gac ggt gtg gtc att gtt att ttg gct gtg 499
Met Gly Leu Val Val Leu Asp Gly Val Val Ile Val Ile Leu Ala Val
120 125 130

tcc ggc ttc cgt gtt gct gtg ttc cgt gcg atc cca gca tcc atg aag 547
Ser Gly Phe Arg Val Ala Val Phe Arg Ala Ile Pro Ala Ser Met Lys
135 140 145

gcg gcc atc agc gtg ggt atc ggc ctg ttc atc gcc atg atc ggc ctc 595
Ala Ala Ile Ser Val Gly Ile Gly Leu Phe Ile Ala Met Ile Gly Leu
150 155 160 165

gtg gat gca ggc ttt gtt cgc cgt att cca gat gct gcc ggt act act 643
Val Asp Ala Gly Phe Val Arg Arg Ile Pro Asp Ala Ala Gly Thr Thr
170 175 180

gtg cca gtg act ttg ggc att gat ggt tcc att gcg tct tgg cca acg 691
Val Pro Val Thr Leu Gly Ile Asp Gly Ser Ile Ala Ser Trp Pro Thr
185 190 195

ttc gtg ttc gtt gtc ggt gtt ctt ctc tgt ggc atc ctt gtt gtc cgt 739
Phe Val Phe Val Val Gly Val Leu Leu Cys Gly Ile Leu Val Val Arg

```
        200                 205                 210

cga gtt cgc ggt gga ctg ttt atc ggc att ttg gga acc acc att ttg   787
Arg Val Arg Gly Gly Leu Phe Ile Gly Ile Leu Gly Thr Thr Ile Leu
    215                 220                 225

gcg atc atc gca gaa gca atc ttt gat tcc ggt gcg tcc ttt gaa aat   835
Ala Ile Ile Ala Glu Ala Ile Phe Asp Ser Gly Ala Ser Phe Glu Asn
230                 235                 240                 245

ggt gaa gca aac gca gaa ggc tgg tca ctc gcc gtt cct ggt ctc cca   883
Gly Glu Ala Asn Ala Glu Gly Trp Ser Leu Ala Val Pro Gly Leu Pro
                250                 255                 260

gac tcc ttc ggt ggc atc ccg gat ctt tcc atc gtc ggc gca gtt gat   931
Asp Ser Phe Gly Gly Ile Pro Asp Leu Ser Ile Val Gly Ala Val Asp
            265                 270                 275

ttg atc ggt gcg ttc agc cgc atc ggt gtg gtc gcc gcg acc ttg ctg   979
Leu Ile Gly Ala Phe Ser Arg Ile Gly Val Val Ala Ala Thr Leu Leu
        280                 285                 290

atc ttt acc ctg gtc ctt gca aac ttc ttc gac gcc atg ggc acc atg   1027
Ile Phe Thr Leu Val Leu Ala Asn Phe Phe Asp Ala Met Gly Thr Met
    295                 300                 305

acc gct ctt ggt aag cag ggc aac ttg gtt gat gat gaa ggc aac ctt   1075
Thr Ala Leu Gly Lys Gln Gly Asn Leu Val Asp Asp Glu Gly Asn Leu
310                 315                 320                 325

cca gac att aag aag gca ctg gtt gtg gaa ggc gca ggt gcc att gtc   1123
Pro Asp Ile Lys Lys Ala Leu Val Val Glu Gly Ala Gly Ala Ile Val
                330                 335                 340

ggt ggt gct ttc tct gca tcc tcc aac acc gtg ttc gct gac tct tct   1171
Gly Gly Ala Phe Ser Ala Ser Ser Asn Thr Val Phe Ala Asp Ser Ser
            345                 350                 355

gca ggt gtt gca gac ggc gca cga acc ggc ctt gcc aac gtg gtc acc   1219
Ala Gly Val Ala Asp Gly Ala Arg Thr Gly Leu Ala Asn Val Val Thr
        360                 365                 370

ggc tcc ttg ttc ttg gct gcc atg ttc ttg acc cca ctg tat gaa atc   1267
Gly Ser Leu Phe Leu Ala Ala Met Phe Leu Thr Pro Leu Tyr Glu Ile
    375                 380                 385

gtc ccc atc gaa gca gca gca cca gtg ctt gta gtt gtt ggc gcg atg   1315
Val Pro Ile Glu Ala Ala Ala Pro Val Leu Val Val Val Gly Ala Met
390                 395                 400                 405

atg atg ggg cag gtt acc gag att gat ttc tcc aag ttc tac atc gca   1363
Met Met Gly Gln Val Thr Glu Ile Asp Phe Ser Lys Phe Tyr Ile Ala
                410                 415                 420

ttc cca gcg ttc ttg acc att gtg atc atg cct ttc acc tac tcc att   1411
Phe Pro Ala Phe Leu Thr Ile Val Ile Met Pro Phe Thr Tyr Ser Ile
            425                 430                 435

gca aac ggc att ggc gtt gga ttc atc atg tac gcc atc atg gct gca   1459
Ala Asn Gly Ile Gly Val Gly Phe Ile Met Tyr Ala Ile Met Ala Ala
        440                 445                 450
```

```
gcg gca ggc aaa gca aag caa gtg cac tgg ctg atg tgg ctg gtc gct   1507
Ala Ala Gly Lys Ala Lys Gln Val His Trp Leu Met Trp Leu Val Ala
    455                 460                 465

gga ctc ttc gtc gtg ttc ttc gcg att gat ccc atc atg gaa gct gtc   1555
Gly Leu Phe Val Val Phe Phe Ala Ile Asp Pro Ile Met Glu Ala Val
470                 475                 480                 485

ggc taatgacaac gcgcacggta att                                    1581
Gly
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<210> 1028
<211> 486
<212> PRT
<213> Corynebacterium glutamicum

<400> 1028

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Met Thr Ser Gly Lys Ser Thr Ser Thr Arg Gly Ala Leu Asp Arg Tyr
  1               5                  10                  15

Phe Lys Ile Ser Glu Arg Gly Ser Ser Ile Gly Thr Glu Ile Arg Ala
             20                  25                  30

Gly Val Val Thr Phe Phe Ala Met Ala Tyr Ile Ile Ile Leu Asn Pro
         35                  40                  45

Leu Ile Leu Gly Thr Thr Pro Asp Val Glu Gly Asn Thr Leu Gly Ile
     50                  55                  60

Ala Gln Val Ala Ala Ala Thr Ala Leu Ala Ala Gly Val Met Thr Ile
 65                  70                  75                  80

Ala Phe Gly Leu Ile Ala Arg Tyr Pro Phe Gly Ile Ala Ala Gly Leu
                 85                  90                  95

Gly Ile Asn Thr Met Val Ala Val Thr Leu Val Ser Gly Glu Gly Leu
            100                 105                 110

Thr Trp Pro Glu Ala Met Gly Leu Val Val Leu Asp Gly Val Val Ile
        115                 120                 125

Val Ile Leu Ala Val Ser Gly Phe Arg Val Ala Val Phe Arg Ala Ile
    130                 135                 140

Pro Ala Ser Met Lys Ala Ala Ile Ser Val Gly Ile Gly Leu Phe Ile
145                 150                 155                 160

Ala Met Ile Gly Leu Val Asp Ala Gly Phe Val Arg Arg Ile Pro Asp
                165                 170                 175

Ala Ala Gly Thr Thr Val Pro Val Thr Leu Gly Ile Asp Gly Ser Ile
            180                 185                 190

Ala Ser Trp Pro Thr Phe Val Phe Val Val Gly Val Leu Leu Cys Gly
        195                 200                 205

Ile Leu Val Val Arg Arg Val Arg Gly Gly Leu Phe Ile Gly Ile Leu
    210                 215                 220
```

```
Gly Thr Thr Ile Leu Ala Ile Ile Ala Glu Ala Ile Phe Asp Ser Gly
225                 230                 235                 240

Ala Ser Phe Glu Asn Gly Glu Ala Asn Ala Glu Gly Trp Ser Leu Ala
                245                 250                 255

Val Pro Gly Leu Pro Asp Ser Phe Gly Gly Ile Pro Asp Leu Ser Ile
            260                 265                 270

Val Gly Ala Val Asp Leu Ile Gly Ala Phe Ser Arg Ile Gly Val Val
        275                 280                 285

Ala Ala Thr Leu Leu Ile Phe Thr Leu Val Leu Ala Asn Phe Phe Asp
    290                 295                 300

Ala Met Gly Thr Met Thr Ala Leu Gly Lys Gln Gly Asn Leu Val Asp
305                 310                 315                 320

Asp Glu Gly Asn Leu Pro Asp Ile Lys Lys Ala Leu Val Val Glu Gly
                325                 330                 335

Ala Gly Ala Ile Val Gly Gly Ala Phe Ser Ala Ser Ser Asn Thr Val
            340                 345                 350

Phe Ala Asp Ser Ser Ala Gly Val Ala Asp Gly Ala Arg Thr Gly Leu
        355                 360                 365

Ala Asn Val Val Thr Gly Ser Leu Phe Leu Ala Ala Met Phe Leu Thr
    370                 375                 380

Pro Leu Tyr Glu Ile Val Pro Ile Glu Ala Ala Ala Pro Val Leu Val
385                 390                 395                 400

Val Val Gly Ala Met Met Met Gly Gln Val Thr Glu Ile Asp Phe Ser
                405                 410                 415

Lys Phe Tyr Ile Ala Phe Pro Ala Phe Leu Thr Ile Val Ile Met Pro
            420                 425                 430

Phe Thr Tyr Ser Ile Ala Asn Gly Ile Gly Val Gly Phe Ile Met Tyr
        435                 440                 445

Ala Ile Met Ala Ala Ala Ala Gly Lys Ala Lys Gln Val His Trp Leu
    450                 455                 460

Met Trp Leu Val Ala Gly Leu Phe Val Val Phe Phe Ala Ile Asp Pro
465                 470                 475                 480

Ile Met Glu Ala Val Gly
                485
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<210> 1029
<211> 1581
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1558)

<223> FRXA02180

<400> 1029

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agctttctca caacttgaat agaaattgag gtatccggca atg acg tca ggg aaa   115
                                          Met Thr Ser Gly Lys
                                            1               5

tca acg agt act agg gga gcc cta gac cgg tat ttc aaa atc tcg gag   163
Ser Thr Ser Thr Arg Gly Ala Leu Asp Arg Tyr Phe Lys Ile Ser Glu
                 10                  15                  20

cga gga tca agc att ggc acg gaa atc cgt gca ggt gtg gtc aca ttc   211
Arg Gly Ser Ser Ile Gly Thr Glu Ile Arg Ala Gly Val Val Thr Phe
             25                  30                  35

ttc gcg atg gcc tac atc atc atc ctc aac ccc ttg atc ctt ggc acc   259
Phe Ala Met Ala Tyr Ile Ile Ile Leu Asn Pro Leu Ile Leu Gly Thr
         40                  45                  50

acc cct gac gta gag ggc aac acc cta ggc atc gca cag gtt gca gcg   307
Thr Pro Asp Val Glu Gly Asn Thr Leu Gly Ile Ala Gln Val Ala Ala
     55                  60                  65

gca aca gcg ctt gcc gct ggt gtc atg acc atc gcg ttt ggt ttg att   355
Ala Thr Ala Leu Ala Ala Gly Val Met Thr Ile Ala Phe Gly Leu Ile
 70                  75                  80                  85

gcg cgt tat cca ttc ggc att gct gct ggc ctg gga att aac acc atg   403
Ala Arg Tyr Pro Phe Gly Ile Ala Ala Gly Leu Gly Ile Asn Thr Met
                 90                  95                 100

gtc gcc gtg aca ctg gtt tca ggt gag ggc ctg acc tgg ccg gaa gca   451
Val Ala Val Thr Leu Val Ser Gly Glu Gly Leu Thr Trp Pro Glu Ala
            105                 110                 115

atg gga ctt gtg gtc ctt gac ggt gtg gtc att gtt att ttg gct gtg   499
Met Gly Leu Val Val Leu Asp Gly Val Val Ile Val Ile Leu Ala Val
        120                 125                 130

tcc ggc ttc cgt gtt gct gtg ttc cgt gcg atc cca gca tcc atg aag   547
Ser Gly Phe Arg Val Ala Val Phe Arg Ala Ile Pro Ala Ser Met Lys
    135                 140                 145

gcg gcc atc agc gtg ggt atc ggc ctg ttc atc gcc atg atc ggc ctc   595
Ala Ala Ile Ser Val Gly Ile Gly Leu Phe Ile Ala Met Ile Gly Leu
150                 155                 160                 165

gtg gat gca ggc ttt gtt cgc cgt att cca gat gct gcc ggt act act   643
Val Asp Ala Gly Phe Val Arg Arg Ile Pro Asp Ala Ala Gly Thr Thr
                170                 175                 180

gtg cca gtg act ttg ggc att gat ggt tcc att gcg tct tgg cca acg   691
Val Pro Val Thr Leu Gly Ile Asp Gly Ser Ile Ala Ser Trp Pro Thr
            185                 190                 195

ttc gtg ttc gtt gtc ggt gtt ctt ctc tgt ggc atc ctt gtt gtc cgt   739
Phe Val Phe Val Val Gly Val Leu Leu Cys Gly Ile Leu Val Val Arg
        200                 205                 210
```

```
cga gtt cgc ggt gga ctg ttt atc ggc att ttg gga acc acc att ttg   787
Arg Val Arg Gly Gly Leu Phe Ile Gly Ile Leu Gly Thr Thr Ile Leu
    215                 220                 225

gcg atc atc gca gaa gca atc ttt gat tcc ggt gcg tcc ttt gaa aat   835
Ala Ile Ile Ala Glu Ala Ile Phe Asp Ser Gly Ala Ser Phe Glu Asn
230                 235                 240                 245

ggt gaa gca aac gca gaa ggc tgg tca ctc gcc gtt cct ggt ctc cca   883
Gly Glu Ala Asn Ala Glu Gly Trp Ser Leu Ala Val Pro Gly Leu Pro
                250                 255                 260

gac tcc ttc ggt ggc atc ccg gat ctt tcc atc gtc ggc gca gtt gat   931
Asp Ser Phe Gly Gly Ile Pro Asp Leu Ser Ile Val Gly Ala Val Asp
            265                 270                 275

ttg atc ggt gcg ttc agc cgc atc ggt gtg gtc gcc gcg acc ttg ctg   979
Leu Ile Gly Ala Phe Ser Arg Ile Gly Val Val Ala Ala Thr Leu Leu
        280                 285                 290

atc ttt acc ctg gtc ctt gca aac ttc ttc gac gcc atg ggc acc atg   1027
Ile Phe Thr Leu Val Leu Ala Asn Phe Phe Asp Ala Met Gly Thr Met
    295                 300                 305

acc gct ctt ggt aag cag ggc aac ttg gtt gat gat gaa ggc aac ctt   1075
Thr Ala Leu Gly Lys Gln Gly Asn Leu Val Asp Asp Glu Gly Asn Leu
310                 315                 320                 325

cca gac att aag aag gca ctg gtt gtg gaa ggc gca ggt gcc att gtc   1123
Pro Asp Ile Lys Lys Ala Leu Val Val Glu Gly Ala Gly Ala Ile Val
                330                 335                 340

ggt ggt gct ttc tct gca tcc tcc aac acc gtg ttc gct gac tct tct   1171
Gly Gly Ala Phe Ser Ala Ser Ser Asn Thr Val Phe Ala Asp Ser Ser
            345                 350                 355

gca ggt gtt gca gac ggc gca cga acc ggc ctt gcc aac gtg gtc acc   1219
Ala Gly Val Ala Asp Gly Ala Arg Thr Gly Leu Ala Asn Val Val Thr
        360                 365                 370

ggc tcc ttg ttc ttg gct gcc atg ttc ttg acc cca ctg tat gaa atc   1267
Gly Ser Leu Phe Leu Ala Ala Met Phe Leu Thr Pro Leu Tyr Glu Ile
    375                 380                 385

gtc ccc atc gaa gca gca gca cca gtg ctt gta gtt gtt ggc gcg atg   1315
Val Pro Ile Glu Ala Ala Ala Pro Val Leu Val Val Val Gly Ala Met
390                 395                 400                 405

atg atg ggg cag gtt acc gag att gat ttc tcc aag ttc tac atc gca   1363
Met Met Gly Gln Val Thr Glu Ile Asp Phe Ser Lys Phe Tyr Ile Ala
                410                 415                 420

ttc cca gcg ttc ttg acc att gtg atc atg cct ttc acc tac tcc att   1411
Phe Pro Ala Phe Leu Thr Ile Val Ile Met Pro Phe Thr Tyr Ser Ile
            425                 430                 435

gca aac ggc att ggc gtt gga ttc atc atg tac gcc atc atg gct gca   1459
Ala Asn Gly Ile Gly Val Gly Phe Ile Met Tyr Ala Ile Met Ala Ala
        440                 445                 450

gcg gca ggc aaa gca aag caa gtg cac tgg ctg atg tgg ctg gtc gct   1507
```

```
Ala Ala Gly Lys Ala Lys Gln Val His Trp Leu Met Trp Leu Val Ala
    455                 460                 465

gga ctc ttc gtc gtg ttc ttc gcg att gat ccc atc atg gaa gct gtc   1555
Gly Leu Phe Val Val Phe Phe Ala Ile Asp Pro Ile Met Glu Ala Val
470                 475                 480                 485

ggc taatgacaac gcgcacggta att                                   1581
Gly
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<210> 1030
<211> 486
<212> PRT
<213> Corynebacterium glutamicum

<400> 1030

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Met Thr Ser Gly Lys Ser Thr Ser Thr Arg Gly Ala Leu Asp Arg Tyr
  1               5                  10                  15

Phe Lys Ile Ser Glu Arg Gly Ser Ser Ile Gly Thr Glu Ile Arg Ala
             20                  25                  30

Gly Val Val Thr Phe Phe Ala Met Ala Tyr Ile Ile Ile Leu Asn Pro
         35                  40                  45

Leu Ile Leu Gly Thr Thr Pro Asp Val Glu Gly Asn Thr Leu Gly Ile
     50                  55                  60

Ala Gln Val Ala Ala Ala Thr Ala Leu Ala Ala Gly Val Met Thr Ile
 65                  70                  75                  80

Ala Phe Gly Leu Ile Ala Arg Tyr Pro Phe Gly Ile Ala Ala Gly Leu
                 85                  90                  95

Gly Ile Asn Thr Met Val Ala Val Thr Leu Val Ser Gly Glu Gly Leu
            100                 105                 110

Thr Trp Pro Glu Ala Met Gly Leu Val Val Leu Asp Gly Val Val Ile
        115                 120                 125

Val Ile Leu Ala Val Ser Gly Phe Arg Val Ala Val Phe Arg Ala Ile
    130                 135                 140

Pro Ala Ser Met Lys Ala Ala Ile Ser Val Gly Ile Gly Leu Phe Ile
145                 150                 155                 160

Ala Met Ile Gly Leu Val Asp Ala Gly Phe Val Arg Arg Ile Pro Asp
                165                 170                 175

Ala Ala Gly Thr Thr Val Pro Val Thr Leu Gly Ile Asp Gly Ser Ile
            180                 185                 190

Ala Ser Trp Pro Thr Phe Val Phe Val Val Gly Val Leu Leu Cys Gly
        195                 200                 205

Ile Leu Val Val Arg Arg Val Arg Gly Gly Leu Phe Ile Gly Ile Leu
    210                 215                 220

Gly Thr Thr Ile Leu Ala Ile Ile Ala Glu Ala Ile Phe Asp Ser Gly
```

```
225                 230                 235                 240

Ala Ser Phe Glu Asn Gly Glu Ala Asn Ala Glu Gly Trp Ser Leu Ala
                245                 250                 255

Val Pro Gly Leu Pro Asp Ser Phe Gly Gly Ile Pro Asp Leu Ser Ile
            260                 265                 270

Val Gly Ala Val Asp Leu Ile Gly Ala Phe Ser Arg Ile Gly Val Val
        275                 280                 285

Ala Ala Thr Leu Leu Ile Phe Thr Leu Val Leu Ala Asn Phe Phe Asp
    290                 295                 300

Ala Met Gly Thr Met Thr Ala Leu Gly Lys Gln Gly Asn Leu Val Asp
305                 310                 315                 320

Asp Glu Gly Asn Leu Pro Asp Ile Lys Lys Ala Leu Val Val Glu Gly
                325                 330                 335

Ala Gly Ala Ile Val Gly Gly Ala Phe Ser Ala Ser Ser Asn Thr Val
            340                 345                 350

Phe Ala Asp Ser Ser Ala Gly Val Ala Asp Gly Ala Arg Thr Gly Leu
        355                 360                 365

Ala Asn Val Val Thr Gly Ser Leu Phe Leu Ala Ala Met Phe Leu Thr
    370                 375                 380

Pro Leu Tyr Glu Ile Val Pro Ile Glu Ala Ala Ala Pro Val Leu Val
385                 390                 395                 400

Val Val Gly Ala Met Met Met Gly Gln Val Thr Glu Ile Asp Phe Ser
                405                 410                 415

Lys Phe Tyr Ile Ala Phe Pro Ala Phe Leu Thr Ile Val Ile Met Pro
            420                 425                 430

Phe Thr Tyr Ser Ile Ala Asn Gly Ile Gly Val Gly Phe Ile Met Tyr
        435                 440                 445

Ala Ile Met Ala Ala Ala Ala Gly Lys Ala Lys Gln Val His Trp Leu
    450                 455                 460

Met Trp Leu Val Ala Gly Leu Phe Val Val Phe Phe Ala Ile Asp Pro
465                 470                 475                 480

Ile Met Glu Ala Val Gly
                485
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<210> 1031
<211> 702
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(679)
<223> RXN02185

<400> 1031
caactccttg gggtgaagcc agacatccac tggcagagca actcctccgc tctaacccga 60

cagctaacct cgacggcgac aaatgagagg aaaacttttc atg gga cgt cac tcc 115
Met Gly Arg His Ser
1 5

act aag act agc tcc gcg ttc acc aag ctc gca gct tcc acc atc gct 163
Thr Lys Thr Ser Ser Ala Phe Thr Lys Leu Ala Ala Ser Thr Ile Ala
10 15 20

ttc ggt gct gct gca acc atc atg gct cct tct gca tct gct gca cct 211
Phe Gly Ala Ala Ala Thr Ile Met Ala Pro Ser Ala Ser Ala Ala Pro
25 30 35

gat tcc gac tgg gat cgc ctc gca cag tgc gag tcc ggt ggt aac tgg 259
Asp Ser Asp Trp Asp Arg Leu Ala Gln Cys Glu Ser Gly Gly Asn Trp
40 45 50

gca atc aac acc ggt aac ggc tac cac ggt ggt ctg cag ttc tcc gct 307
Ala Ile Asn Thr Gly Asn Gly Tyr His Gly Gly Leu Gln Phe Ser Ala
55 60 65

agc acc tgg gct gct tac ggc ggc cag gag ttc gct acc tac gca tac 355
Ser Thr Trp Ala Ala Tyr Gly Gly Gln Glu Phe Ala Thr Tyr Ala Tyr
70 75 80 85

cag gca acc cgt gag cag cag atc gct gtt gca gag cgc acc ttg gct 403
Gln Ala Thr Arg Glu Gln Gln Ile Ala Val Ala Glu Arg Thr Leu Ala
90 95 100

ggt cag ggc tgg ggc gca tgg cct gct tgc tcc gct tcc ctt gga ctg 451
Gly Gln Gly Trp Gly Ala Trp Pro Ala Cys Ser Ala Ser Leu Gly Leu
105 110 115

aac tcc gct cca acc cag cgt gac ctc tcc gct acc acc tcc acc cca 499
Asn Ser Ala Pro Thr Gln Arg Asp Leu Ser Ala Thr Thr Ser Thr Pro
120 125 130

gag cca gct gca gct gca cca gct gtt gct gag tac aac gct cct gca 547
Glu Pro Ala Ala Ala Ala Pro Ala Val Ala Glu Tyr Asn Ala Pro Ala
135 140 145

gcc aac atc gca gtt ggc tcc acc gac ttg aac acc atc aag tcc acc 595
Ala Asn Ile Ala Val Gly Ser Thr Asp Leu Asn Thr Ile Lys Ser Thr
150 155 160 165

tac ggc gct gtc acc ggc acc ctc gct cag tac ggc atc acc gtt cca 643
Tyr Gly Ala Val Thr Gly Thr Leu Ala Gln Tyr Gly Ile Thr Val Pro
170 175 180

gct gag gtt gag tct tac tac aac gct ttc gtc ggc taaatctagc 689
Ala Glu Val Glu Ser Tyr Tyr Asn Ala Phe Val Gly
185 190

tgcacttttt aaa 702

<210> 1032
<211> 193
<212> PRT

<213> Corynebacterium glutamicum

<400> 1032
Met Gly Arg His Ser Thr Lys Thr Ser Ser Ala Phe Thr Lys Leu Ala
1 5 10 15

Ala Ser Thr Ile Ala Phe Gly Ala Ala Ala Thr Ile Met Ala Pro Ser
20 25 30

Ala Ser Ala Ala Pro Asp Ser Asp Trp Asp Arg Leu Ala Gln Cys Glu
35 40 45

Ser Gly Gly Asn Trp Ala Ile Asn Thr Gly Asn Gly Tyr His Gly Gly
50 55 60

Leu Gln Phe Ser Ala Ser Thr Trp Ala Ala Tyr Gly Gly Gln Glu Phe
65 70 75 80

Ala Thr Tyr Ala Tyr Gln Ala Thr Arg Glu Gln Gln Ile Ala Val Ala
85 90 95

Glu Arg Thr Leu Ala Gly Gln Gly Trp Gly Ala Trp Pro Ala Cys Ser
100 105 110

Ala Ser Leu Gly Leu Asn Ser Ala Pro Thr Gln Arg Asp Leu Ser Ala
115 120 125

Thr Thr Ser Thr Pro Glu Pro Ala Ala Ala Ala Pro Ala Val Ala Glu
130 135 140

Tyr Asn Ala Pro Ala Ala Asn Ile Ala Val Gly Ser Thr Asp Leu Asn
145 150 155 160

Thr Ile Lys Ser Thr Tyr Gly Ala Val Thr Gly Thr Leu Ala Gln Tyr
165 170 175

Gly Ile Thr Val Pro Ala Glu Val Glu Ser Tyr Tyr Asn Ala Phe Val
180 185 190

Gly

<210> 1033
<211> 702
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(679)
<223> FRXA02185

<400> 1033
caactccttg gggtgaagcc agacatccac tggcagagca actcctccgc tctaacccga 60

cagctaacct cgacggcgac aaatgagagg aaaactttc atg gga cgt cac tcc 115
Met Gly Arg His Ser
1 5

act aag act agc tcc gcg ttc acc aag ctc gca gct tcc acc atc gct 163

```
Thr Lys Thr Ser Ser Ala Phe Thr Lys Leu Ala Ala Ser Thr Ile Ala
                10                  15                  20

ttc ggt gct gct gca acc atc atg gct cct tct gca tct gct gca cct   211
Phe Gly Ala Ala Ala Thr Ile Met Ala Pro Ser Ala Ser Ala Ala Pro
            25                  30                  35

gat tcc gac tgg gat cgc ctc gca cag tgc gag tcc ggt ggt aac tgg   259
Asp Ser Asp Trp Asp Arg Leu Ala Gln Cys Glu Ser Gly Gly Asn Trp
        40                  45                  50

gca atc aac acc ggt aac ggc tac cac ggt ggt ctg cag ttc tcc gct   307
Ala Ile Asn Thr Gly Asn Gly Tyr His Gly Gly Leu Gln Phe Ser Ala
    55                  60                  65

agc acc tgg gct gct tac ggc ggc cag gag ttc gct acc tac gca tac   355
Ser Thr Trp Ala Ala Tyr Gly Gly Gln Glu Phe Ala Thr Tyr Ala Tyr
70                  75                  80                  85

cag gca acc cgt gag cag cag atc gct gtt gca gag cgc acc ttg gct   403
Gln Ala Thr Arg Glu Gln Gln Ile Ala Val Ala Glu Arg Thr Leu Ala
                90                  95                  100

ggt cag ggc tgg ggc gca tgg cct gct tgc tcc gct tcc ctt gga ctg   451
Gly Gln Gly Trp Gly Ala Trp Pro Ala Cys Ser Ala Ser Leu Gly Leu
            105                 110                 115

aac tcc gct cca acc cag cgt gac ctc tcc gct acc acc tcc acc cca   499
Asn Ser Ala Pro Thr Gln Arg Asp Leu Ser Ala Thr Thr Ser Thr Pro
        120                 125                 130

gag cca gct gca gct gca cca gct gtt gct gag tac aac gct cct gca   547
Glu Pro Ala Ala Ala Ala Pro Ala Val Ala Glu Tyr Asn Ala Pro Ala
    135                 140                 145

gcc aac atc gca gtt ggc tcc acc gac ttg aac acc atc aag tcc acc   595
Ala Asn Ile Ala Val Gly Ser Thr Asp Leu Asn Thr Ile Lys Ser Thr
150                 155                 160                 165

tac ggc gct gtc acc ggc acc ctc gct cag tac ggc atc acc gtt cca   643
Tyr Gly Ala Val Thr Gly Thr Leu Ala Gln Tyr Gly Ile Thr Val Pro
                170                 175                 180

gct gag gtt gag tct tac tac aac gct ttc gtc ggc taaatctagc        689
Ala Glu Val Glu Ser Tyr Tyr Asn Ala Phe Val Gly
            185                 190

tgcacttttt aaa                                                   702


<210> 1034
<211> 193
<212> PRT
<213> Corynebacterium glutamicum

<400> 1034
Met Gly Arg His Ser Thr Lys Thr Ser Ser Ala Phe Thr Lys Leu Ala
  1               5                  10                  15

Ala Ser Thr Ile Ala Phe Gly Ala Ala Ala Thr Ile Met Ala Pro Ser
            20                  25                  30
```

```
Ala Ser Ala Ala Pro Asp Ser Asp Trp Asp Arg Leu Ala Gln Cys Glu
         35                  40                  45

Ser Gly Gly Asn Trp Ala Ile Asn Thr Gly Asn Gly Tyr His Gly Gly
     50                  55                  60

Leu Gln Phe Ser Ala Ser Thr Trp Ala Ala Tyr Gly Gly Gln Glu Phe
 65                  70                  75                  80

Ala Thr Tyr Ala Tyr Gln Ala Thr Arg Glu Gln Gln Ile Ala Val Ala
                 85                  90                  95

Glu Arg Thr Leu Ala Gly Gln Gly Trp Gly Ala Trp Pro Ala Cys Ser
            100                 105                 110

Ala Ser Leu Gly Leu Asn Ser Ala Pro Thr Gln Arg Asp Leu Ser Ala
        115                 120                 125

Thr Thr Ser Thr Pro Glu Pro Ala Ala Ala Ala Pro Ala Val Ala Glu
    130                 135                 140

Tyr Asn Ala Pro Ala Ala Asn Ile Ala Val Gly Ser Thr Asp Leu Asn
145                 150                 155                 160

Thr Ile Lys Ser Thr Tyr Gly Ala Val Thr Gly Thr Leu Ala Gln Tyr
                165                 170                 175

Gly Ile Thr Val Pro Ala Glu Val Glu Ser Tyr Tyr Asn Ala Phe Val
            180                 185                 190

Gly
```

<210> 1035
<211> 321
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(298)
<223> RXN02186

<400> 1035
tccaaccacc ccttgagggt ggggatgggg gagtcttttt tcatgatgtt gttaagttta 60

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agccttgttg aggtgacttt tgttcccaga gtttgaaaga atg tat gac atg gca   115
                                            Met Tyr Asp Met Ala
                                              1               5

aac gta gag aag aag cac ttc gtc gat ccg gca tgg ccg gag cac aat   163
Asn Val Glu Lys Lys His Phe Val Asp Pro Ala Trp Pro Glu His Asn
                 10                  15                  20

cca gct gac gga cac gtc gtt act gaa ctc atc tcc aag gtc gca ggc   211
Pro Ala Asp Gly His Val Val Thr Glu Leu Ile Ser Lys Val Ala Gly
             25                  30                  35

gcg tcc agc cca tgg ggc gat gac aag gaa ttc cca gtt tct gca gaa   259
```

```
Ala Ser Ser Pro Trp Gly Asp Asp Lys Glu Phe Pro Val Ser Ala Glu
         40                  45                  50

gag acc gga tac gtt cac ccg tac acc cgg atc aac cgc taagaaactt    308
Glu Thr Gly Tyr Val His Pro Tyr Thr Arg Ile Asn Arg
     55                  60                  65

aaaaaagagg caa                                                   321


<210> 1036
<211> 66
<212> PRT
<213> Corynebacterium glutamicum

<400> 1036
Met Tyr Asp Met Ala Asn Val Glu Lys Lys His Phe Val Asp Pro Ala
  1               5                  10                  15

Trp Pro Glu His Asn Pro Ala Asp Gly His Val Val Thr Glu Leu Ile
             20                  25                  30

Ser Lys Val Ala Gly Ala Ser Ser Pro Trp Gly Asp Asp Lys Glu Phe
         35                  40                  45

Pro Val Ser Ala Glu Glu Thr Gly Tyr Val His Pro Tyr Thr Arg Ile
     50                  55                  60

Asn Arg
 65


<210> 1037
<211> 342
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(319)
<223> FRXA02186

<400> 1037
agctgatcat cactttgagt atccaaccac cccttgaggg tggggatggg ggagtctttt 60

ttcatgatgt tgttaagttt aagccttgtt gaggtgactt ttg ttc cca gag ttt   115
                                          Leu Phe Pro Glu Phe
                                            1               5

gaa aga atg tat gac atg gca aac gta gag aag aag cac ttc gtc gat   163
Glu Arg Met Tyr Asp Met Ala Asn Val Glu Lys Lys His Phe Val Asp
                 10                  15                  20

ccg gca tgg ccg gag cac aat cca gct gac gga cac gtc gtt act gaa   211
Pro Ala Trp Pro Glu His Asn Pro Ala Asp Gly His Val Val Thr Glu
             25                  30                  35

ctc atc tcc aag gtc gca ggc gcg tcc agc cca tgg ggc gat gac aag   259
Leu Ile Ser Lys Val Ala Gly Ala Ser Ser Pro Trp Gly Asp Asp Lys
         40                  45                  50
```

```
gaa ttc cca gtt tct gca gaa gag acc gga tac gtt cac ccg tac acc   307
Glu Phe Pro Val Ser Ala Glu Glu Thr Gly Tyr Val His Pro Tyr Thr
     55                  60                  65

cgg atc aac cgc taagaaactt aaaaaagagg caa                        342
Arg Ile Asn Arg
 70
```

<210> 1038
<211> 73
<212> PRT
<213> Corynebacterium glutamicum

<400> 1038

```
Leu Phe Pro Glu Phe Glu Arg Met Tyr Asp Met Ala Asn Val Glu Lys
  1               5                  10                  15

Lys His Phe Val Asp Pro Ala Trp Pro Glu His Asn Pro Ala Asp Gly
             20                  25                  30

His Val Val Thr Glu Leu Ile Ser Lys Val Ala Gly Ala Ser Ser Pro
         35                  40                  45

Trp Gly Asp Asp Lys Glu Phe Pro Val Ser Ala Glu Glu Thr Gly Tyr
     50                  55                  60

Val His Pro Tyr Thr Arg Ile Asn Arg
 65                  70
```

<210> 1039
<211> 898
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(898)
<223> RXN02207

<400> 1039

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gaatcggtga ctttgccaac accaatcaca caagcccttg atgatgtctc cctgtgactt 60

ggtccaatta cattcactgg taatctgaaa ccttgtgaat atg cgc cgt cga tcc   115
                                              Met Arg Arg Arg Ser
                                                1               5

cgt gtg tcc cgt ttg ctt ccc gcc aca gct ttg ctg gcc tca act gca   163
Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu Leu Ala Ser Thr Ala
                10                  15                  20

ctt ctt tta agt gca tgt acg caa ggg gta acg gac tcc ccg gat atg   211
Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr Asp Ser Pro Asp Met
             25                  30                  35

ggc aag gca act ccc gct gtc tcc ccc gca gca agc aac ccg gat ggc   259
Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala Ser Asn Pro Asp Gly
         40                  45                  50

caa gta att gag ttc ggc aac atc act gac atg gaa gtc act gat ggt   307
```

```
Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met Glu Val Thr Asp Gly
     55                  60                  65

gac atc ctc ggt gta cgc acc gaa gac gca ctc gct att ggt aca gtc   355
Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu Ala Ile Gly Thr Val
 70                  75                  80                  85

tcc gac ttc gaa gcg ggt agc cag gtg gaa ctg gac gtc gat aag caa   403
Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu Asp Val Asp Lys Gln
                 90                  95                 100

tgc ggc gac ctg acc gca acc ggc ggc act ttc gtg ctc ccc tgc gcc   451
Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe Val Leu Pro Cys Ala
            105                 110                 115

gat ggc gtt tat ttg att gat gcc aag gac ccg gat ctg gat gag ttg   499
Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro Asp Leu Asp Glu Leu
        120                 125                 130

cgt gca act gac aag cca gtc acg gtg gca gcc ttg acc agc gat gat   547
Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala Leu Thr Ser Asp Asp
    135                 140                 145

cag ctt ctg gtg ggc aat ggt gaa gat gaa gaa ctc acc atc tac cgc   595
Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu Leu Thr Ile Tyr Arg
150                 155                 160                 165

gag ggc gaa gag cca gaa acc ttc acc gtc gcg ggt ccc aat acc cag   643
Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala Gly Pro Asn Thr Gln
                170                 175                 180

ctc atc gcc gtt cct gtc att gat cgc cac gac gcc gtt gtg cgc acc   691
Leu Ile Ala Val Pro Val Ile Asp Arg His Asp Ala Val Val Arg Thr
            185                 190                 195

tgg aac gaa aac acc acg att caa gat gtg gac tac ccc aac gac cgt   739
Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp Tyr Pro Asn Asp Arg
        200                 205                 210

gaa ggc gcg acc ctt cgc gtg gga ctc ggc gtt ggt caa atg gct ggt   787
Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val Gly Gln Met Ala Gly
    215                 220                 225

ggc gaa gac ggc ctg ctg gtg gtc tct gat gaa atg ggt ggc caa att   835
Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu Met Gly Gly Gln Ile
230                 235                 240                 245

gcc atc tac aac gct gat gat gtc atc cga ctt caa aat gac cgc ccc   883
Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu Gln Asn Asp Arg Pro
                250                 255                 260

cac cga cga gga acc                                              898
His Arg Arg Gly Thr
            265
```

<210> 1040
<211> 266
<212> PRT
<213> Corynebacterium glutamicum

<400> 1040
Met Arg Arg Arg Ser Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu
1 5 10 15

Leu Ala Ser Thr Ala Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr
20 25 30

Asp Ser Pro Asp Met Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala
35 40 45

Ser Asn Pro Asp Gly Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met
50 55 60

Glu Val Thr Asp Gly Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu
65 70 75 80

Ala Ile Gly Thr Val Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu
85 90 95

Asp Val Asp Lys Gln Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe
100 105 110

Val Leu Pro Cys Ala Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro
115 120 125

Asp Leu Asp Glu Leu Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala
130 135 140

Leu Thr Ser Asp Asp Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu
145 150 155 160

Leu Thr Ile Tyr Arg Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala
165 170 175

Gly Pro Asn Thr Gln Leu Ile Ala Val Pro Val Ile Asp Arg His Asp
180 185 190

Ala Val Val Arg Thr Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp
195 200 205

Tyr Pro Asn Asp Arg Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val
210 215 220

Gly Gln Met Ala Gly Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu
225 230 235 240

Met Gly Gly Gln Ile Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu
245 250 255

Gln Asn Asp Arg Pro His Arg Arg Gly Thr
260 265

<210> 1041
<211> 859
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(859)

<223> FRXA02207

<400> 1041

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gaatcggtga ctttgccaac accaatcaca caagcccttg atgatgtctc cctgtgactt 60

ggtccaatta cattcactgg taatctgaaa ccttgtgaat atg cgc cgt cga tcc   115
                                              Met Arg Arg Arg Ser
                                                1               5

cgt gtg tcc cgt ttg ctt ccc gcc aca gct ttg ctg gcc tca act gca   163
Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu Leu Ala Ser Thr Ala
                10                  15                  20

ctt ctt tta agt gca tgt acg caa ggg gta acg gac tcc ccg gat atg   211
Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr Asp Ser Pro Asp Met
            25                  30                  35

ggc aag gca act ccc gct gtc tcc ccc gca gca agc aac ccg gat ggc   259
Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala Ser Asn Pro Asp Gly
        40                  45                  50

caa gta att gag ttc ggc aac atc act gac atg gaa gtc act gat ggt   307
Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met Glu Val Thr Asp Gly
    55                  60                  65

gac atc ctc ggt gta cgc acc gaa gac gca ctc gct att ggt aca gtc   355
Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu Ala Ile Gly Thr Val
70                  75                  80                  85

tcc gac ttc gaa gcg ggt agc cag gtg gaa ctg gac gtc gat aag caa   403
Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu Asp Val Asp Lys Gln
                90                  95                  100

tgc ggc gac ctg acc gca acc ggc ggc act ttc gtg ctc ccc tgc gcc   451
Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe Val Leu Pro Cys Ala
            105                 110                 115

gat ggc gtt tat ttg att gat gcc aag gac ccg gat ctg gat gag ttg   499
Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro Asp Leu Asp Glu Leu
        120                 125                 130

cgt gca act gac aag cca gtc acg gtg gca gcc ttg acc agc gat gat   547
Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala Leu Thr Ser Asp Asp
    135                 140                 145

cag ctt ctg gtg ggc aat ggt gaa gat gaa gaa ctc acc atc tac cgc   595
Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu Leu Thr Ile Tyr Arg
150                 155                 160                 165

gag ggc gaa gag cca gaa acc ttc acc gtc gcg ggt ccc aat acc cag   643
Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala Gly Pro Asn Thr Gln
                170                 175                 180

ctc atc gcc gtt cct gtc att gat cgc cac gac gcc gtt gtg cgc acc   691
Leu Ile Ala Val Pro Val Ile Asp Arg His Asp Ala Val Val Arg Thr
            185                 190                 195

tgg aac gaa aac acc acg att caa gat gtg gac tac ccc aac gac cgt   739
Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp Tyr Pro Asn Asp Arg
        200                 205                 210
```

```
gaa ggc gcg acc ctt cgc gtg gga ctc ggc gtt ggt caa atg gct ggt   787
Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val Gly Gln Met Ala Gly
    215                 220                 225

ggc gaa gac ggc ctg ctg gtg gtc tct gat gaa atg ggt ggc caa att   835
Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu Met Gly Gly Gln Ile
230                 235                 240                 245

gcc atc tac aac gct gat gat gtc                                  859
Ala Ile Tyr Asn Ala Asp Asp Val
                250
```

<210> 1042
<211> 253
<212> PRT
<213> Corynebacterium glutamicum

<400> 1042

```
Met Arg Arg Arg Ser Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu
  1               5                  10                  15

Leu Ala Ser Thr Ala Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr
             20                  25                  30

Asp Ser Pro Asp Met Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala
         35                  40                  45

Ser Asn Pro Asp Gly Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met
     50                  55                  60

Glu Val Thr Asp Gly Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu
 65                  70                  75                  80

Ala Ile Gly Thr Val Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu
                 85                  90                  95

Asp Val Asp Lys Gln Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe
            100                 105                 110

Val Leu Pro Cys Ala Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro
        115                 120                 125

Asp Leu Asp Glu Leu Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala
    130                 135                 140

Leu Thr Ser Asp Asp Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu
145                 150                 155                 160

Leu Thr Ile Tyr Arg Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala
                165                 170                 175

Gly Pro Asn Thr Gln Leu Ile Ala Val Pro Val Ile Asp Arg His Asp
            180                 185                 190

Ala Val Val Arg Thr Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp
        195                 200                 205

Tyr Pro Asn Asp Arg Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val
    210                 215                 220
```

```
Gly Gln Met Ala Gly Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu
225                 230                 235                 240

Met Gly Gly Gln Ile Ala Ile Tyr Asn Ala Asp Asp Val
                245                 250


<210> 1043
<211> 601
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(601)
<223> RXN02223

<400> 1043
cttgcttttg agggccgcta cgcgcagctg tatcaacgat ggagtgctca atagttcaaa 60

tccaccacaa actctagaga tttggggtag aaacgaagac atg agc acc tac caa   115
                                            Met Ser Thr Tyr Gln
                                              1               5

gac gat cgt ttc cca ggc cca gac ccc tac gca ccg ctt ggt gaa aag   163
Asp Asp Arg Phe Pro Gly Pro Asp Pro Tyr Ala Pro Leu Gly Glu Lys
                 10                  15                  20

cca agc ttt acc ctc acc tcc acc gac ttg gaa aac ggt gca aag ctg   211
Pro Ser Phe Thr Leu Thr Ser Thr Asp Leu Glu Asn Gly Ala Lys Leu
             25                  30                  35

gcc gaa gcc caa ctc ggt ggc acc gat att tcc cca cag ctg tcc tgg   259
Ala Glu Ala Gln Leu Gly Gly Thr Asp Ile Ser Pro Gln Leu Ser Trp
         40                  45                  50

tca gat ctt cca gaa ggc acc aaa tcc ctc gcg atc acc tgc ctc gac   307
Ser Asp Leu Pro Glu Gly Thr Lys Ser Leu Ala Ile Thr Cys Leu Asp
     55                  60                  65

cca gat gcc cca acc ggc gct ggt ttc tgg cac tgg gca gtg ttt aac   355
Pro Asp Ala Pro Thr Gly Ala Gly Phe Trp His Trp Ala Val Phe Asn
 70                  75                  80                  85

atc ccc aca act gtc acg gag atc ccc acc ggt gct ggc gat gaa acc   403
Ile Pro Thr Thr Val Thr Glu Ile Pro Thr Gly Ala Gly Asp Glu Thr
                 90                  95                 100

ctc ggc ggc atc gaa ggc gta gtt tcc ctc aag ggt gat tcc ggc aag   451
Leu Gly Gly Ile Glu Gly Val Val Ser Leu Lys Gly Asp Ser Gly Lys
            105                 110                 115

cgt ggc ttc tac gga gcg caa cct cca gct ggc cac gca ccg cac cgt   499
Arg Gly Phe Tyr Gly Ala Gln Pro Pro Ala Gly His Ala Pro His Arg
        120                 125                 130

tac ctc ttc gca gtt cat gca ctt gat gtg gaa aaa ctc gac atc gcc   547
Tyr Leu Phe Ala Val His Ala Leu Asp Val Glu Lys Leu Asp Ile Ala
    135                 140                 145

ccc gac gct acc ccc act ggt cta ggc ttc aac ctg tat ttc cac act   595
```

Pro Asp Ala Thr Pro Thr Gly Leu Gly Phe Asn Leu Tyr Phe His Thr
150 155 160 165

ctt ggc 601
Leu Gly

<210> 1044
<211> 167
<212> PRT
<213> Corynebacterium glutamicum

<400> 1044
Met Ser Thr Tyr Gln Asp Asp Arg Phe Pro Gly Pro Asp Pro Tyr Ala
1 5 10 15

Pro Leu Gly Glu Lys Pro Ser Phe Thr Leu Thr Ser Thr Asp Leu Glu
20 25 30

Asn Gly Ala Lys Leu Ala Glu Ala Gln Leu Gly Gly Thr Asp Ile Ser
35 40 45

Pro Gln Leu Ser Trp Ser Asp Leu Pro Glu Gly Thr Lys Ser Leu Ala
50 55 60

Ile Thr Cys Leu Asp Pro Asp Ala Pro Thr Gly Ala Gly Phe Trp His
65 70 75 80

Trp Ala Val Phe Asn Ile Pro Thr Thr Val Thr Glu Ile Pro Thr Gly
85 90 95

Ala Gly Asp Glu Thr Leu Gly Gly Ile Glu Gly Val Val Ser Leu Lys
100 105 110

Gly Asp Ser Gly Lys Arg Gly Phe Tyr Gly Ala Gln Pro Pro Ala Gly
115 120 125

His Ala Pro His Arg Tyr Leu Phe Ala Val His Ala Leu Asp Val Glu
130 135 140

Lys Leu Asp Ile Ala Pro Asp Ala Thr Pro Thr Gly Leu Gly Phe Asn
145 150 155 160

Leu Tyr Phe His Thr Leu Gly
165

<210> 1045
<211> 520
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(520)
<223> FRXA02223

<400> 1045
cttgcttttg agggccgcta cgcgcagctg tatcaacgat ggagtgctca atagttcaaa 60

```
tccaccacaa actctagaga tttggggtag aaacgaagac atg agc acc tac caa   115
                                            Met Ser Thr Tyr Gln
                                              1               5

gac gat cgt ttc cca ggc cca gac ccc tac gca ccg ctt ggt gaa aag   163
Asp Asp Arg Phe Pro Gly Pro Asp Pro Tyr Ala Pro Leu Gly Glu Lys
               10                  15                  20

cca agc ttt acc ctc acc tcc acc gac ttg gaa aac ggt gca aag ctg   211
Pro Ser Phe Thr Leu Thr Ser Thr Asp Leu Glu Asn Gly Ala Lys Leu
            25                  30                  35

gcc gaa gcc caa ctc ggt ggc acc gat att tcc cca cag ctg tcc tgg   259
Ala Glu Ala Gln Leu Gly Gly Thr Asp Ile Ser Pro Gln Leu Ser Trp
         40                  45                  50

tca gat ctt cca gaa ggc acc aaa tcc ctc gcg atc acc tgc ctc gac   307
Ser Asp Leu Pro Glu Gly Thr Lys Ser Leu Ala Ile Thr Cys Leu Asp
     55                  60                  65

cca gat gcc cca acc ggc gct ggt ttc tgg cac tgg gca gtg ttt aac   355
Pro Asp Ala Pro Thr Gly Ala Gly Phe Trp His Trp Ala Val Phe Asn
 70                  75                  80                  85

atc ccc aca act gtc acg gag atc ccc acc ggt gct ggc gat gaa acc   403
Ile Pro Thr Thr Val Thr Glu Ile Pro Thr Gly Ala Gly Asp Glu Thr
               90                  95                 100

ctc ggc ggc atc gaa ggc gta gtt tcc ctc aag ggt gat tcc ggc aag   451
Leu Gly Gly Ile Glu Gly Val Val Ser Leu Lys Gly Asp Ser Gly Lys
            105                 110                 115

cgt ggc ttc tac gga gcg caa cct cca gct ggc cac gca ccg cac cgt   499
Arg Gly Phe Tyr Gly Ala Gln Pro Pro Ala Gly His Ala Pro His Arg
        120                 125                 130

tac ctc ttc gca gtt cat gca                                      520
Tyr Leu Phe Ala Val His Ala
    135                 140
```

Do not add any new matter to this page

<210> 1046
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

<400> 1046

```
Met Ser Thr Tyr Gln Asp Asp Arg Phe Pro Gly Pro Asp Pro Tyr Ala
  1               5                  10                  15

Pro Leu Gly Glu Lys Pro Ser Phe Thr Leu Thr Ser Thr Asp Leu Glu
            20                  25                  30

Asn Gly Ala Lys Leu Ala Glu Ala Gln Leu Gly Gly Thr Asp Ile Ser
         35                  40                  45

Pro Gln Leu Ser Trp Ser Asp Leu Pro Glu Gly Thr Lys Ser Leu Ala
     50                  55                  60

Ile Thr Cys Leu Asp Pro Asp Ala Pro Thr Gly Ala Gly Phe Trp His
 65                  70                  75                  80
```

```
Trp Ala Val Phe Asn Ile Pro Thr Thr Val Thr Glu Ile Pro Thr Gly
                 85                  90                  95

Ala Gly Asp Glu Thr Leu Gly Gly Ile Glu Gly Val Val Ser Leu Lys
            100                 105                 110

Gly Asp Ser Gly Lys Arg Gly Phe Tyr Gly Ala Gln Pro Pro Ala Gly
        115                 120                 125

His Ala Pro His Arg Tyr Leu Phe Ala Val His Ala
    130                 135                 140


<210> 1047
<211> 1156
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1156)
<223> RXN02226

<400> 1047
ctgacacctc ctatggcacg cggtatgttt aataaacgta attcgagttt cggcggccgt 60

gtcgcgcggc caggacgacc ctagctttta aggacccacc atg act gag aac cag   115
                                            Met Thr Glu Asn Gln
                                              1               5

act ccc agc tcc acc tct gca ccg aag ccg gga cct cgc ccg ggc cca   163
Thr Pro Ser Ser Thr Ser Ala Pro Lys Pro Gly Pro Arg Pro Gly Pro
                10                  15                  20

cgg cca gga ccc cga cct ggg gct cag gtt gct gca aag aaa gct gcg   211
Arg Pro Gly Pro Arg Pro Gly Ala Gln Val Ala Ala Lys Lys Ala Ala
            25                  30                  35

gtt gct aca cct gcg ccg atc gcc aaa act tct aac gat cct gca aag   259
Val Ala Thr Pro Ala Pro Ile Ala Lys Thr Ser Asn Asp Pro Ala Lys
        40                  45                  50

ttt ggt cgc gtt gag gca gac gga tct gca tat gtc acc acc tct gct   307
Phe Gly Arg Val Glu Ala Asp Gly Ser Ala Tyr Val Thr Thr Ser Ala
    55                  60                  65

ggc gag cgt ctg att ggt tct tgg cag gcc ggc acc cct gag gaa ggt   355
Gly Glu Arg Leu Ile Gly Ser Trp Gln Ala Gly Thr Pro Glu Glu Gly
70                  75                  80                  85

ctt gct cac tac ggc gcc cgt ttt gat gat ctg gcc acc gaa gtt gag   403
Leu Ala His Tyr Gly Ala Arg Phe Asp Asp Leu Ala Thr Glu Val Glu
                90                  95                  100

ctc atg gaa cag cgc cta atc tcc cac cct gat gat gcg acc tcc atc   451
Leu Met Glu Gln Arg Leu Ile Ser His Pro Asp Asp Ala Thr Ser Ile
            105                 110                 115

cgc acg aag gct gaa gaa ctc aag gca acc ctg ccc acc atc gct gcg   499
Arg Thr Lys Ala Glu Glu Leu Lys Ala Thr Leu Pro Thr Ile Ala Ala
```

```
        120                 125                 130

atc ggt gac ctt gat ggc gtt gaa gct cgc ctg tcc aag atc atc aac   547
Ile Gly Asp Leu Asp Gly Val Glu Ala Arg Leu Ser Lys Ile Ile Asn
    135                 140                 145

aac tcc gag gaa gcc aac gag cgc gcc aag gaa caa aag gct aaa aac   595
Asn Ser Glu Glu Ala Asn Glu Arg Ala Lys Glu Gln Lys Ala Lys Asn
150                 155                 160                 165

cgt gag cgc gca gta gct cgc aag gaa gag ctc gct gtt gag gct gaa   643
Arg Glu Arg Ala Val Ala Arg Lys Glu Glu Leu Ala Val Glu Ala Glu
                170                 175                 180

acc ttg gca gaa aac tcc tcc gac tgg aag gtt gct ggc gac cgc atc   691
Thr Leu Ala Glu Asn Ser Ser Asp Trp Lys Val Ala Gly Asp Arg Ile
            185                 190                 195

cgc gcc atc ctg gat gag tgg aag tcc atc cac ggc atc gac cgc aag   739
Arg Ala Ile Leu Asp Glu Trp Lys Ser Ile His Gly Ile Asp Arg Lys
        200                 205                 210

acc gat gat gaa ctg tgg aaa cgc tac tcc cgt gcg cgt gac tcc ttc   787
Thr Asp Asp Glu Leu Trp Lys Arg Tyr Ser Arg Ala Arg Asp Ser Phe
    215                 220                 225

aac cgt cgc cgc ggc gca cac ttc gca gag ctg gat cgc acc cgc gca   835
Asn Arg Arg Arg Gly Ala His Phe Ala Glu Leu Asp Arg Thr Arg Ala
230                 235                 240                 245

tct gca cgc aaa ctc aag gaa gaa ctc gtt gag cgc gcc aat gct ctc   883
Ser Ala Arg Lys Leu Lys Glu Glu Leu Val Glu Arg Ala Asn Ala Leu
                250                 255                 260

aag gaa tcc act gag tgg aac gac acc gcc cgc gca ttc cgc gat ctc   931
Lys Glu Ser Thr Glu Trp Asn Asp Thr Ala Arg Ala Phe Arg Asp Leu
            265                 270                 275

atg acc gaa tgg aaa gcc gcc ggc cgc gca cca cgc gaa atc gac gac   979
Met Thr Glu Trp Lys Ala Ala Gly Arg Ala Pro Arg Glu Ile Asp Asp
        280                 285                 290

aag ctg tgg gca gca ttc aag ggc gcc cag gac tac ttc ttt gat aag   1027
Lys Leu Trp Ala Ala Phe Lys Gly Ala Gln Asp Tyr Phe Phe Asp Lys
    295                 300                 305

cgc aac gcc gta gcc aag gaa cgc gac cag gaa ttc gaa gcc aac gca   1075
Arg Asn Ala Val Ala Lys Glu Arg Asp Gln Glu Phe Glu Ala Asn Ala
310                 315                 320                 325

acc gca aag cag cag ctc atc gac gaa tac gac gca cag atc aac ccc   1123
Thr Ala Lys Gln Gln Leu Ile Asp Glu Tyr Asp Ala Gln Ile Asn Pro
                330                 335                 340

gag cag ggc ctc gat gga gcg cgc agc aag ctc                      1156
Glu Gln Gly Leu Asp Gly Ala Arg Ser Lys Leu
            345                 350
```

<210> 1048
<211> 352

<212> PRT
<213> Corynebacterium glutamicum

<400> 1048

```
Met Thr Glu Asn Gln Thr Pro Ser Ser Thr Ser Ala Pro Lys Pro Gly
  1               5                  10                  15

Pro Arg Pro Gly Pro Arg Pro Gly Pro Arg Pro Gly Ala Gln Val Ala
             20                  25                  30

Ala Lys Lys Ala Ala Val Ala Thr Pro Ala Pro Ile Ala Lys Thr Ser
         35                  40                  45

Asn Asp Pro Ala Lys Phe Gly Arg Val Glu Ala Asp Gly Ser Ala Tyr
     50                  55                  60

Val Thr Thr Ser Ala Gly Glu Arg Leu Ile Gly Ser Trp Gln Ala Gly
 65                  70                  75                  80

Thr Pro Glu Glu Gly Leu Ala His Tyr Gly Ala Arg Phe Asp Asp Leu
                 85                  90                  95

Ala Thr Glu Val Glu Leu Met Glu Gln Arg Leu Ile Ser His Pro Asp
            100                 105                 110

Asp Ala Thr Ser Ile Arg Thr Lys Ala Glu Glu Leu Lys Ala Thr Leu
        115                 120                 125

Pro Thr Ile Ala Ala Ile Gly Asp Leu Asp Gly Val Glu Ala Arg Leu
    130                 135                 140

Ser Lys Ile Ile Asn Asn Ser Glu Glu Ala Asn Glu Arg Ala Lys Glu
145                 150                 155                 160

Gln Lys Ala Lys Asn Arg Glu Arg Ala Val Ala Arg Lys Glu Glu Leu
                165                 170                 175

Ala Val Glu Ala Glu Thr Leu Ala Glu Asn Ser Ser Asp Trp Lys Val
            180                 185                 190

Ala Gly Asp Arg Ile Arg Ala Ile Leu Asp Glu Trp Lys Ser Ile His
        195                 200                 205

Gly Ile Asp Arg Lys Thr Asp Asp Glu Leu Trp Lys Arg Tyr Ser Arg
    210                 215                 220

Ala Arg Asp Ser Phe Asn Arg Arg Arg Gly Ala His Phe Ala Glu Leu
225                 230                 235                 240

Asp Arg Thr Arg Ala Ser Ala Arg Lys Leu Lys Glu Glu Leu Val Glu
                245                 250                 255

Arg Ala Asn Ala Leu Lys Glu Ser Thr Glu Trp Asn Asp Thr Ala Arg
            260                 265                 270

Ala Phe Arg Asp Leu Met Thr Glu Trp Lys Ala Ala Gly Arg Ala Pro
        275                 280                 285

Arg Glu Ile Asp Asp Lys Leu Trp Ala Ala Phe Lys Gly Ala Gln Asp
    290                 295                 300
```

```
Tyr Phe Phe Asp Lys Arg Asn Ala Val Ala Lys Glu Arg Asp Gln Glu
305                 310                 315                 320

Phe Glu Ala Asn Ala Thr Ala Lys Gln Gln Leu Ile Asp Glu Tyr Asp
                325                 330                 335

Ala Gln Ile Asn Pro Glu Gln Gly Leu Asp Gly Ala Arg Ser Lys Leu
            340                 345                 350
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<210> 1049
<211> 1156
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1156)
<223> FRXA02226

<400> 1049

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ctgacacctc ctatggcacg cggtatgttt aataaacgta attcgagttt cggcggccgt 60

gtcgcgcggc caggacgacc ctagctttta aggacccacc atg act gag aac cag   115
                                            Met Thr Glu Asn Gln
                                              1               5

act ccc agc tcc acc tct gca ccg aag ccg gga cct cgc ccg ggc cca   163
Thr Pro Ser Ser Thr Ser Ala Pro Lys Pro Gly Pro Arg Pro Gly Pro
                10                  15                  20

cgg cca gga ccc cga cct ggg gct cag gtt gct gca aag aaa gct gcg   211
Arg Pro Gly Pro Arg Pro Gly Ala Gln Val Ala Ala Lys Lys Ala Ala
            25                  30                  35

gtt gct aca cct gcg ccg atc gcc aaa act tct aac gat cct gca aag   259
Val Ala Thr Pro Ala Pro Ile Ala Lys Thr Ser Asn Asp Pro Ala Lys
        40                  45                  50

ttt ggt cgc gtt gag gca gac gga tct gca tat gtc acc acc tct gct   307
Phe Gly Arg Val Glu Ala Asp Gly Ser Ala Tyr Val Thr Thr Ser Ala
    55                  60                  65

ggc gag cgt ctg att ggt tct tgg cag gcc ggc acc cct gag gaa ggt   355
Gly Glu Arg Leu Ile Gly Ser Trp Gln Ala Gly Thr Pro Glu Glu Gly
70                  75                  80                  85

ctt gct cac tac ggc gcc cgt ttt gat gat ctg gcc acc gaa gtt gag   403
Leu Ala His Tyr Gly Ala Arg Phe Asp Asp Leu Ala Thr Glu Val Glu
                90                  95                  100

ctc atg gaa cag cgc cta atc tcc cac cct gat gat gcg acc tcc atc   451
Leu Met Glu Gln Arg Leu Ile Ser His Pro Asp Asp Ala Thr Ser Ile
            105                 110                 115

cgc acg aag gct gaa gaa ctc aag gca acc ctg ccc acc atc gct gcg   499
Arg Thr Lys Ala Glu Glu Leu Lys Ala Thr Leu Pro Thr Ile Ala Ala
        120                 125                 130
```

```
atc ggt gac ctt gat ggc gtt gaa gct cgc ctg tcc aag atc atc aac   547
Ile Gly Asp Leu Asp Gly Val Glu Ala Arg Leu Ser Lys Ile Ile Asn
    135                 140                 145

aac tcc gag gaa gcc aac gag cgc gcc aag gaa caa aag gct aaa aac   595
Asn Ser Glu Glu Ala Asn Glu Arg Ala Lys Glu Gln Lys Ala Lys Asn
150                 155                 160                 165

cgt gag cgc gca gta gct cgc aag gaa gag ctc gct gtt gag gct gaa   643
Arg Glu Arg Ala Val Ala Arg Lys Glu Glu Leu Ala Val Glu Ala Glu
                170                 175                 180

acc ttg gca gaa aac tcc tcc gac tgg aag gtt gct ggc gac cgc atc   691
Thr Leu Ala Glu Asn Ser Ser Asp Trp Lys Val Ala Gly Asp Arg Ile
            185                 190                 195

cgc gcc atc ctg gat gag tgg aag tcc atc cac ggc atc gac cgc aag   739
Arg Ala Ile Leu Asp Glu Trp Lys Ser Ile His Gly Ile Asp Arg Lys
        200                 205                 210

acc gat gat gaa ctg tgg aaa cgc tac tcc cgt gcg cgt gac tcc ttc   787
Thr Asp Asp Glu Leu Trp Lys Arg Tyr Ser Arg Ala Arg Asp Ser Phe
    215                 220                 225

aac cgt cgc cgc ggc gca cac ttc gca gag ctg gat cgc acc cgc gca   835
Asn Arg Arg Arg Gly Ala His Phe Ala Glu Leu Asp Arg Thr Arg Ala
230                 235                 240                 245

tct gca cgc aaa ctc aag gaa gaa ctc gtt gag cgc gcc aat gct ctc   883
Ser Ala Arg Lys Leu Lys Glu Glu Leu Val Glu Arg Ala Asn Ala Leu
                250                 255                 260

aag gaa tcc act gag tgg aac gac acc gcc cgc gca ttc cgc gat ctc   931
Lys Glu Ser Thr Glu Trp Asn Asp Thr Ala Arg Ala Phe Arg Asp Leu
            265                 270                 275

atg acc gaa tgg aaa gcc gcc ggc cgc gca cca cgc gaa atc gac gac   979
Met Thr Glu Trp Lys Ala Ala Gly Arg Ala Pro Arg Glu Ile Asp Asp
        280                 285                 290

aag ctg tgg gca gca ttc aag ggc gcc cag gac tac ttc ttt gat aag   1027
Lys Leu Trp Ala Ala Phe Lys Gly Ala Gln Asp Tyr Phe Phe Asp Lys
    295                 300                 305

cgc aac gcc gta gcc aag gaa cgc gac cag gaa ttc gaa gcc aac gca   1075
Arg Asn Ala Val Ala Lys Glu Arg Asp Gln Glu Phe Glu Ala Asn Ala
310                 315                 320                 325

acc gca aag cag cag ctc atc gac gaa tac gac gca cag atc aac ccc   1123
Thr Ala Lys Gln Gln Leu Ile Asp Glu Tyr Asp Ala Gln Ile Asn Pro
                330                 335                 340

gag cag ggc ctc gat gga gcg cgc agc aag ctc                      1156
Glu Gln Gly Leu Asp Gly Ala Arg Ser Lys Leu
            345                 350
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<210> 1050
<211> 352
<212> PRT

<213> Corynebacterium glutamicum

<400> 1050

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Met Thr Glu Asn Gln Thr Pro Ser Ser Thr Ser Ala Pro Lys Pro Gly
  1               5                  10                  15

Pro Arg Pro Gly Pro Arg Pro Gly Pro Arg Pro Gly Ala Gln Val Ala
             20                  25                  30

Ala Lys Lys Ala Ala Val Ala Thr Pro Ala Pro Ile Ala Lys Thr Ser
         35                  40                  45

Asn Asp Pro Ala Lys Phe Gly Arg Val Glu Ala Asp Gly Ser Ala Tyr
     50                  55                  60

Val Thr Thr Ser Ala Gly Glu Arg Leu Ile Gly Ser Trp Gln Ala Gly
 65                  70                  75                  80

Thr Pro Glu Glu Gly Leu Ala His Tyr Gly Ala Arg Phe Asp Asp Leu
                 85                  90                  95

Ala Thr Glu Val Glu Leu Met Glu Gln Arg Leu Ile Ser His Pro Asp
            100                 105                 110

Asp Ala Thr Ser Ile Arg Thr Lys Ala Glu Glu Leu Lys Ala Thr Leu
        115                 120                 125

Pro Thr Ile Ala Ala Ile Gly Asp Leu Asp Gly Val Glu Ala Arg Leu
    130                 135                 140

Ser Lys Ile Ile Asn Asn Ser Glu Glu Ala Asn Glu Arg Ala Lys Glu
145                 150                 155                 160

Gln Lys Ala Lys Asn Arg Glu Arg Ala Val Ala Arg Lys Glu Glu Leu
                165                 170                 175

Ala Val Glu Ala Glu Thr Leu Ala Glu Asn Ser Ser Asp Trp Lys Val
            180                 185                 190

Ala Gly Asp Arg Ile Arg Ala Ile Leu Asp Glu Trp Lys Ser Ile His
        195                 200                 205

Gly Ile Asp Arg Lys Thr Asp Asp Glu Leu Trp Lys Arg Tyr Ser Arg
    210                 215                 220

Ala Arg Asp Ser Phe Asn Arg Arg Arg Gly Ala His Phe Ala Glu Leu
225                 230                 235                 240

Asp Arg Thr Arg Ala Ser Ala Arg Lys Leu Lys Glu Glu Leu Val Glu
                245                 250                 255

Arg Ala Asn Ala Leu Lys Glu Ser Thr Glu Trp Asn Asp Thr Ala Arg
            260                 265                 270

Ala Phe Arg Asp Leu Met Thr Glu Trp Lys Ala Ala Gly Arg Ala Pro
        275                 280                 285

Arg Glu Ile Asp Asp Lys Leu Trp Ala Ala Phe Lys Gly Ala Gln Asp
    290                 295                 300

Tyr Phe Phe Asp Lys Arg Asn Ala Val Ala Lys Glu Arg Asp Gln Glu
```

```
305                 310                 315                 320

Phe Glu Ala Asn Ala Thr Ala Lys Gln Gln Leu Ile Asp Glu Tyr Asp
                325                 330                 335

Ala Gln Ile Asn Pro Glu Gln Gly Leu Asp Gly Ala Arg Ser Lys Leu
            340                 345                 350
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<210> 1051
<211> 408
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(385)
<223> RXN02238

<400> 1051

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ggcgcttagc caaaacatag agcggtaggg tatgcttatc cgattgagca acctttcccg 60

ctcttaacac tactgtccat atacttttga aaaggtgtca gtg acc aac gtg agc   115
                                            Val Thr Asn Val Ser
                                              1               5

aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att   163
Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
                 10                  15                  20

acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac   211
Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
             25                  30                  35

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc   259
Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
         40                  45                  50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt   307
Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
     55                  60                  65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc   355
Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
 70                  75                  80                  85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca     405
Asn Ala Gly Leu Leu Asp His Glu Glu Gly
                 90                  95

cac                                                               408
```

<210> 1052
<211> 95
<212> PRT
<213> Corynebacterium glutamicum

<400> 1052
Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp
1 5 10 15

Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys
20 25 30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
35 40 45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
50 55 60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
65 70 75 80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly
85 90 95

<210> 1053
<211> 408
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(385)
<223> FRXA02238

<400> 1053
ggcgcttagc caaaacatag agcggtaggg tatgcttatc cgattgagca acctttcccg 60

ctcttaacac tactgtccat atacttttga aaaggtgtca gtg acc aac gtg agc 115
Val Thr Asn Val Ser
1 5

aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
10 15 20

acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
25 30 35

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
40 45 50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
55 60 65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355
Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
70 75 80 85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405
Asn Ala Gly Leu Leu Asp His Glu Glu Gly
90 95

```
cac                                                                    408


<210> 1054
<211> 95
<212> PRT
<213> Corynebacterium glutamicum

<400> 1054
Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp
  1               5                  10                  15

Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys
             20                  25                  30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
         35                  40                  45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
     50                  55                  60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
 65                  70                  75                  80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly
                 85                  90                  95


<210> 1055
<211> 800
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(777)
<223> RXN02254

<400> 1055
atc gcc gtt gcc gaa gaa ggc gga ttg tgg gaa aac ctc ctg cag cac   48
Ile Ala Val Ala Glu Glu Gly Gly Leu Trp Glu Asn Leu Leu Gln His
  1               5                  10                  15

cgc ttc ggt gga cat ggt gcg cta gct ggt cac gcc ttg gga aac ctc   96
Arg Phe Gly Gly His Gly Ala Leu Ala Gly His Ala Leu Gly Asn Leu
             20                  25                  30

gtg atc gcg gcg ttg acc gac att ttg ggc acc tcc cag cat gcg ctt   144
Val Ile Ala Ala Leu Thr Asp Ile Leu Gly Thr Ser Gln His Ala Leu
         35                  40                  45

gat caa atc gct caa ctc gct gga gcc aaa gga cgc atc atc ccg gta   192
Asp Gln Ile Ala Gln Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val
     50                  55                  60

tgt gct gaa cct ttg gat ctt gaa gcg gaa gta tca ggt cta gac tct   240
Cys Ala Glu Pro Leu Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser
 65                  70                  75                  80

gat gct cga gtc atg cgt caa gtt cgt ggt caa gtg gcg gta gct gca   288
Asp Ala Arg Val Met Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala
```

```
                 85                  90                  95

acc ccc ggg cag gtg cga cgc gtt cga atc att ccg gac aat cca gaa   336
Thr Pro Gly Gln Val Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu
            100                 105                 110

ccg aac ccc gct gcc atc gag gcc att ctc gat gca gat ttg gtc acc   384
Pro Asn Pro Ala Ala Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr
        115                 120                 125

ctt ggc cca ggt tcc tgg ttc tcc tct gtg att cca cac att ttg gtc   432
Leu Gly Pro Gly Ser Trp Phe Ser Ser Val Ile Pro His Ile Leu Val
    130                 135                 140

cca ggg atc gtt gat gcc ttg gcg cag aca aaa gca acc aaa acc gtg   480
Pro Gly Ile Val Asp Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val
145                 150                 155                 160

gtg tta aac ctg acg tcc gag cca ggg gag acc gcg gga ttc tct gca   528
Val Leu Asn Leu Thr Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala
                165                 170                 175

gaa cga cac atc cat gtg ctc cgc cag cat gct cga aac ctt cag gtt   576
Glu Arg His Ile His Val Leu Arg Gln His Ala Arg Asn Leu Gln Val
            180                 185                 190

gac caa gtc att gtc gat gcc aag aca ctg tcc tca caa acc gaa cgc   624
Asp Gln Val Ile Val Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg
        195                 200                 205

aat cat gta gaa cga gct gct cgc acc ctt ggt gca gaa gtc tcc ttc   672
Asn His Val Glu Arg Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe
    210                 215                 220

cat gat gtc cag gct gaa gat ggc cgt ggt cga ttc acc agt att cac   720
His Asp Val Gln Ala Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His
225                 230                 235                 240

gat cca gca aag ctg tgt gca gcg ttg ctg gca agt ttt gct gga gca   768
Asp Pro Ala Lys Leu Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala
                245                 250                 255

cga aag cgt taaggagtag gcgtgtcact gac                            800
Arg Lys Arg
```

<210> 1056
<211> 259
<212> PRT
<213> Corynebacterium glutamicum

<400> 1056

```
Ile Ala Val Ala Glu Glu Gly Gly Leu Trp Glu Asn Leu Leu Gln His
  1               5                  10                  15

Arg Phe Gly Gly His Gly Ala Leu Ala Gly His Ala Leu Gly Asn Leu
             20                  25                  30

Val Ile Ala Ala Leu Thr Asp Ile Leu Gly Thr Ser Gln His Ala Leu
         35                  40                  45
```

```
Asp Gln Ile Ala Gln Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val
     50                  55                  60

Cys Ala Glu Pro Leu Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser
 65                  70                  75                  80

Asp Ala Arg Val Met Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala
                 85                  90                  95

Thr Pro Gly Gln Val Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu
            100                 105                 110

Pro Asn Pro Ala Ala Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr
        115                 120                 125

Leu Gly Pro Gly Ser Trp Phe Ser Ser Val Ile Pro His Ile Leu Val
    130                 135                 140

Pro Gly Ile Val Asp Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val
145                 150                 155                 160

Val Leu Asn Leu Thr Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala
                165                 170                 175

Glu Arg His Ile His Val Leu Arg Gln His Ala Arg Asn Leu Gln Val
            180                 185                 190

Asp Gln Val Ile Val Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg
        195                 200                 205

Asn His Val Glu Arg Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe
    210                 215                 220

His Asp Val Gln Ala Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His
225                 230                 235                 240

Asp Pro Ala Lys Leu Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala
                245                 250                 255

Arg Lys Arg
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<210> 1057
<211> 804
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(781)
<223> FRXA02254

<400> 1057
ttgatcgccg atgccgaaga aggcggattg tgggaaaacc tcctgcagca ccgcttcagg 60

tggacatggt gcgctagctg gtcacgcctt gggaaacctc gtg atc gcg gcg ttg 115
                                        Val Ile Ala Ala Leu
                                          1   5

```
acc gac att ttg ggc acc tcc cag cat gcg ctt gat caa atc gct caa   163
Thr Asp Ile Leu Gly Thr Ser Gln His Ala Leu Asp Gln Ile Ala Gln
                10                  15                  20

ctc gct gga gcc aaa gga cgc atc atc ccg gta tgt gct gaa cct ttg   211
Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val Cys Ala Glu Pro Leu
            25                  30                  35

gat ctt gaa gcg gaa gta tca ggt cta gac tct gat gct cga gtc atg   259
Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser Asp Ala Arg Val Met
        40                  45                  50

cgt caa gtt cgt ggt caa gtg gcg gta gct gca acc ccc ggg cag gtg   307
Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala Thr Pro Gly Gln Val
    55                  60                  65

cga cgc gtt cga atc att ccg gac aat cca gaa ccg aac ccc gct gcc   355
Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu Pro Asn Pro Ala Ala
70                  75                  80                  85

atc gag gcc att ctc gat gca gat ttg gtc acc ctt ggc cca ggt tcc   403
Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr Leu Gly Pro Gly Ser
                90                  95                  100

tgg ttc tcc tct gtg att cca cac att ttg gtc cca ggg atc gtt gat   451
Trp Phe Ser Ser Val Ile Pro His Ile Leu Val Pro Gly Ile Val Asp
            105                 110                 115

gcc ttg gcg cag aca aaa gca acc aaa acc gtg gtg tta aac ctg acg   499
Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val Val Leu Asn Leu Thr
        120                 125                 130

tcc gag cca ggg gag acc gcg gga ttc tct gca gaa cga cac atc cat   547
Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala Glu Arg His Ile His
    135                 140                 145

gtg ctc cgc cag cat gct cga aac ctt cag gtt gac caa gtc att gtc   595
Val Leu Arg Gln His Ala Arg Asn Leu Gln Val Asp Gln Val Ile Val
150                 155                 160                 165

gat gcc aag aca ctg tcc tca caa acc gaa cgc aat cat gta gaa cga   643
Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg Asn His Val Glu Arg
                170                 175                 180

gct gct cgc acc ctt ggt gca gaa gtc tcc ttc cat gat gtc cag gct   691
Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe His Asp Val Gln Ala
            185                 190                 195

gaa gat ggc cgt ggt cga ttc acc agt att cac gat cca gca aag ctg   739
Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His Asp Pro Ala Lys Leu
        200                 205                 210

tgt gca gcg ttg ctg gca agt ttt gct gga gca cga aag cgt           781
Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala Arg Lys Arg
    215                 220                 225

taaggagtag gcgtgtcact gac                                       804
```

<210> 1058
<211> 227

<212> PRT
<213> Corynebacterium glutamicum

<400> 1058
Val Ile Ala Ala Leu Thr Asp Ile Leu Gly Thr Ser Gln His Ala Leu
1 5 10 15

Asp Gln Ile Ala Gln Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val
20 25 30

Cys Ala Glu Pro Leu Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser
35 40 45

Asp Ala Arg Val Met Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala
50 55 60

Thr Pro Gly Gln Val Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu
65 70 75 80

Pro Asn Pro Ala Ala Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr
85 90 95

Leu Gly Pro Gly Ser Trp Phe Ser Ser Val Ile Pro His Ile Leu Val
100 105 110

Pro Gly Ile Val Asp Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val
115 120 125

Val Leu Asn Leu Thr Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala
130 135 140

Glu Arg His Ile His Val Leu Arg Gln His Ala Arg Asn Leu Gln Val
145 150 155 160

Asp Gln Val Ile Val Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg
165 170 175

Asn His Val Glu Arg Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe
180 185 190

His Asp Val Gln Ala Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His
195 200 205

Asp Pro Ala Lys Leu Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala
210 215 220

Arg Lys Arg
225

<210> 1059
<211> 681
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(658)
<223> RXN02271

<400> 1059

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cactccccta tcctaagcca catctcggtt tattaaactg ttagtgaatt ctcacccgca 60

acactggtgt atttcagtta catccgtatg gttattggtt atg agc ttt ctt aac   115
                                            Met Ser Phe Leu Asn
                                              1               5

tct gca aaa acc aag acc gta gcc ctc acc gca acc ttc gtt ggt gca   163
Ser Ala Lys Thr Lys Thr Val Ala Leu Thr Ala Thr Phe Val Gly Ala
                 10                  15                  20

gca acc ctt gca act cct gca atc gca tcc gct gac atc gtc gac aac   211
Ala Thr Leu Ala Thr Pro Ala Ile Ala Ser Ala Asp Ile Val Asp Asn
             25                  30                  35

gcc ctc gca gcc ctc cca tcc ggt gag atc agc tgc tcc cag gct gaa   259
Ala Leu Ala Ala Leu Pro Ser Gly Glu Ile Ser Cys Ser Gln Ala Glu
         40                  45                  50

aag tac tgg acc acc gaa gct gat tac aac agc aag gtt gca cag gcc   307
Lys Tyr Trp Thr Thr Glu Ala Asp Tyr Asn Ser Lys Val Ala Gln Ala
     55                  60                  65

aac gcc ttg gca atg ttt gac tcc cgc ggc cca cag atc cag gca gct   355
Asn Ala Leu Ala Met Phe Asp Ser Arg Gly Pro Gln Ile Gln Ala Ala
 70                  75                  80                  85

ctc gca cgc gtt gac gaa gca gca aac cgc tgc gga ctc aag ggc ggc   403
Leu Ala Arg Val Asp Glu Ala Ala Asn Arg Cys Gly Leu Lys Gly Gly
                 90                  95                 100

acc gta gct gcg cag gct gag gca act gag gct gcg cct gcc gct cca   451
Thr Val Ala Ala Gln Ala Glu Ala Thr Glu Ala Ala Pro Ala Ala Pro
            105                 110                 115

gca cct gca ccg cag gat aac acc ggc act tct cag act gcc cct gcc   499
Ala Pro Ala Pro Gln Asp Asn Thr Gly Thr Ser Gln Thr Ala Pro Ala
        120                 125                 130

cca gca gca cca gca gca cca gca gct acc cct gtg gtt aac ctt gca   547
Pro Ala Ala Pro Ala Ala Pro Ala Ala Thr Pro Val Val Asn Leu Ala
    135                 140                 145

cct gca gga tca cca act ttc acc att gaa gtt cca gga gtt ggc ggg   595
Pro Ala Gly Ser Pro Thr Phe Thr Ile Glu Val Pro Gly Val Gly Gly
150                 155                 160                 165

gtt cag ctg cca gat cta tac caa atc gtc caa cag ttc ttg gca cag   643
Val Gln Leu Pro Asp Leu Tyr Gln Ile Val Gln Gln Phe Leu Ala Gln
                170                 175                 180

ttc gga atc aag atc taaatctatt cacatccctt aac                    681
Phe Gly Ile Lys Ile
            185
```

<210> 1060
<211> 186
<212> PRT
<213> Corynebacterium glutamicum

<400> 1060

```
Met Ser Phe Leu Asn Ser Ala Lys Thr Lys Thr Val Ala Leu Thr Ala
  1               5                  10                  15

Thr Phe Val Gly Ala Ala Thr Leu Ala Thr Pro Ala Ile Ala Ser Ala
            20                  25                  30

Asp Ile Val Asp Asn Ala Leu Ala Ala Leu Pro Ser Gly Glu Ile Ser
        35                  40                  45

Cys Ser Gln Ala Glu Lys Tyr Trp Thr Thr Glu Ala Asp Tyr Asn Ser
    50                  55                  60

Lys Val Ala Gln Ala Asn Ala Leu Ala Met Phe Asp Ser Arg Gly Pro
65                  70                  75                  80

Gln Ile Gln Ala Ala Leu Ala Arg Val Asp Glu Ala Ala Asn Arg Cys
                85                  90                  95

Gly Leu Lys Gly Gly Thr Val Ala Ala Gln Ala Glu Ala Thr Glu Ala
            100                 105                 110

Ala Pro Ala Ala Pro Ala Pro Ala Pro Gln Asp Asn Thr Gly Thr Ser
        115                 120                 125

Gln Thr Ala Pro Ala Pro Ala Ala Pro Ala Ala Pro Ala Ala Thr Pro
    130                 135                 140

Val Val Asn Leu Ala Pro Ala Gly Ser Pro Thr Phe Thr Ile Glu Val
145                 150                 155                 160

Pro Gly Val Gly Gly Val Gln Leu Pro Asp Leu Tyr Gln Ile Val Gln
                165                 170                 175

Gln Phe Leu Ala Gln Phe Gly Ile Lys Ile
            180                 185
```

<210> 1061
<211> 681
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(658)
<223> FRXA02271

<400> 1061
cactccccta tcctaagcca catctcggtt tattaaactg ttagtgaatt ctcacccgca 60

acactggtgt atttcagtta catccgtatg gttattggtt atg agc ttt ctt aac 115
                                                Met Ser Phe Leu Asn
                                                  1   5

tct gca aaa acc aag acc gta gcc ctc acc gca acc ttc gtt ggt gca 163
Ser Ala Lys Thr Lys Thr Val Ala Leu Thr Ala Thr Phe Val Gly Ala
                10   15   20

gca acc ctt gca act cct gca atc gca tcc gct gac atc gtc gac aac 211
Ala Thr Leu Ala Thr Pro Ala Ile Ala Ser Ala Asp Ile Val Asp Asn
            25   30   35

```
gcc ctc gca gcc ctc cca tcc ggt gag atc agc tgc tcc cag gct gaa   259
Ala Leu Ala Ala Leu Pro Ser Gly Glu Ile Ser Cys Ser Gln Ala Glu
         40                  45                  50

aag tac tgg acc acc gaa gct gat tac aac agc aag gtt gca cag gcc   307
Lys Tyr Trp Thr Thr Glu Ala Asp Tyr Asn Ser Lys Val Ala Gln Ala
     55                  60                  65

aac gcc ttg gca atg ttt gac tcc cgc ggc cca cag atc cag gca gct   355
Asn Ala Leu Ala Met Phe Asp Ser Arg Gly Pro Gln Ile Gln Ala Ala
 70                  75                  80                  85

ctc gca cgc gtt gac gaa gca gca aac cgc tgc gga ctc aag ggc ggc   403
Leu Ala Arg Val Asp Glu Ala Ala Asn Arg Cys Gly Leu Lys Gly Gly
                 90                  95                 100

acc gta gct gcg cag gct gag gca act gag gct gcg cct gcc gct cca   451
Thr Val Ala Ala Gln Ala Glu Ala Thr Glu Ala Ala Pro Ala Ala Pro
            105                 110                 115

gca cct gca ccg cag gat aac acc ggc act tct cag act gcc cct gcc   499
Ala Pro Ala Pro Gln Asp Asn Thr Gly Thr Ser Gln Thr Ala Pro Ala
        120                 125                 130

cca gca gca cca gca gca cca gca gct acc cct gtg gtt aac ctt gca   547
Pro Ala Ala Pro Ala Ala Pro Ala Ala Thr Pro Val Val Asn Leu Ala
    135                 140                 145

cct gca gga tca cca act ttc acc att gaa gtt cca gga gtt ggc ggg   595
Pro Ala Gly Ser Pro Thr Phe Thr Ile Glu Val Pro Gly Val Gly Gly
150                 155                 160                 165

gtt cag ctg cca gat cta tac caa atc gtc caa cag ttc ttg gca cag   643
Val Gln Leu Pro Asp Leu Tyr Gln Ile Val Gln Gln Phe Leu Ala Gln
                170                 175                 180

ttc gga atc aag atc taaatctatt cacatccctt aac                    681
Phe Gly Ile Lys Ile
            185
```

<210> 1062
<211> 186
<212> PRT
<213> Corynebacterium glutamicum

<400> 1062

```
Met Ser Phe Leu Asn Ser Ala Lys Thr Lys Thr Val Ala Leu Thr Ala
  1               5                  10                  15

Thr Phe Val Gly Ala Ala Thr Leu Ala Thr Pro Ala Ile Ala Ser Ala
             20                  25                  30

Asp Ile Val Asp Asn Ala Leu Ala Ala Leu Pro Ser Gly Glu Ile Ser
         35                  40                  45

Cys Ser Gln Ala Glu Lys Tyr Trp Thr Thr Glu Ala Asp Tyr Asn Ser
     50                  55                  60

Lys Val Ala Gln Ala Asn Ala Leu Ala Met Phe Asp Ser Arg Gly Pro
```

```
 65                  70                  75                  80

Gln Ile Gln Ala Ala Leu Ala Arg Val Asp Glu Ala Ala Asn Arg Cys
                85                  90                  95

Gly Leu Lys Gly Gly Thr Val Ala Ala Gln Ala Glu Ala Thr Glu Ala
            100                 105                 110

Ala Pro Ala Ala Pro Ala Pro Ala Pro Gln Asp Asn Thr Gly Thr Ser
        115                 120                 125

Gln Thr Ala Pro Ala Pro Ala Ala Pro Ala Ala Pro Ala Ala Thr Pro
    130                 135                 140

Val Val Asn Leu Ala Pro Ala Gly Ser Pro Thr Phe Thr Ile Glu Val
145                 150                 155                 160

Pro Gly Val Gly Gly Val Gln Leu Pro Asp Leu Tyr Gln Ile Val Gln
                165                 170                 175

Gln Phe Leu Ala Gln Phe Gly Ile Lys Ile
            180                 185
```

<210> 1063
<211> 1581
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1558)
<223> RXN02279

<400> 1063

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ggtaagaggg cattttccga tgcgcagcga ttcttgctca acgccgacga gctcgcggag 60

ctttctgatt atgagcgtct ggcttatgcc atcaccttgc ttg atc agc ctg gaa   115
                                          Leu Ile Ser Leu Glu
                                            1               5

aag aag cag aag gac gcg aac ttt ttc ctt tcg gag ctt cgc cgc cag   163
Lys Lys Gln Lys Asp Ala Asn Phe Phe Leu Ser Glu Leu Arg Arg Gln
                10                  15                  20

ggc tac cgc gct gtc gat ttc ttg gaa tcc cag act gtt gac cag ctg   211
Gly Tyr Arg Ala Val Asp Phe Leu Glu Ser Gln Thr Val Asp Gln Leu
            25                  30                  35

aat aac ccc gat gtc cag act tac ctc acc gaa gcg gaa ctg att cgc   259
Asn Asn Pro Asp Val Gln Thr Tyr Leu Thr Glu Ala Glu Leu Ile Arg
        40                  45                  50

gat gac ttg agg tct tgg gca gtc atc aat caa atg gca ttg gac aac   307
Asp Asp Leu Arg Ser Trp Ala Val Ile Asn Gln Met Ala Leu Asp Asn
    55                  60                  65

atc gat ctt gtt cca tac ggc gag gaa aac gac gag cca ctt gca atc   355
Ile Asp Leu Val Pro Tyr Gly Glu Glu Asn Asp Glu Pro Leu Ala Ile
70                  75                  80                  85
```

```
gcc cgc aag atc atc gag gaa acc gct tcc cat cct gag ctg aga ttc   403
Ala Arg Lys Ile Ile Glu Glu Thr Ala Ser His Pro Glu Leu Arg Phe
                 90                  95                 100

gaa aac ctc gag gcc cag ttc tcc gag ttc acc atc ttg ctt gct caa   451
Glu Asn Leu Glu Ala Gln Phe Ser Glu Phe Thr Ile Leu Leu Ala Gln
            105                 110                 115

agc ccg gag aac ctc gac gta gcc cgc tac cag gag ctt cgt aca cag   499
Ser Pro Glu Asn Leu Asp Val Ala Arg Tyr Gln Glu Leu Arg Thr Gln
        120                 125                 130

gga aac ttt gtt caa gaa ctc gcc ttg gac agc att ttc ggc caa cat   547
Gly Asn Phe Val Gln Glu Leu Ala Leu Asp Ser Ile Phe Gly Gln His
    135                 140                 145

gcc gtt gtt caa gac acc gga aac ggc gaa gcc atc cta gat gaa act   595
Ala Val Val Gln Asp Thr Gly Asn Gly Glu Ala Ile Leu Asp Glu Thr
150                 155                 160                 165

atc ggg tac atg atc ggc gcc ggc atg cgt gaa acc act gcc cgc acc   643
Ile Gly Tyr Met Ile Gly Ala Gly Met Arg Glu Thr Thr Ala Arg Thr
                170                 175                 180

gcc agc cag ttc gcg cag ctt tac tca ttt gtg ggc agg cag gaa cgc   691
Ala Ser Gln Phe Ala Gln Leu Tyr Ser Phe Val Gly Arg Gln Glu Arg
            185                 190                 195

tcc att gaa atg gca cga ctc gct ttc gag gaa ctt caa gcg gca gga   739
Ser Ile Glu Met Ala Arg Leu Ala Phe Glu Glu Leu Gln Ala Ala Gly
        200                 205                 210

ctt ccc cac cgt gag gaa gaa ctg cga ttg ggc atg caa ctc gcc cag   787
Leu Pro His Arg Glu Glu Glu Leu Arg Leu Gly Met Gln Leu Ala Gln
    215                 220                 225

gtt gaa cca att gaa gcc cgc gaa atc ctg gaa aag ctg ctg ctg cct   835
Val Glu Pro Ile Glu Ala Arg Glu Ile Leu Glu Lys Leu Leu Leu Pro
230                 235                 240                 245

aaa ttc gag cag aat ctg aca ctt gat gaa ctt gaa act gaa gca ctc   883
Lys Phe Glu Gln Asn Leu Thr Leu Asp Glu Leu Glu Thr Glu Ala Leu
                250                 255                 260

ctt cct ttg ggt gct acc gtt gct atc cac gac ccc cag gct gcc gca   931
Leu Pro Leu Gly Ala Thr Val Ala Ile His Asp Pro Gln Ala Ala Ala
            265                 270                 275

gca att ttg cgc cac gct cgc gaa aac gcc gca ggg ttc ggc aac ttc   979
Ala Ile Leu Arg His Ala Arg Glu Asn Ala Ala Gly Phe Gly Asn Phe
        280                 285                 290

gaa ctc gca gtc caa gcg atg acc atg atc acg gat gtc ctc tac acc   1027
Glu Leu Ala Val Gln Ala Met Thr Met Ile Thr Asp Val Leu Tyr Thr
    295                 300                 305

caa aac atg cac gag caa ctg ctg gag gag ctc aac cac tct ctc ccc   1075
Gln Asn Met His Glu Gln Leu Leu Glu Glu Leu Asn His Ser Leu Pro
310                 315                 320                 325

tat gct caa atg ctt gat gat caa cac caa gct gaa ctg aaa ctg ctg   1123
```

```
Tyr Ala Gln Met Leu Asp Asp Gln His Gln Ala Glu Leu Lys Leu Leu
                330                 335                 340

gac agc atc gcc atc gtc cag gca gac ctc ggt tcc acc gaa gcg ctg   1171
Asp Ser Ile Ala Ile Val Gln Ala Asp Leu Gly Ser Thr Glu Ala Leu
            345                 350                 355

gaa acc ctg ggc acc gca atg gga ctc gca gaa acc aca gct cag aag   1219
Glu Thr Leu Gly Thr Ala Met Gly Leu Ala Glu Thr Thr Ala Gln Lys
        360                 365                 370

cta tac gtg cag gaa tcc ctc aac cgc gca tac ttc act ttt gcc cgc   1267
Leu Tyr Val Gln Glu Ser Leu Asn Arg Ala Tyr Phe Thr Phe Ala Arg
    375                 380                 385

cct gaa gat tgc atc agc gga gca gcc gac gct tct gcc ctg gcc atg   1315
Pro Glu Asp Cys Ile Ser Gly Ala Ala Asp Ala Ser Ala Leu Ala Met
390                 395                 400                 405

caa aac gat gac cct tcc aat gca gct gcc cag ttg gag cag tgt gca   1363
Gln Asn Asp Asp Pro Ser Asn Ala Ala Ala Gln Leu Glu Gln Cys Ala
                410                 415                 420

cag tac ttg ttc caa ttg ggc cac gaa act gac ggc gca agc ctg ctg   1411
Gln Tyr Leu Phe Gln Leu Gly His Glu Thr Asp Gly Ala Ser Leu Leu
            425                 430                 435

gaa tct gca ttc agg gtt gaa ggc atc ccc act gag cag gca ctg tac   1459
Glu Ser Ala Phe Arg Val Glu Gly Ile Pro Thr Glu Gln Ala Leu Tyr
        440                 445                 450

tac gca aat gca ctg tct tcc atc tat gaa gat ttc ggc gat tcc gcg   1507
Tyr Ala Asn Ala Leu Ser Ser Ile Tyr Glu Asp Phe Gly Asp Ser Ala
    455                 460                 465

aag tcg cag tac tgg gag cag cag gcg cag gaa aag cag cag ctt ctg   1555
Lys Ser Gln Tyr Trp Glu Gln Gln Ala Gln Glu Lys Gln Gln Leu Leu
470                 475                 480                 485

gag taacggccgt ttaaagagtc gaa                                    1581
Glu
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<210> 1064
<211> 486
<212> PRT
<213> Corynebacterium glutamicum

<400> 1064

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Leu Ile Ser Leu Glu Lys Lys Gln Lys Asp Ala Asn Phe Phe Leu Ser
  1               5                  10                  15

Glu Leu Arg Arg Gln Gly Tyr Arg Ala Val Asp Phe Leu Glu Ser Gln
             20                  25                  30

Thr Val Asp Gln Leu Asn Asn Pro Asp Val Gln Thr Tyr Leu Thr Glu
         35                  40                  45

Ala Glu Leu Ile Arg Asp Asp Leu Arg Ser Trp Ala Val Ile Asn Gln
     50                  55                  60
```

```
Met Ala Leu Asp Asn Ile Asp Leu Val Pro Tyr Gly Glu Glu Asn Asp
 65                  70                  75                  80

Glu Pro Leu Ala Ile Ala Arg Lys Ile Ile Glu Glu Thr Ala Ser His
                85                  90                  95

Pro Glu Leu Arg Phe Glu Asn Leu Glu Ala Gln Phe Ser Glu Phe Thr
            100                 105                 110

Ile Leu Leu Ala Gln Ser Pro Glu Asn Leu Asp Val Ala Arg Tyr Gln
        115                 120                 125

Glu Leu Arg Thr Gln Gly Asn Phe Val Gln Glu Leu Ala Leu Asp Ser
    130                 135                 140

Ile Phe Gly Gln His Ala Val Val Gln Asp Thr Gly Asn Gly Glu Ala
145                 150                 155                 160

Ile Leu Asp Glu Thr Ile Gly Tyr Met Ile Gly Ala Gly Met Arg Glu
                165                 170                 175

Thr Thr Ala Arg Thr Ala Ser Gln Phe Ala Gln Leu Tyr Ser Phe Val
            180                 185                 190

Gly Arg Gln Glu Arg Ser Ile Glu Met Ala Arg Leu Ala Phe Glu Glu
        195                 200                 205

Leu Gln Ala Ala Gly Leu Pro His Arg Glu Glu Glu Leu Arg Leu Gly
    210                 215                 220

Met Gln Leu Ala Gln Val Glu Pro Ile Glu Ala Arg Glu Ile Leu Glu
225                 230                 235                 240

Lys Leu Leu Leu Pro Lys Phe Glu Gln Asn Leu Thr Leu Asp Glu Leu
                245                 250                 255

Glu Thr Glu Ala Leu Leu Pro Leu Gly Ala Thr Val Ala Ile His Asp
            260                 265                 270

Pro Gln Ala Ala Ala Ala Ile Leu Arg His Ala Arg Glu Asn Ala Ala
        275                 280                 285

Gly Phe Gly Asn Phe Glu Leu Ala Val Gln Ala Met Thr Met Ile Thr
    290                 295                 300

Asp Val Leu Tyr Thr Gln Asn Met His Glu Gln Leu Leu Glu Glu Leu
305                 310                 315                 320

Asn His Ser Leu Pro Tyr Ala Gln Met Leu Asp Asp Gln His Gln Ala
                325                 330                 335

Glu Leu Lys Leu Leu Asp Ser Ile Ala Ile Val Gln Ala Asp Leu Gly
            340                 345                 350

Ser Thr Glu Ala Leu Glu Thr Leu Gly Thr Ala Met Gly Leu Ala Glu
        355                 360                 365

Thr Thr Ala Gln Lys Leu Tyr Val Gln Glu Ser Leu Asn Arg Ala Tyr
    370                 375                 380
```

```
Phe Thr Phe Ala Arg Pro Glu Asp Cys Ile Ser Gly Ala Ala Asp Ala
385                 390                 395                 400

Ser Ala Leu Ala Met Gln Asn Asp Asp Pro Ser Asn Ala Ala Ala Gln
                405                 410                 415

Leu Glu Gln Cys Ala Gln Tyr Leu Phe Gln Leu Gly His Glu Thr Asp
            420                 425                 430

Gly Ala Ser Leu Leu Glu Ser Ala Phe Arg Val Glu Gly Ile Pro Thr
        435                 440                 445

Glu Gln Ala Leu Tyr Tyr Ala Asn Ala Leu Ser Ser Ile Tyr Glu Asp
    450                 455                 460

Phe Gly Asp Ser Ala Lys Ser Gln Tyr Trp Glu Gln Gln Ala Gln Glu
465                 470                 475                 480

Lys Gln Gln Leu Leu Glu
                485
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Sequence Listing

<210> 1065
<211> 1427
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1404)
<223> FRXA02279

<400> 1065

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Xaa Ala Arg Ala Thr Ala Leu Val Asp Phe Leu Glu Ser Gln Thr Val
  1               5                  10                  15

gac cag ctg aat aac ccc gat gtc cag act tac ctc acc gaa gcg gaa   96
Asp Gln Leu Asn Asn Pro Asp Val Gln Thr Tyr Leu Thr Glu Ala Glu
             20                  25                  30

ctg att cgc gat gac ttg agg tct tgg gca gtc atc aaa tca aat ggc   144
Leu Ile Arg Asp Asp Leu Arg Ser Trp Ala Val Ile Lys Ser Asn Gly
         35                  40                  45

att gga caa cat cga tct tgt tcc ata cgg cga gga aac gac gag cca   192
Ile Gly Gln His Arg Ser Cys Ser Ile Arg Arg Gly Asn Asp Glu Pro
     50                  55                  60

ctt gca atc gcc cgc aag atc atc gag gaa acc gct tcc cat cct gag   240
Leu Ala Ile Ala Arg Lys Ile Ile Glu Glu Thr Ala Ser His Pro Glu
 65                  70                  75                  80

ctg aga ttc gaa aac ctc gag gcc cag ttc tcc gag ttc acc atc ttg   288
Leu Arg Phe Glu Asn Leu Glu Ala Gln Phe Ser Glu Phe Thr Ile Leu
                 85                  90                  95

ctt gct caa agc ccg gag aac ctc gac gta gcc cgc tac cag gag ctt   336
Leu Ala Gln Ser Pro Glu Asn Leu Asp Val Ala Arg Tyr Gln Glu Leu
            100                 105                 110
```

```
cgt aca cag gga aac ttt gtt caa gaa ctc gcc ttg gac agc att ttc   384
Arg Thr Gln Gly Asn Phe Val Gln Glu Leu Ala Leu Asp Ser Ile Phe
        115                 120                 125

ggc caa cat gcc gtt gtt caa gac acc gga aac ggc gaa gcc atc cta   432
Gly Gln His Ala Val Val Gln Asp Thr Gly Asn Gly Glu Ala Ile Leu
    130                 135                 140

gat gaa act atc ggg tac atg atc ggc gcc ggc atg cgt gaa acc act   480
Asp Glu Thr Ile Gly Tyr Met Ile Gly Ala Gly Met Arg Glu Thr Thr
145                 150                 155                 160

gcc cgc acc gcc agc cag ttc gcg cag ctt tac tca ttt gtg ggc agg   528
Ala Arg Thr Ala Ser Gln Phe Ala Gln Leu Tyr Ser Phe Val Gly Arg
                165                 170                 175

cag gaa cgc tcc att gaa atg gca cga ctc gct ttc gag gaa ctt caa   576
Gln Glu Arg Ser Ile Glu Met Ala Arg Leu Ala Phe Glu Glu Leu Gln
            180                 185                 190

gcg gca gga ctt ccc cac cgt gag gaa gaa ctg cga ttg ggc atg caa   624
Ala Ala Gly Leu Pro His Arg Glu Glu Glu Leu Arg Leu Gly Met Gln
        195                 200                 205

ctc gcc cag gtt gaa cca att gaa gcc cgc gaa atc ctg gaa aag ctg   672
Leu Ala Gln Val Glu Pro Ile Glu Ala Arg Glu Ile Leu Glu Lys Leu
    210                 215                 220

ctg ctg cct aaa ttc gag cag aat ctg aca ctt gat gaa ctt gaa act   720
Leu Leu Pro Lys Phe Glu Gln Asn Leu Thr Leu Asp Glu Leu Glu Thr
225                 230                 235                 240

gaa gca ctc ctt cct ttg ggt gct acc gtt gct atc cac gac ccc cag   768
Glu Ala Leu Leu Pro Leu Gly Ala Thr Val Ala Ile His Asp Pro Gln
                245                 250                 255

gct gcc gca gca att ttg cgc cac gct cgc gaa aac gcc gca ggg ttc   816
Ala Ala Ala Ala Ile Leu Arg His Ala Arg Glu Asn Ala Ala Gly Phe
            260                 265                 270

ggc aac ttc gaa ctc gca gtc caa gcg atg acc atg atc acg gat gtc   864
Gly Asn Phe Glu Leu Ala Val Gln Ala Met Thr Met Ile Thr Asp Val
        275                 280                 285

ctc tac acc caa aac atg cac gag caa ctg ctg gag gag ctc aac cac   912
Leu Tyr Thr Gln Asn Met His Glu Gln Leu Leu Glu Glu Leu Asn His
    290                 295                 300

tct ctc ccc tat gct caa atg ctt gat gat caa cac caa gct gaa ctg   960
Ser Leu Pro Tyr Ala Gln Met Leu Asp Asp Gln His Gln Ala Glu Leu
305                 310                 315                 320

aaa ctg ctg gac agc atc gcc atc gtc cag gca gac ctc ggt tcc acc   1008
Lys Leu Leu Asp Ser Ile Ala Ile Val Gln Ala Asp Leu Gly Ser Thr
                325                 330                 335

gaa gcg ctg gaa acc ctg ggc acc gca atg gga ctc gca gaa acc aca   1056
Glu Ala Leu Glu Thr Leu Gly Thr Ala Met Gly Leu Ala Glu Thr Thr
            340                 345                 350

gct cag aag cta tac gtg cag gaa tcc ctc aac cgc gca tac ttc act   1104
```

```
Ala Gln Lys Leu Tyr Val Gln Glu Ser Leu Asn Arg Ala Tyr Phe Thr
        355                 360                 365

ttt gcc cgc cct gaa gat tgc atc agc gga gca gcc gac gct tct gcc   1152
Phe Ala Arg Pro Glu Asp Cys Ile Ser Gly Ala Ala Asp Ala Ser Ala
    370                 375                 380

ctg gcc atg caa aac gat gac cct tcc aat gca gct gcc cag ttg gag   1200
Leu Ala Met Gln Asn Asp Asp Pro Ser Asn Ala Ala Ala Gln Leu Glu
385                 390                 395                 400

cag tgt gca cag tac ttg ttc caa ttg ggc cac gaa act gac ggc gca   1248
Gln Cys Ala Gln Tyr Leu Phe Gln Leu Gly His Glu Thr Asp Gly Ala
                405                 410                 415

agc ctg ctg gaa tct gca ttc agg gtt gaa ggc atc ccc act gag cag   1296
Ser Leu Leu Glu Ser Ala Phe Arg Val Glu Gly Ile Pro Thr Glu Gln
            420                 425                 430

gca ctg tac tac gca aat gca ctg tct tcc atc tat gaa gat ttc ggc   1344
Ala Leu Tyr Tyr Ala Asn Ala Leu Ser Ser Ile Tyr Glu Asp Phe Gly
        435                 440                 445

gat tcc gcg aag tcg cag tac tgg gag cag cag gcg cag gaa aag cag   1392
Asp Ser Ala Lys Ser Gln Tyr Trp Glu Gln Gln Ala Gln Glu Lys Gln
    450                 455                 460

cag ctt ctg gag taacggccgt ttaaagagtc gaa                        1427
Gln Leu Leu Glu
465
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<210> 1066
<211> 468
<212> PRT
<213> Corynebacterium glutamicum

<400> 1066

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Xaa Ala Arg Ala Thr Ala Leu Val Asp Phe Leu Glu Ser Gln Thr Val
  1               5                  10                  15

Asp Gln Leu Asn Asn Pro Asp Val Gln Thr Tyr Leu Thr Glu Ala Glu
             20                  25                  30

Leu Ile Arg Asp Asp Leu Arg Ser Trp Ala Val Ile Lys Ser Asn Gly
         35                  40                  45

Ile Gly Gln His Arg Ser Cys Ser Ile Arg Arg Gly Asn Asp Glu Pro
     50                  55                  60

Leu Ala Ile Ala Arg Lys Ile Ile Glu Glu Thr Ala Ser His Pro Glu
 65                  70                  75                  80

Leu Arg Phe Glu Asn Leu Glu Ala Gln Phe Ser Glu Phe Thr Ile Leu
                 85                  90                  95

Leu Ala Gln Ser Pro Glu Asn Leu Asp Val Ala Arg Tyr Gln Glu Leu
            100                 105                 110

Arg Thr Gln Gly Asn Phe Val Gln Glu Leu Ala Leu Asp Ser Ile Phe
        115                 120                 125
```

Gly Gln His Ala Val Val Gln Asp Thr Gly Asn Gly Glu Ala Ile Leu
130 135 140

Asp Glu Thr Ile Gly Tyr Met Ile Gly Ala Gly Met Arg Glu Thr Thr
145 150 155 160

Ala Arg Thr Ala Ser Gln Phe Ala Gln Leu Tyr Ser Phe Val Gly Arg
165 170 175

Gln Glu Arg Ser Ile Glu Met Ala Arg Leu Ala Phe Glu Glu Leu Gln
180 185 190

Ala Ala Gly Leu Pro His Arg Glu Glu Glu Leu Arg Leu Gly Met Gln
195 200 205

Leu Ala Gln Val Glu Pro Ile Glu Ala Arg Glu Ile Leu Glu Lys Leu
210 215 220

Leu Leu Pro Lys Phe Glu Gln Asn Leu Thr Leu Asp Glu Leu Glu Thr
225 230 235 240

Glu Ala Leu Leu Pro Leu Gly Ala Thr Val Ala Ile His Asp Pro Gln
245 250 255

Ala Ala Ala Ala Ile Leu Arg His Ala Arg Glu Asn Ala Ala Gly Phe
260 265 270

Gly Asn Phe Glu Leu Ala Val Gln Ala Met Thr Met Ile Thr Asp Val
275 280 285

Leu Tyr Thr Gln Asn Met His Glu Gln Leu Leu Glu Glu Leu Asn His
290 295 300

Ser Leu Pro Tyr Ala Gln Met Leu Asp Asp Gln His Gln Ala Glu Leu
305 310 315 320

Lys Leu Leu Asp Ser Ile Ala Ile Val Gln Ala Asp Leu Gly Ser Thr
325 330 335

Glu Ala Leu Glu Thr Leu Gly Thr Ala Met Gly Leu Ala Glu Thr Thr
340 345 350

Ala Gln Lys Leu Tyr Val Gln Glu Ser Leu Asn Arg Ala Tyr Phe Thr
355 360 365

Phe Ala Arg Pro Glu Asp Cys Ile Ser Gly Ala Ala Asp Ala Ser Ala
370 375 380

Leu Ala Met Gln Asn Asp Asp Pro Ser Asn Ala Ala Ala Gln Leu Glu
385 390 395 400

Gln Cys Ala Gln Tyr Leu Phe Gln Leu Gly His Glu Thr Asp Gly Ala
405 410 415

Ser Leu Leu Glu Ser Ala Phe Arg Val Glu Gly Ile Pro Thr Glu Gln
420 425 430

Ala Leu Tyr Tyr Ala Asn Ala Leu Ser Ser Ile Tyr Glu Asp Phe Gly
435 440 445

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Asp Ser Ala Lys Ser Gln Tyr Trp Glu Gln Gln Ala Gln Glu Lys Gln
    450                 455                 460

Gln Leu Leu Glu
465
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<210> 1067
<211> 612
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(589)
<223> RXN02296

<400> 1067

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gcatcatttg tgttgtttaa agtatatggc tgttgaagtg ccattttcgc ggattagcat 60

gggaatcacc agtatttctg gacggttaag gatgattcat atg cgt aat caa aca   115
                                            Met Arg Asn Gln Thr
                                              1               5

atc gct gcg gtc gca gct ttg gtc ctg ctc acc gcc gcc acg ccc gcg   163
Ile Ala Ala Val Ala Ala Leu Val Leu Leu Thr Ala Ala Thr Pro Ala
                 10                  15                  20

atc gct gcc acc ccg gcg aca gct gga aac gga ctc tat tcc att gac   211
Ile Ala Ala Thr Pro Ala Thr Ala Gly Asn Gly Leu Tyr Ser Ile Asp
             25                  30                  35

atg ggc gac gag caa aag ctt acc tgc gtg ctt ttc gat gag ccc tcc   259
Met Gly Asp Glu Gln Lys Leu Thr Cys Val Leu Phe Asp Glu Pro Ser
         40                  45                  50

acc gaa gcg cac gtc gtc gcc agc tgt gct gcg act ttc ccg gtg acc   307
Thr Glu Ala His Val Val Ala Ser Cys Ala Ala Thr Phe Pro Val Thr
     55                  60                  65

tgg aag ctt ctc gac ggc gct cac gaa caa gcc gcg aaa ctt gaa atc   355
Trp Lys Leu Leu Asp Gly Ala His Glu Gln Ala Ala Lys Leu Glu Ile
 70                  75                  80                  85

acc cag gct caa gac ggt gaa ctc tcg gtg aca gcc agc aag cag ccg   403
Thr Gln Ala Gln Asp Gly Glu Leu Ser Val Thr Ala Ser Lys Gln Pro
                 90                  95                 100

ttg atc acc acg atg att gcg ccc acc agc atc act aag ccc atc act   451
Leu Ile Thr Thr Met Ile Ala Pro Thr Ser Ile Thr Lys Pro Ile Thr
            105                 110                 115

gtc aat agg ctt gtg gtt gtt cct ggt gag aat gag gtt cgc ttt tat   499
Val Asn Arg Leu Val Val Val Pro Gly Glu Asn Glu Val Arg Phe Tyr
        120                 125                 130

gct acc gat cct gat gtt tta cca gtg ctg atc acg cct gac tcc tat   547
Ala Thr Asp Pro Asp Val Leu Pro Val Leu Ile Thr Pro Asp Ser Tyr
    135                 140                 145

gaa gtg ttg acc gat tcc gct gct aaa gtg aaa gcg aca tta           589
```

Glu Val Leu Thr Asp Ser Ala Ala Lys Val Lys Ala Thr Leu
150 155 160

tgaaataaac gtggatcaag gag 612

<210> 1068
<211> 163
<212> PRT
<213> Corynebacterium glutamicum

<400> 1068
Met Arg Asn Gln Thr Ile Ala Ala Val Ala Ala Leu Val Leu Leu Thr
1 5 10 15

Ala Ala Thr Pro Ala Ile Ala Ala Thr Pro Ala Thr Ala Gly Asn Gly
20 25 30

Leu Tyr Ser Ile Asp Met Gly Asp Glu Gln Lys Leu Thr Cys Val Leu
35 40 45

Phe Asp Glu Pro Ser Thr Glu Ala His Val Val Ala Ser Cys Ala Ala
50 55 60

Thr Phe Pro Val Thr Trp Lys Leu Leu Asp Gly Ala His Glu Gln Ala
65 70 75 80

Ala Lys Leu Glu Ile Thr Gln Ala Gln Asp Gly Glu Leu Ser Val Thr
85 90 95

Ala Ser Lys Gln Pro Leu Ile Thr Thr Met Ile Ala Pro Thr Ser Ile
100 105 110

Thr Lys Pro Ile Thr Val Asn Arg Leu Val Val Val Pro Gly Glu Asn
115 120 125

Glu Val Arg Phe Tyr Ala Thr Asp Pro Asp Val Leu Pro Val Leu Ile
130 135 140

Thr Pro Asp Ser Tyr Glu Val Leu Thr Asp Ser Ala Ala Lys Val Lys
145 150 155 160

Ala Thr Leu

<210> 1069
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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(589)
<223> FRXA02296

<400> 1069
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gggaatcacc agtatttctg gacggttaag gatgattcat atg cgt aat caa aca 115
Met Arg Asn Gln Thr

```
                                                    1               5

atc gct gcg gtc gca gct ttg gtc ctg ctc acc gcc gcc acg ccc gcg   163
Ile Ala Ala Val Ala Ala Leu Val Leu Leu Thr Ala Ala Thr Pro Ala
                10                  15                  20

atc gct gcc acc ccg gcg aca gct gga aac gga ctc tat tcc att gac   211
Ile Ala Ala Thr Pro Ala Thr Ala Gly Asn Gly Leu Tyr Ser Ile Asp
            25                  30                  35

atg ggc gac gag caa aag ctt acc tgc gtg ctt ttc gat gag ccc tcc   259
Met Gly Asp Glu Gln Lys Leu Thr Cys Val Leu Phe Asp Glu Pro Ser
        40                  45                  50

acc gaa gcg cac gtc gtc gcc agc tgt gct gcg act ttc ccg gtg acc   307
Thr Glu Ala His Val Val Ala Ser Cys Ala Ala Thr Phe Pro Val Thr
    55                  60                  65

tgg aag ctt ctc gac ggc gct cac gaa caa gcc gcg aaa ctt gaa atc   355
Trp Lys Leu Leu Asp Gly Ala His Glu Gln Ala Ala Lys Leu Glu Ile
70                  75                  80                  85

acc cag gct caa gac ggt gaa ctc tcg gtg aca gcc agc aag cag ccg   403
Thr Gln Ala Gln Asp Gly Glu Leu Ser Val Thr Ala Ser Lys Gln Pro
                90                  95                  100

ttg atc acc acg atg att gcg ccc acc agc atc act aag ccc atc act   451
Leu Ile Thr Thr Met Ile Ala Pro Thr Ser Ile Thr Lys Pro Ile Thr
            105                 110                 115

gtc aat agg ctt gtg gtt gtt cct ggt gag aat gag gtt cgc ttt tat   499
Val Asn Arg Leu Val Val Val Pro Gly Glu Asn Glu Val Arg Phe Tyr
        120                 125                 130

gct acc gat cct gat gtt tta cca gtg ctg atc acg cct gac tcc tat   547
Ala Thr Asp Pro Asp Val Leu Pro Val Leu Ile Thr Pro Asp Ser Tyr
    135                 140                 145

gaa gtg ttg acc gat tcc gct gct aaa gtg aaa gcg aca tta           589
Glu Val Leu Thr Asp Ser Ala Ala Lys Val Lys Ala Thr Leu
150                 155                 160

tgaaataaac gtggatcaag gag                                        612


<210> 1070
<211> 163
<212> PRT
<213> Corynebacterium glutamicum

<400> 1070
Met Arg Asn Gln Thr Ile Ala Ala Val Ala Ala Leu Val Leu Leu Thr
  1               5                  10                  15

Ala Ala Thr Pro Ala Ile Ala Ala Thr Pro Ala Thr Ala Gly Asn Gly
            20                  25                  30

Leu Tyr Ser Ile Asp Met Gly Asp Glu Gln Lys Leu Thr Cys Val Leu
        35                  40                  45

Phe Asp Glu Pro Ser Thr Glu Ala His Val Val Ala Ser Cys Ala Ala
```

```
     50                  55                  60

Thr Phe Pro Val Thr Trp Lys Leu Leu Asp Gly Ala His Glu Gln Ala
 65                  70                  75                  80

Ala Lys Leu Glu Ile Thr Gln Ala Gln Asp Gly Glu Leu Ser Val Thr
                85                  90                  95

Ala Ser Lys Gln Pro Leu Ile Thr Thr Met Ile Ala Pro Thr Ser Ile
            100                 105                 110

Thr Lys Pro Ile Thr Val Asn Arg Leu Val Val Val Pro Gly Glu Asn
        115                 120                 125

Glu Val Arg Phe Tyr Ala Thr Asp Pro Asp Val Leu Pro Val Leu Ile
    130                 135                 140

Thr Pro Asp Ser Tyr Glu Val Leu Thr Asp Ser Ala Ala Lys Val Lys
145                 150                 155                 160

Ala Thr Leu
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Do not add any new matter to this document

<210> 1071
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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(433)
<223> RXN02300

<400> 1071

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caatgctgtc caaagcggag cgtaaagata aggatcagaa atg aaa act tat gca   115
                                            Met Lys Thr Tyr Ala
                                              1               5

gta cta att gcg gtg gca ggg ttg gca ctt gct ggg tgt agc tcg tcg   163
Val Leu Ile Ala Val Ala Gly Leu Ala Leu Ala Gly Cys Ser Ser Ser
                 10                  15                  20

gct cct gga atc tgg cgt gcc act gaa ccc gca gat gcc tac ctt gaa   211
Ala Pro Gly Ile Trp Arg Ala Thr Glu Pro Ala Asp Ala Tyr Leu Glu
             25                  30                  35

ata gcc gat gac ggc acg ctg tcc gga acc gac ggc tgc aac aga ctt   259
Ile Ala Asp Asp Gly Thr Leu Ser Gly Thr Asp Gly Cys Asn Arg Leu
         40                  45                  50

ttt ggt ggc tgg gaa aaa gac ggc tct acc atc act ttc ggc gcc atc   307
Phe Gly Gly Trp Glu Lys Asp Gly Ser Thr Ile Thr Phe Gly Ala Ile
     55                  60                  65

ggt atg aca gaa atg tac tgc gaa ggc gtc aac gat tgg ctg tcc cag   355
Gly Met Thr Glu Met Tyr Cys Glu Gly Val Asn Asp Trp Leu Ser Gln
 70                  75                  80                  85
```

```
atg cac acc gcc acc gtc acc gat gcc acc atg acc att ttc aac gag   403
Met His Thr Ala Thr Val Thr Asp Ala Thr Met Thr Ile Phe Asn Glu
                 90                  95                  100

gcc ggc agc aat att ggc gag cta aaa cgc taaatgcttc tcgacgtcaa     453
Ala Gly Ser Asn Ile Gly Glu Leu Lys Arg
            105                 110

aag                                                               456
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<210> 1072
<211> 111
<212> PRT
<213> Corynebacterium glutamicum

<400> 1072

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Met Lys Thr Tyr Ala Val Leu Ile Ala Val Ala Gly Leu Ala Leu Ala
  1               5                  10                  15

Gly Cys Ser Ser Ser Ala Pro Gly Ile Trp Arg Ala Thr Glu Pro Ala
             20                  25                  30

Asp Ala Tyr Leu Glu Ile Ala Asp Asp Gly Thr Leu Ser Gly Thr Asp
         35                  40                  45

Gly Cys Asn Arg Leu Phe Gly Gly Trp Glu Lys Asp Gly Ser Thr Ile
     50                  55                  60

Thr Phe Gly Ala Ile Gly Met Thr Glu Met Tyr Cys Glu Gly Val Asn
 65                  70                  75                  80

Asp Trp Leu Ser Gln Met His Thr Ala Thr Val Thr Asp Ala Thr Met
                 85                  90                  95

Thr Ile Phe Asn Glu Ala Gly Ser Asn Ile Gly Glu Leu Lys Arg
            100                 105                 110
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<210> 1073
<211> 456
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(433)
<223> FRXA02300

<400> 1073

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gggtcattcc ggtgaacacg gatttcgcgc cggtgaatct gacggtcagc caattgcggg 60

caatgctgtc caaagcggag cgtaaagata aggatcagaa atg aaa act tat gca   115
                                              Met Lys Thr Tyr Ala
                                                1               5

gta cta att gcg gtg gca ggg ttg gca ctt gct ggg tgt agc tcg tcg   163
Val Leu Ile Ala Val Ala Gly Leu Ala Leu Ala Gly Cys Ser Ser Ser
                10                  15                  20

gct cct gga atc tgg cgt gcc act gaa ccc gca gat gcc tac ctt gaa   211
```

```
Ala Pro Gly Ile Trp Arg Ala Thr Glu Pro Ala Asp Ala Tyr Leu Glu
            25                  30                  35

ata gcc gat gac ggc acg ctg tcc gga acc gac ggc tgc aac aga ctt   259
Ile Ala Asp Asp Gly Thr Leu Ser Gly Thr Asp Gly Cys Asn Arg Leu
        40                  45                  50

ttt ggt ggc tgg gaa aaa gac ggc tct acc atc act ttc ggc gcc atc   307
Phe Gly Gly Trp Glu Lys Asp Gly Ser Thr Ile Thr Phe Gly Ala Ile
    55                  60                  65

ggt atg aca gaa atg tac tgc gaa ggc gtc aac gat tgg ctg tcc cag   355
Gly Met Thr Glu Met Tyr Cys Glu Gly Val Asn Asp Trp Leu Ser Gln
70                  75                  80                  85

atg cac acc gcc acc gtc acc gat gcc acc atg acc att ttc aac gag   403
Met His Thr Ala Thr Val Thr Asp Ala Thr Met Thr Ile Phe Asn Glu
                90                  95                  100

gcc ggc agc aat att ggc gag cta aaa cgc taaatgcttc tcgacgtcaa     453
Ala Gly Ser Asn Ile Gly Glu Leu Lys Arg
            105                 110

aag                                                               456
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Do not enter or alter anything above this line

<210> 1074
<211> 111
<212> PRT
<213> Corynebacterium glutamicum

<400> 1074

```
Met Lys Thr Tyr Ala Val Leu Ile Ala Val Ala Gly Leu Ala Leu Ala
  1               5                  10                  15

Gly Cys Ser Ser Ser Ala Pro Gly Ile Trp Arg Ala Thr Glu Pro Ala
            20                  25                  30

Asp Ala Tyr Leu Glu Ile Ala Asp Asp Gly Thr Leu Ser Gly Thr Asp
        35                  40                  45

Gly Cys Asn Arg Leu Phe Gly Gly Trp Glu Lys Asp Gly Ser Thr Ile
    50                  55                  60

Thr Phe Gly Ala Ile Gly Met Thr Glu Met Tyr Cys Glu Gly Val Asn
65                  70                  75                  80

Asp Trp Leu Ser Gln Met His Thr Ala Thr Val Thr Asp Ala Thr Met
                85                  90                  95

Thr Ile Phe Asn Glu Ala Gly Ser Asn Ile Gly Glu Leu Lys Arg
            100                 105                 110
```

<210> 1075
<211> 840
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(817)
<223> RXN02301

<400> 1075
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taaccgaacc tggccagtgc aacaggatta tgtttaaagc atg gat ctt gca ctg 115
Met Asp Leu Ala Leu
1 5

gct cag gtt gat tcc acc gtt tcg ggg ctt tat gac gcc ctc gat ctc 163
Ala Gln Val Asp Ser Thr Val Ser Gly Leu Tyr Asp Ala Leu Asp Leu
10 15 20

atc ggc gtg ctg ctg aac gga ata atc ggt gga acg atc gcc agg caa 211
Ile Gly Val Leu Leu Asn Gly Ile Ile Gly Gly Thr Ile Ala Arg Gln
25 30 35

cga ggc tat gac atc att ggc ttt ctg ttc ctg gcg tta ttt tct gcg 259
Arg Gly Tyr Asp Ile Ile Gly Phe Leu Phe Leu Ala Leu Phe Ser Ala
40 45 50

ctg ggt ggc gga atg atc cgt gac atg ctg att cag cag ggg act gtc 307
Leu Gly Gly Gly Met Ile Arg Asp Met Leu Ile Gln Gln Gly Thr Val
55 60 65

gcg gcg atc gat aat cag atc tac ctt gcg ctc gcg ttt tct ggc gcg 355
Ala Ala Ile Asp Asn Gln Ile Tyr Leu Ala Leu Ala Phe Ser Gly Ala
70 75 80 85

ctg att gcc atg gcg gtg aac ttt aaa ggc agg gtg tgg gag ctg ttt 403
Leu Ile Ala Met Ala Val Asn Phe Lys Gly Arg Val Trp Glu Leu Phe
90 95 100

aaa gtt cac ggc gat gcc att gtg ttg ggc gtc tgg gcg gtg acg ggt 451
Lys Val His Gly Asp Ala Ile Val Leu Gly Val Trp Ala Val Thr Gly
105 110 115

tcc gtg aag gcg atg aat gcg ggg gtg gct ccg ctg ccg agt att ttc 499
Ser Val Lys Ala Met Asn Ala Gly Val Ala Pro Leu Pro Ser Ile Phe
120 125 130

atg ggc gtg ctc acc gcg gtg ggt ggt ggc atg gtg cgt gat gtg gct 547
Met Gly Val Leu Thr Ala Val Gly Gly Gly Met Val Arg Asp Val Ala
135 140 145

act ggc cag acg ccg acg att ttt ggt ggc gga act ctt tac gct gtg 595
Thr Gly Gln Thr Pro Thr Ile Phe Gly Gly Gly Thr Leu Tyr Ala Val
150 155 160 165

cct gcg acg ctt tct gcc acg tca atg gtt att ttt cat agc ttt gac 643
Pro Ala Thr Leu Ser Ala Thr Ser Met Val Ile Phe His Ser Phe Asp
170 175 180

cag gta att ctg ggt atg att att tca ccg ttc ttg ggt atc gcg ttg 691
Gln Val Ile Leu Gly Met Ile Ile Ser Pro Phe Leu Gly Ile Ala Leu
185 190 195

gcg gtt act gcg tat tgg tgc ggt tgg gtc att ccg gtg aac acg gat 739
Ala Val Thr Ala Tyr Trp Cys Gly Trp Val Ile Pro Val Asn Thr Asp
200 205 210

```
ttc gcg ccg gtg aat ctg acg gtc agc caa ttg cgg gca atg ctg tcc   787
Phe Ala Pro Val Asn Leu Thr Val Ser Gln Leu Arg Ala Met Leu Ser
    215                 220                 225

aaa gcg gag cgt aaa gat aag gat cag aaa tgaaaactta tgcagtacta     837
Lys Ala Glu Arg Lys Asp Lys Asp Gln Lys
230                 235

att                                                               840
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<210> 1076
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

<400> 1076

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Met Asp Leu Ala Leu Ala Gln Val Asp Ser Thr Val Ser Gly Leu Tyr
  1               5                  10                  15

Asp Ala Leu Asp Leu Ile Gly Val Leu Leu Asn Gly Ile Ile Gly Gly
             20                  25                  30

Thr Ile Ala Arg Gln Arg Gly Tyr Asp Ile Ile Gly Phe Leu Phe Leu
         35                  40                  45

Ala Leu Phe Ser Ala Leu Gly Gly Gly Met Ile Arg Asp Met Leu Ile
     50                  55                  60

Gln Gln Gly Thr Val Ala Ala Ile Asp Asn Gln Ile Tyr Leu Ala Leu
 65                  70                  75                  80

Ala Phe Ser Gly Ala Leu Ile Ala Met Ala Val Asn Phe Lys Gly Arg
                 85                  90                  95

Val Trp Glu Leu Phe Lys Val His Gly Asp Ala Ile Val Leu Gly Val
            100                 105                 110

Trp Ala Val Thr Gly Ser Val Lys Ala Met Asn Ala Gly Val Ala Pro
        115                 120                 125

Leu Pro Ser Ile Phe Met Gly Val Leu Thr Ala Val Gly Gly Gly Met
    130                 135                 140

Val Arg Asp Val Ala Thr Gly Gln Thr Pro Thr Ile Phe Gly Gly Gly
145                 150                 155                 160

Thr Leu Tyr Ala Val Pro Ala Thr Leu Ser Ala Thr Ser Met Val Ile
                165                 170                 175

Phe His Ser Phe Asp Gln Val Ile Leu Gly Met Ile Ile Ser Pro Phe
            180                 185                 190

Leu Gly Ile Ala Leu Ala Val Thr Ala Tyr Trp Cys Gly Trp Val Ile
        195                 200                 205

Pro Val Asn Thr Asp Phe Ala Pro Val Asn Leu Thr Val Ser Gln Leu
    210                 215                 220

Arg Ala Met Leu Ser Lys Ala Glu Arg Lys Asp Lys Asp Gln Lys
```

```
225                 230                 235


<210> 1077
<211> 840
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(817)
<223> FRXA02301

<400> 1077
gcttcgcata tgtctggatc ttattggatg tatgagtcag agatcaggga gatcgcgcac 60

taaccgaacc tggccagtgc aacaggatta tgtttaaagc atg gat ctt gca ctg   115
                                              Met Asp Leu Ala Leu
                                                1               5

gct cag gtt gat tcc acc gtt tcg ggg ctt tat gac gcc ctc gat ctc   163
Ala Gln Val Asp Ser Thr Val Ser Gly Leu Tyr Asp Ala Leu Asp Leu
                10                  15                  20

atc ggc gtg ctg ctg aac gga ata atc ggt gga acg atc gcc agg caa   211
Ile Gly Val Leu Leu Asn Gly Ile Ile Gly Gly Thr Ile Ala Arg Gln
            25                  30                  35

cga ggc tat gac atc att ggc ttt ctg ttc ctg gcg tta ttt tct gcg   259
Arg Gly Tyr Asp Ile Ile Gly Phe Leu Phe Leu Ala Leu Phe Ser Ala
        40                  45                  50

ctg ggt ggc gga atg atc cgt gac atg ctg att cag cag ggg act gtc   307
Leu Gly Gly Gly Met Ile Arg Asp Met Leu Ile Gln Gln Gly Thr Val
    55                  60                  65

gcg gcg atc gat aat cag atc tac ctt gcg ctc gcg ttt tct ggc gcg   355
Ala Ala Ile Asp Asn Gln Ile Tyr Leu Ala Leu Ala Phe Ser Gly Ala
70                  75                  80                  85

ctg att gcc atg gcg gtg aac ttt aaa ggc agg gtg tgg gag ctg ttt   403
Leu Ile Ala Met Ala Val Asn Phe Lys Gly Arg Val Trp Glu Leu Phe
                90                  95                  100

aaa gtt cac ggc gat gcc att gtg ttg ggc gtc tgg gcg gtg acg ggt   451
Lys Val His Gly Asp Ala Ile Val Leu Gly Val Trp Ala Val Thr Gly
            105                 110                 115

tcc gtg aag gcg atg aat gcg ggg gtg gct ccg ctg ccg agt att ttc   499
Ser Val Lys Ala Met Asn Ala Gly Val Ala Pro Leu Pro Ser Ile Phe
        120                 125                 130

atg ggc gtg ctc acc gcg gtg ggt ggt ggc atg gtg cgt gat gtg gct   547
Met Gly Val Leu Thr Ala Val Gly Gly Gly Met Val Arg Asp Val Ala
    135                 140                 145

act ggc cag acg ccg acg att ttt ggt ggc gga act ctt tac gct gtg   595
Thr Gly Gln Thr Pro Thr Ile Phe Gly Gly Gly Thr Leu Tyr Ala Val
150                 155                 160                 165

cct gcg acg ctt tct gcc acg tca atg gtt att ttt cat agc ttt gac   643
```

```
Pro Ala Thr Leu Ser Ala Thr Ser Met Val Ile Phe His Ser Phe Asp
                170                 175                 180

cag gta att ctg ggt atg att att tca ccg ttc ttg ggt atc gcg ttg   691
Gln Val Ile Leu Gly Met Ile Ile Ser Pro Phe Leu Gly Ile Ala Leu
            185                 190                 195

gcg gtt act gcg tat tgg tgc ggt tgg gtc att ccg gtg aac acg gat   739
Ala Val Thr Ala Tyr Trp Cys Gly Trp Val Ile Pro Val Asn Thr Asp
        200                 205                 210

ttc gcg ccg gtg aat ctg acg gtc agc caa ttg cgg gca atg ctg tcc   787
Phe Ala Pro Val Asn Leu Thr Val Ser Gln Leu Arg Ala Met Leu Ser
    215                 220                 225

aaa gcg gag cgt aaa gat aag gat cag aaa tgaaaactta tgcagtacta     837
Lys Ala Glu Arg Lys Asp Lys Asp Gln Lys
230                 235

att                                                               840
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Sequence Listing

<210> 1078
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

<400> 1078

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Met Asp Leu Ala Leu Ala Gln Val Asp Ser Thr Val Ser Gly Leu Tyr
  1               5                  10                  15

Asp Ala Leu Asp Leu Ile Gly Val Leu Leu Asn Gly Ile Ile Gly Gly
             20                  25                  30

Thr Ile Ala Arg Gln Arg Gly Tyr Asp Ile Ile Gly Phe Leu Phe Leu
         35                  40                  45

Ala Leu Phe Ser Ala Leu Gly Gly Gly Met Ile Arg Asp Met Leu Ile
     50                  55                  60

Gln Gln Gly Thr Val Ala Ala Ile Asp Asn Gln Ile Tyr Leu Ala Leu
 65                  70                  75                  80

Ala Phe Ser Gly Ala Leu Ile Ala Met Ala Val Asn Phe Lys Gly Arg
                 85                  90                  95

Val Trp Glu Leu Phe Lys Val His Gly Asp Ala Ile Val Leu Gly Val
            100                 105                 110

Trp Ala Val Thr Gly Ser Val Lys Ala Met Asn Ala Gly Val Ala Pro
        115                 120                 125

Leu Pro Ser Ile Phe Met Gly Val Leu Thr Ala Val Gly Gly Gly Met
    130                 135                 140

Val Arg Asp Val Ala Thr Gly Gln Thr Pro Thr Ile Phe Gly Gly Gly
145                 150                 155                 160

Thr Leu Tyr Ala Val Pro Ala Thr Leu Ser Ala Thr Ser Met Val Ile
                165                 170                 175
```

```
Phe His Ser Phe Asp Gln Val Ile Leu Gly Met Ile Ile Ser Pro Phe
            180                 185                 190

Leu Gly Ile Ala Leu Ala Val Thr Ala Tyr Trp Cys Gly Trp Val Ile
        195                 200                 205

Pro Val Asn Thr Asp Phe Ala Pro Val Asn Leu Thr Val Ser Gln Leu
    210                 215                 220

Arg Ala Met Leu Ser Lys Ala Glu Arg Lys Asp Lys Asp Gln Lys
225                 230                 235
```

<210> 1079
<211> 1002
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(979)
<223> RXN02302

<400> 1079

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ggccaggttc ggttagtgcg cgatctccct gatctctgac tcatacatcc aataagatcc 60

agacatatgc gaagctaatg aaggaaacga ggagctgata gtg gca aca aat cgt   115
                                              Val Ala Thr Asn Arg
                                                1               5

aca tct tcc gct ggt gtc atc acg tct gtt ctc gca tcc gct ttg ttc   163
Thr Ser Ser Ala Gly Val Ile Thr Ser Val Leu Ala Ser Ala Leu Phe
                10                  15                  20

gga gcg atc ttt ttc atc tct ggg gcg att gag gca aag gcg gaa aca   211
Gly Ala Ile Phe Phe Ile Ser Gly Ala Ile Glu Ala Lys Ala Glu Thr
            25                  30                  35

ctt gtt gct tgg cgt gtc ctt cta aca gcg gca tgc tat ttg ctt gcc   259
Leu Val Ala Trp Arg Val Leu Leu Thr Ala Ala Cys Tyr Leu Leu Ala
        40                  45                  50

ctt ctg cac cct gct ggt cgg aag gtg ttt aag gaa ttt tgg gac aca   307
Leu Leu His Pro Ala Gly Arg Lys Val Phe Lys Glu Phe Trp Asp Thr
    55                  60                  65

cta agg tcc caa cct cgt caa att ctg tac ttt atc ttc ctc gtt gta   355
Leu Arg Ser Gln Pro Arg Gln Ile Leu Tyr Phe Ile Phe Leu Val Val
70                  75                  80                  85

ctc atc acg ctt cag ctg tgg ctg ttt tct tgg tcg cct aag agt cat   403
Leu Ile Thr Leu Gln Leu Trp Leu Phe Ser Trp Ser Pro Lys Ser His
                90                  95                  100

gct tta gat gcc tca ctt ggt tac ctg tta ctg ccc att ttc cta gta   451
Ala Leu Asp Ala Ser Leu Gly Tyr Leu Leu Leu Pro Ile Phe Leu Val
            105                 110                 115

att gtg ggg cgg ttt ttc ttc gct gat tac atc acc agg ctg cag tgg   499
Ile Val Gly Arg Phe Phe Phe Ala Asp Tyr Ile Thr Arg Leu Gln Trp
        120                 125                 130
```

```
att gcg gtg gga atc gcg ctg atc gca gta acc ttg aaa ttt gtc att   547
Ile Ala Val Gly Ile Ala Leu Ile Ala Val Thr Leu Lys Phe Val Ile
    135                 140                 145

agt gcg caa tta tcg tgg gta act ttt gcc atc gct gcg ggt tat gca   595
Ser Ala Gln Leu Ser Trp Val Thr Phe Ala Ile Ala Ala Gly Tyr Ala
150                 155                 160                 165

ctg tat ttt gcg ctt cgt aaa tac tcg ggg ctg aac aac gct ttt gct   643
Leu Tyr Phe Ala Leu Arg Lys Tyr Ser Gly Leu Asn Asn Ala Phe Ala
                170                 175                 180

tac ggc gca gaa gtt tta gcg tta agt ccc ctg gca ttt ttc atg ctc   691
Tyr Gly Ala Glu Val Leu Ala Leu Ser Pro Leu Ala Phe Phe Met Leu
            185                 190                 195

gcc act gtc gag gat ccg ctg tct aac gcc atg ttg tca atg gtt att   739
Ala Thr Val Glu Asp Pro Leu Ser Asn Ala Met Leu Ser Met Val Ile
        200                 205                 210

ctg gcg ggc ctc gct ggc gca tta gct atg gcg ttg tat cta gcc gcc   787
Leu Ala Gly Leu Ala Gly Ala Leu Ala Met Ala Leu Tyr Leu Ala Ala
    215                 220                 225

tca act ctg ctt agt atg ccg atg ttt ggc ctg ctc agt tat ggt gaa   835
Ser Thr Leu Leu Ser Met Pro Met Phe Gly Leu Leu Ser Tyr Gly Glu
230                 235                 240                 245

cca atc ttg ctg ttt gtt gca gca cta tta ctt ggt gaa acg ttg aat   883
Pro Ile Leu Leu Phe Val Ala Ala Leu Leu Leu Gly Glu Thr Leu Asn
                250                 255                 260

ctc agc gac gcc att gtc tac tca cta ctg gcg tgc gcc ctg gcg tta   931
Leu Ser Asp Ala Ile Val Tyr Ser Leu Leu Ala Cys Ala Leu Ala Leu
            265                 270                 275

ctg gga ttt gat ggg ata cga agg tct cga aaa aac ctc gag acc gat   979
Leu Gly Phe Asp Gly Ile Arg Arg Ser Arg Lys Asn Leu Glu Thr Asp
        280                 285                 290

taacttctgc tcaacttccc acc                                        1002


<210> 1080
<211> 293
<212> PRT
<213> Corynebacterium glutamicum

<400> 1080
Val Ala Thr Asn Arg Thr Ser Ser Ala Gly Val Ile Thr Ser Val Leu
  1               5                  10                  15

Ala Ser Ala Leu Phe Gly Ala Ile Phe Phe Ile Ser Gly Ala Ile Glu
             20                  25                  30

Ala Lys Ala Glu Thr Leu Val Ala Trp Arg Val Leu Leu Thr Ala Ala
         35                  40                  45

Cys Tyr Leu Leu Ala Leu Leu His Pro Ala Gly Arg Lys Val Phe Lys
     50                  55                  60
```

```
Glu Phe Trp Asp Thr Leu Arg Ser Gln Pro Arg Gln Ile Leu Tyr Phe
 65                  70                  75                  80

Ile Phe Leu Val Val Leu Ile Thr Leu Gln Leu Trp Leu Phe Ser Trp
                85                  90                  95

Ser Pro Lys Ser His Ala Leu Asp Ala Ser Leu Gly Tyr Leu Leu Leu
            100                 105                 110

Pro Ile Phe Leu Val Ile Val Gly Arg Phe Phe Phe Ala Asp Tyr Ile
        115                 120                 125

Thr Arg Leu Gln Trp Ile Ala Val Gly Ile Ala Leu Ile Ala Val Thr
    130                 135                 140

Leu Lys Phe Val Ile Ser Ala Gln Leu Ser Trp Val Thr Phe Ala Ile
145                 150                 155                 160

Ala Ala Gly Tyr Ala Leu Tyr Phe Ala Leu Arg Lys Tyr Ser Gly Leu
                165                 170                 175

Asn Asn Ala Phe Ala Tyr Gly Ala Glu Val Leu Ala Leu Ser Pro Leu
            180                 185                 190

Ala Phe Phe Met Leu Ala Thr Val Glu Asp Pro Leu Ser Asn Ala Met
        195                 200                 205

Leu Ser Met Val Ile Leu Ala Gly Leu Ala Gly Ala Leu Ala Met Ala
    210                 215                 220

Leu Tyr Leu Ala Ala Ser Thr Leu Leu Ser Met Pro Met Phe Gly Leu
225                 230                 235                 240

Leu Ser Tyr Gly Glu Pro Ile Leu Leu Phe Val Ala Ala Leu Leu Leu
                245                 250                 255

Gly Glu Thr Leu Asn Leu Ser Asp Ala Ile Val Tyr Ser Leu Leu Ala
            260                 265                 270

Cys Ala Leu Ala Leu Leu Gly Phe Asp Gly Ile Arg Arg Ser Arg Lys
        275                 280                 285

Asn Leu Glu Thr Asp
    290


<210> 1081
<211> 865
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(865)
<223> FRXA02302

<400> 1081
ggccaggttc ggttagtgcg cgatctccct gatctctgac tcatacatcc aataagatcc 60

agacatatgc gaagctaatg aaggaaacga ggagctgata gtg gca aca aat cgt   115
```

```
                                                  Val Ala Thr Asn Arg
                                                    1               5

aca tct tcc gct ggt gtc atc acg tct gtt ctc gca tcc gct ttg ttc   163
Thr Ser Ser Ala Gly Val Ile Thr Ser Val Leu Ala Ser Ala Leu Phe
                10                  15                  20

gga gcg atc ttt ttc atc tct ggg gcg att gag gca aag gcg gaa aca   211
Gly Ala Ile Phe Phe Ile Ser Gly Ala Ile Glu Ala Lys Ala Glu Thr
            25                  30                  35

ctt gtt gct tgg cgt gtc ctt cta aca gcg gca tgc tat ttg ctt gcc   259
Leu Val Ala Trp Arg Val Leu Leu Thr Ala Ala Cys Tyr Leu Leu Ala
        40                  45                  50

ctt ctg cac cct gct ggt cgg aag gtg ttt aag gaa ttt tgg gac aca   307
Leu Leu His Pro Ala Gly Arg Lys Val Phe Lys Glu Phe Trp Asp Thr
    55                  60                  65

cta agg tcc caa cct cgt caa att ctg tac ttt atc ttc ctc gtt gta   355
Leu Arg Ser Gln Pro Arg Gln Ile Leu Tyr Phe Ile Phe Leu Val Val
70                  75                  80                  85

ctc atc acg ctt cag ctg tgg ctg ttt tct tgg tcg cct aag agt cat   403
Leu Ile Thr Leu Gln Leu Trp Leu Phe Ser Trp Ser Pro Lys Ser His
                90                  95                  100

gct tta gat gcc tca ctt ggt tac ctg tta ctg ccc att ttc cta gta   451
Ala Leu Asp Ala Ser Leu Gly Tyr Leu Leu Leu Pro Ile Phe Leu Val
            105                 110                 115

att gtg ggg cgg ttt ttc ttc gct gat tac atc acc agg ctg cag tgg   499
Ile Val Gly Arg Phe Phe Phe Ala Asp Tyr Ile Thr Arg Leu Gln Trp
        120                 125                 130

att gcg gtg gga atc gcg ctg atc gca gta acc ttg aaa ttt gtc att   547
Ile Ala Val Gly Ile Ala Leu Ile Ala Val Thr Leu Lys Phe Val Ile
    135                 140                 145

agt gcg caa tta tcg tgg gta act ttt gcc atc gct gcg ggt tat gca   595
Ser Ala Gln Leu Ser Trp Val Thr Phe Ala Ile Ala Ala Gly Tyr Ala
150                 155                 160                 165

ctg tat ttt gcg ctt cgt aaa tac tcg ggg ctg aac aac gct ttt gct   643
Leu Tyr Phe Ala Leu Arg Lys Tyr Ser Gly Leu Asn Asn Ala Phe Ala
                170                 175                 180

tac ggc gca gaa gtt tta gcg tta agt ccc ctg gca ttt ttc atg ctc   691
Tyr Gly Ala Glu Val Leu Ala Leu Ser Pro Leu Ala Phe Phe Met Leu
            185                 190                 195

gcc act gtc gag gat ccg ctg tct aac gcc atg ttg tca atg gtt att   739
Ala Thr Val Glu Asp Pro Leu Ser Asn Ala Met Leu Ser Met Val Ile
        200                 205                 210

ctg gcg ggc ctc gct ggc gca tta gct atg gcg ttg tat cta gcc gcc   787
Leu Ala Gly Leu Ala Gly Ala Leu Ala Met Ala Leu Tyr Leu Ala Ala
    215                 220                 225

tca act ctg ctt agt atg ccg atg ttt ggc ctg ctc agt tat ggt gaa   835
Ser Thr Leu Leu Ser Met Pro Met Phe Gly Leu Leu Ser Tyr Gly Glu
```

```
230                 235                 240                 245

cca atc ttg ctg ttt gtt gca gca cta tta                              865
Pro Ile Leu Leu Phe Val Ala Ala Leu Leu
                250                 255


<210> 1082
<211> 255
<212> PRT
<213> Corynebacterium glutamicum

<400> 1082
Val Ala Thr Asn Arg Thr Ser Ser Ala Gly Val Ile Thr Ser Val Leu
  1               5                  10                  15

Ala Ser Ala Leu Phe Gly Ala Ile Phe Phe Ile Ser Gly Ala Ile Glu
             20                  25                  30

Ala Lys Ala Glu Thr Leu Val Ala Trp Arg Val Leu Leu Thr Ala Ala
         35                  40                  45

Cys Tyr Leu Leu Ala Leu Leu His Pro Ala Gly Arg Lys Val Phe Lys
     50                  55                  60

Glu Phe Trp Asp Thr Leu Arg Ser Gln Pro Arg Gln Ile Leu Tyr Phe
 65                  70                  75                  80

Ile Phe Leu Val Val Leu Ile Thr Leu Gln Leu Trp Leu Phe Ser Trp
                 85                  90                  95

Ser Pro Lys Ser His Ala Leu Asp Ala Ser Leu Gly Tyr Leu Leu Leu
            100                 105                 110

Pro Ile Phe Leu Val Ile Val Gly Arg Phe Phe Phe Ala Asp Tyr Ile
        115                 120                 125

Thr Arg Leu Gln Trp Ile Ala Val Gly Ile Ala Leu Ile Ala Val Thr
    130                 135                 140

Leu Lys Phe Val Ile Ser Ala Gln Leu Ser Trp Val Thr Phe Ala Ile
145                 150                 155                 160

Ala Ala Gly Tyr Ala Leu Tyr Phe Ala Leu Arg Lys Tyr Ser Gly Leu
                165                 170                 175

Asn Asn Ala Phe Ala Tyr Gly Ala Glu Val Leu Ala Leu Ser Pro Leu
            180                 185                 190

Ala Phe Phe Met Leu Ala Thr Val Glu Asp Pro Leu Ser Asn Ala Met
        195                 200                 205

Leu Ser Met Val Ile Leu Ala Gly Leu Ala Gly Ala Leu Ala Met Ala
    210                 215                 220

Leu Tyr Leu Ala Ala Ser Thr Leu Leu Ser Met Pro Met Phe Gly Leu
225                 230                 235                 240

Leu Ser Tyr Gly Glu Pro Ile Leu Leu Phe Val Ala Ala Leu Leu
                245                 250                 255
```

<210> 1083
<211> 1029
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1006)
<223> RXN02303

<400> 1083
gcccgggccg aaatcattcc aatctcaccc ccacccaaaa cactgttgat attttcactt 60

tccaaccagc gacgtgagcg cacgcactaa ggttgtgccc atg gct gaa aac aac 115
Met Ala Glu Asn Asn
1 5

acc cca caa gaa act gaa caa gat cag gaa gca cgc ttc cgt gag gag 163
Thr Pro Gln Glu Thr Glu Gln Asp Gln Glu Ala Arg Phe Arg Glu Glu
10 15 20

ttc gag gtt ggc ggt aag gat cgt cag ctt tct gaa gaa gaa cag ctg 211
Phe Glu Val Gly Gly Lys Asp Arg Gln Leu Ser Glu Glu Glu Gln Leu
25 30 35

gag cag ctc gga tcg tat att gat gcg cac tac cct gtt cca gat ttc 259
Glu Gln Leu Gly Ser Tyr Ile Asp Ala His Tyr Pro Val Pro Asp Phe
40 45 50

acg ccc cct tgg gca ggt ggc gcc ggc gat cct gat cca gca gac cgc 307
Thr Pro Pro Trp Ala Gly Gly Ala Gly Asp Pro Asp Pro Ala Asp Arg
55 60 65

tat att gca cat ctt ccc gat cgc acc acg cat act gcg atg atc atg 355
Tyr Ile Ala His Leu Pro Asp Arg Thr Thr His Thr Ala Met Ile Met
70 75 80 85

ttg ggt tct ggc ctt gat cat tcc atg ccg ggt gtc gca ttt atc ggt 403
Leu Gly Ser Gly Leu Asp His Ser Met Pro Gly Val Ala Phe Ile Gly
90 95 100

ggt gtg agc gtc gat gac gtc ccg gag gtc gga ggc gcg att ttc cac 451
Gly Val Ser Val Asp Asp Val Pro Glu Val Gly Gly Ala Ile Phe His
105 110 115

ccg tcg aat ccg acg ggc cgc tgg gct gta tcg ttc cac agc ggt ggt 499
Pro Ser Asn Pro Thr Gly Arg Trp Ala Val Ser Phe His Ser Gly Gly
120 125 130

tgg tgg cgc ggt tcc ggt gat gcg ttg gag ttc cag tgg cgt cca gag 547
Trp Trp Arg Gly Ser Gly Asp Ala Leu Glu Phe Gln Trp Arg Pro Glu
135 140 145

gtc gcg gca gct gcg gaa ttg tcc ggc aca acc atc ctt gac ctg gac 595
Val Ala Ala Ala Ala Glu Leu Ser Gly Thr Thr Ile Leu Asp Leu Asp
150 155 160 165

tat ccg ctg gcc cca ggc cat aac ctc cac gat atg aat gag gtt gtg 643
Tyr Pro Leu Ala Pro Gly His Asn Leu His Asp Met Asn Glu Val Val
170 175 180

```
ggc aag gcg gtc ggt tac gcc cgc cac cat aat ccg gtg tcg atc acg   691
Gly Lys Ala Val Gly Tyr Ala Arg His His Asn Pro Val Ser Ile Thr
            185                 190                 195

ggt tgg ggt tat tcc tcg ggc gcg gcg tta gcc gcg att aat gca tcg   739
Gly Trp Gly Tyr Ser Ser Gly Ala Ala Leu Ala Ala Ile Asn Ala Ser
        200                 205                 210

ctt ttc gac gcc ctg gtc ctc acc ttt ccg gac ctg ggt agc gtc gag   787
Leu Phe Asp Ala Leu Val Leu Thr Phe Pro Asp Leu Gly Ser Val Glu
    215                 220                 225

aag ctc cct gcc gaa att cgt gga gac gct gta gtg ccc gcg gcg gct   835
Lys Leu Pro Ala Glu Ile Arg Gly Asp Ala Val Val Pro Ala Ala Ala
230                 235                 240                 245

gcg tgg ccg acg acc ttt gtg cag atc gcg gcg cag gat gag atc gcg   883
Ala Trp Pro Thr Thr Phe Val Gln Ile Ala Ala Gln Asp Glu Ile Ala
                250                 255                 260

gag cgg cca gga gag ctt ggc gac gcg acc gtg aag gaa tac gtt tcc   931
Glu Arg Pro Gly Glu Leu Gly Asp Ala Thr Val Lys Glu Tyr Val Ser
            265                 270                 275

cgc cac cgt att tcc aca ccg aag gtc gcg cgc gaa aaa atc acc gac   979
Arg His Arg Ile Ser Thr Pro Lys Val Ala Arg Glu Lys Ile Thr Asp
        280                 285                 290

gtg gcg gag ttc ctt aaa act gtt tgc taatgtgcca gcaggttgta        1026
Val Ala Glu Phe Leu Lys Thr Val Cys
    295                 300

aat                                                             1029
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<210> 1084
<211> 302
<212> PRT
<213> Corynebacterium glutamicum

<400> 1084

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Met Ala Glu Asn Asn Thr Pro Gln Glu Thr Glu Gln Asp Gln Glu Ala
  1               5                  10                  15

Arg Phe Arg Glu Glu Phe Glu Val Gly Gly Lys Asp Arg Gln Leu Ser
             20                  25                  30

Glu Glu Glu Gln Leu Glu Gln Leu Gly Ser Tyr Ile Asp Ala His Tyr
         35                  40                  45

Pro Val Pro Asp Phe Thr Pro Pro Trp Ala Gly Gly Ala Gly Asp Pro
     50                  55                  60

Asp Pro Ala Asp Arg Tyr Ile Ala His Leu Pro Asp Arg Thr Thr His
 65                  70                  75                  80

Thr Ala Met Ile Met Leu Gly Ser Gly Leu Asp His Ser Met Pro Gly
                 85                  90                  95

Val Ala Phe Ile Gly Gly Val Ser Val Asp Asp Val Pro Glu Val Gly
```

```
            100                 105                 110

Gly Ala Ile Phe His Pro Ser Asn Pro Thr Gly Arg Trp Ala Val Ser
        115                 120                 125

Phe His Ser Gly Gly Trp Trp Arg Gly Ser Gly Asp Ala Leu Glu Phe
    130                 135                 140

Gln Trp Arg Pro Glu Val Ala Ala Ala Ala Glu Leu Ser Gly Thr Thr
145                 150                 155                 160

Ile Leu Asp Leu Asp Tyr Pro Leu Ala Pro Gly His Asn Leu His Asp
                165                 170                 175

Met Asn Glu Val Val Gly Lys Ala Val Gly Tyr Ala Arg His His Asn
            180                 185                 190

Pro Val Ser Ile Thr Gly Trp Gly Tyr Ser Ser Gly Ala Ala Leu Ala
        195                 200                 205

Ala Ile Asn Ala Ser Leu Phe Asp Ala Leu Val Leu Thr Phe Pro Asp
    210                 215                 220

Leu Gly Ser Val Glu Lys Leu Pro Ala Glu Ile Arg Gly Asp Ala Val
225                 230                 235                 240

Val Pro Ala Ala Ala Ala Trp Pro Thr Thr Phe Val Gln Ile Ala Ala
                245                 250                 255

Gln Asp Glu Ile Ala Glu Arg Pro Gly Glu Leu Gly Asp Ala Thr Val
            260                 265                 270

Lys Glu Tyr Val Ser Arg His Arg Ile Ser Thr Pro Lys Val Ala Arg
        275                 280                 285

Glu Lys Ile Thr Asp Val Ala Glu Phe Leu Lys Thr Val Cys
    290                 295                 300


<210> 1085
<211> 743
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(720)
<223> FRXA02303

<400> 1085
gat cct gat cca gca gac cgc tat att gca cat ctt ccc gat cgc acc   48
Asp Pro Asp Pro Ala Asp Arg Tyr Ile Ala His Leu Pro Asp Arg Thr
  1               5                  10                  15

acg cat act gcg atg atc atg ttg ggt tct ggc ctt gat cat tcc atg   96
Thr His Thr Ala Met Ile Met Leu Gly Ser Gly Leu Asp His Ser Met
             20                  25                  30

ccg ggt gtc gca ttt atc ggt ggt gtg agc gtc gat gac gtc ccg gag   144
Pro Gly Val Ala Phe Ile Gly Gly Val Ser Val Asp Asp Val Pro Glu
         35                  40                  45
```

```
gtc gga ggc gcg att ttc cac ccg tcg aat ccg acg ggc cgc tgg gct   192
Val Gly Gly Ala Ile Phe His Pro Ser Asn Pro Thr Gly Arg Trp Ala
     50                  55                  60

gta tcg ttc cac agc ggt ggt tgg tgg cgc ggt tcc ggt gat gcg ttg   240
Val Ser Phe His Ser Gly Gly Trp Trp Arg Gly Ser Gly Asp Ala Leu
 65                  70                  75                  80

gag ttc cag tgg cgt cca gag gtc gcg gca gct gcg gaa ttg tcc ggc   288
Glu Phe Gln Trp Arg Pro Glu Val Ala Ala Ala Ala Glu Leu Ser Gly
                85                  90                  95

aca acc atc ctt gac ctg gac tat ccg ctg gcc cca ggc cat aac ctc   336
Thr Thr Ile Leu Asp Leu Asp Tyr Pro Leu Ala Pro Gly His Asn Leu
            100                 105                 110

cac gat atg aat gag gtt gtg ggc aag gcg gtc ggt tac gcc cgc cac   384
His Asp Met Asn Glu Val Val Gly Lys Ala Val Gly Tyr Ala Arg His
        115                 120                 125

cat aat ccg gtg tcg atc acg ggt tgg ggt tat tcc tcg ggc gcg gcg   432
His Asn Pro Val Ser Ile Thr Gly Trp Gly Tyr Ser Ser Gly Ala Ala
    130                 135                 140

tta gcc gcg att aat gca tcg ctt ttc gac gcc ctg gtc ctc acc ttt   480
Leu Ala Ala Ile Asn Ala Ser Leu Phe Asp Ala Leu Val Leu Thr Phe
145                 150                 155                 160

ccg gac ctg ggt agc gtc gag aag ctc cct gcc gaa att cgt gga gac   528
Pro Asp Leu Gly Ser Val Glu Lys Leu Pro Ala Glu Ile Arg Gly Asp
                165                 170                 175

gct gta gtg ccc gcg gcg gct gcg tgg ccg acg acc ttt gtg cag atc   576
Ala Val Val Pro Ala Ala Ala Ala Trp Pro Thr Thr Phe Val Gln Ile
            180                 185                 190

gcg gcg cag gat gag atc gcg gag cgg cca gga gag ctt ggc gac gcg   624
Ala Ala Gln Asp Glu Ile Ala Glu Arg Pro Gly Glu Leu Gly Asp Ala
        195                 200                 205

acc gtg aag gaa tac gtt tcc cgc cac cgt att tcc aca ccg aag gtc   672
Thr Val Lys Glu Tyr Val Ser Arg His Arg Ile Ser Thr Pro Lys Val
    210                 215                 220

gcg cgc gaa aaa atc acc gac gtg gcg gag ttc ctt aaa act gtt tgc   720
Ala Arg Glu Lys Ile Thr Asp Val Ala Glu Phe Leu Lys Thr Val Cys
225                 230                 235                 240

taatgtgcca gcaggttgta aat                                        743


<210> 1086
<211> 240
<212> PRT
<213> Corynebacterium glutamicum

<400> 1086
Asp Pro Asp Pro Ala Asp Arg Tyr Ile Ala His Leu Pro Asp Arg Thr
  1               5                  10                  15
```

```
Thr His Thr Ala Met Ile Met Leu Gly Ser Gly Leu Asp His Ser Met
            20                  25                  30

Pro Gly Val Ala Phe Ile Gly Gly Val Ser Val Asp Asp Val Pro Glu
        35                  40                  45

Val Gly Gly Ala Ile Phe His Pro Ser Asn Pro Thr Gly Arg Trp Ala
    50                  55                  60

Val Ser Phe His Ser Gly Gly Trp Trp Arg Gly Ser Gly Asp Ala Leu
65                  70                  75                  80

Glu Phe Gln Trp Arg Pro Glu Val Ala Ala Ala Ala Glu Leu Ser Gly
                85                  90                  95

Thr Thr Ile Leu Asp Leu Asp Tyr Pro Leu Ala Pro Gly His Asn Leu
            100                 105                 110

His Asp Met Asn Glu Val Val Gly Lys Ala Val Gly Tyr Ala Arg His
        115                 120                 125

His Asn Pro Val Ser Ile Thr Gly Trp Gly Tyr Ser Ser Gly Ala Ala
    130                 135                 140

Leu Ala Ala Ile Asn Ala Ser Leu Phe Asp Ala Leu Val Leu Thr Phe
145                 150                 155                 160

Pro Asp Leu Gly Ser Val Glu Lys Leu Pro Ala Glu Ile Arg Gly Asp
                165                 170                 175

Ala Val Val Pro Ala Ala Ala Ala Trp Pro Thr Thr Phe Val Gln Ile
            180                 185                 190

Ala Ala Gln Asp Glu Ile Ala Glu Arg Pro Gly Glu Leu Gly Asp Ala
        195                 200                 205

Thr Val Lys Glu Tyr Val Ser Arg His Arg Ile Ser Thr Pro Lys Val
    210                 215                 220

Ala Arg Glu Lys Ile Thr Asp Val Ala Glu Phe Leu Lys Thr Val Cys
225                 230                 235                 240
```

<210> 1087
<211> 744
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(721)
<223> RXN02307

<400> 1087
ttttgcatta accccaggta ggggcattgt cgcaaagccc aactacagca aggtgcgtac 60

gctggtggcc aactgaatac gtttgaggag aaggttttct atg agt ggc acc gcc 115
                                                Met Ser Gly Thr Ala

```
                                                    1               5

atc atg tac gac acg aca gtt gtt cca tcg aag aaa gaa atc gcg cag   163
Ile Met Tyr Asp Thr Thr Val Val Pro Ser Lys Lys Glu Ile Ala Gln
                10                  15                  20

gct tgg act ggt tat gtg gat ctt cag gga agc tac cgc ctg gta gat   211
Ala Trp Thr Gly Tyr Val Asp Leu Gln Gly Ser Tyr Arg Leu Val Asp
            25                  30                  35

acg gtg gat ggg gaa gtt ggc gtt gag gtg ctg att tcc aag gat cgg   259
Thr Val Asp Gly Glu Val Gly Val Glu Val Leu Ile Ser Lys Asp Arg
        40                  45                  50

gag ggg cgt tta ctc cag att ccg ttt agt tat cgt tcg gca gag att   307
Glu Gly Arg Leu Leu Gln Ile Pro Phe Ser Tyr Arg Ser Ala Glu Ile
    55                  60                  65

aac cca gag cag aca ctt tcc aca ttg gag cat ggt gtg ttg ggc aag   355
Asn Pro Glu Gln Thr Leu Ser Thr Leu Glu His Gly Val Leu Gly Lys
70                  75                  80                  85

cgt tgg gtg act aat gcg ttg ggt gac ccg gtg gca gtg cgg gag ttt   403
Arg Trp Val Thr Asn Ala Leu Gly Asp Pro Val Ala Val Arg Glu Phe
                90                  95                  100

att cgc act att ttg acg ggc gat gat ggt gca gct cgt agc gat ggc   451
Ile Arg Thr Ile Leu Thr Gly Asp Asp Gly Ala Ala Arg Ser Asp Gly
            105                 110                 115

gtg aag ggc tat ctg gat att aaa ggt tcc ggc gat gct gag tcg gtg   499
Val Lys Gly Tyr Leu Asp Ile Lys Gly Ser Gly Asp Ala Glu Ser Val
        120                 125                 130

gat tta cag gat gta aag ctt act gag gtt aca agg cag cgt gcg att   547
Asp Leu Gln Asp Val Lys Leu Thr Glu Val Thr Arg Gln Arg Ala Ile
    135                 140                 145

ggt tcg gta acc atc aac ggt gag cga aag caa ttc tcg ctg cgg ttg   595
Gly Ser Val Thr Ile Asn Gly Glu Arg Lys Gln Phe Ser Leu Arg Leu
150                 155                 160                 165

cct cag ttg ctg aag aat ttc agg gag aca gcc gcg ggc cat aca gct   643
Pro Gln Leu Leu Lys Asn Phe Arg Glu Thr Ala Ala Gly His Thr Ala
                170                 175                 180

acg act ctt cgt att gtg gcg act cat ccg gaa aag gac gat gtt gag   691
Thr Thr Leu Arg Ile Val Ala Thr His Pro Glu Lys Asp Asp Val Glu
            185                 190                 195

ctg ctg gtc gct gag ttc aac tgg atg gaa taatccgaga cagctcctga     741
Leu Leu Val Ala Glu Phe Asn Trp Met Glu
        200                 205

aag                                                               744
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<210> 1088
<211> 207
<212> PRT
<213> Corynebacterium glutamicum

<400> 1088
Met Ser Gly Thr Ala Ile Met Tyr Asp Thr Thr Val Val Pro Ser Lys
1 5 10 15

Lys Glu Ile Ala Gln Ala Trp Thr Gly Tyr Val Asp Leu Gln Gly Ser
20 25 30

Tyr Arg Leu Val Asp Thr Val Asp Gly Glu Val Gly Val Glu Val Leu
35 40 45

Ile Ser Lys Asp Arg Glu Gly Arg Leu Leu Gln Ile Pro Phe Ser Tyr
50 55 60

Arg Ser Ala Glu Ile Asn Pro Glu Gln Thr Leu Ser Thr Leu Glu His
65 70 75 80

Gly Val Leu Gly Lys Arg Trp Val Thr Asn Ala Leu Gly Asp Pro Val
85 90 95

Ala Val Arg Glu Phe Ile Arg Thr Ile Leu Thr Gly Asp Asp Gly Ala
100 105 110

Ala Arg Ser Asp Gly Val Lys Gly Tyr Leu Asp Ile Lys Gly Ser Gly
115 120 125

Asp Ala Glu Ser Val Asp Leu Gln Asp Val Lys Leu Thr Glu Val Thr
130 135 140

Arg Gln Arg Ala Ile Gly Ser Val Thr Ile Asn Gly Glu Arg Lys Gln
145 150 155 160

Phe Ser Leu Arg Leu Pro Gln Leu Leu Lys Asn Phe Arg Glu Thr Ala
165 170 175

Ala Gly His Thr Ala Thr Thr Leu Arg Ile Val Ala Thr His Pro Glu
180 185 190

Lys Asp Asp Val Glu Leu Leu Val Ala Glu Phe Asn Trp Met Glu
195 200 205

<210> 1089
<211> 490
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(490)
<223> FRXA02307

<400> 1089
ttttgcatta accccaggta ggggcattgt cgcaaagccc aactacagca aggtgcgtac 60

gctggtggcc aactgaatac gtttgaggag aaggttttct atg agt ggc acc gcc 115
Met Ser Gly Thr Ala
1 5

atc atg tac gac acg aca gtt gtt cca tcg aag aaa gaa atc gcg cag 163
Ile Met Tyr Asp Thr Thr Val Val Pro Ser Lys Lys Glu Ile Ala Gln

```
                10                  15                  20

gct tgg act ggt tat gtg gat ctt cag gga agc tac cgc ctg gta gat   211
Ala Trp Thr Gly Tyr Val Asp Leu Gln Gly Ser Tyr Arg Leu Val Asp
            25                  30                  35

acg gtg gat ggg gaa gtt ggc gtt gag gtg ctg att tcc aag gat cgg   259
Thr Val Asp Gly Glu Val Gly Val Glu Val Leu Ile Ser Lys Asp Arg
        40                  45                  50

gag ggg cgt tta ctc cag att ccg ttt agt tat cgt tcg gca gag att   307
Glu Gly Arg Leu Leu Gln Ile Pro Phe Ser Tyr Arg Ser Ala Glu Ile
    55                  60                  65

aac cca gag cag aca ctt tcc aca ttg gag cat ggt gtg ttg ggc aag   355
Asn Pro Glu Gln Thr Leu Ser Thr Leu Glu His Gly Val Leu Gly Lys
70                  75                  80                  85

cgt tgg gtg act aat gcg ttg ggt gac ccg gtg gca gtg cgg gag ttt   403
Arg Trp Val Thr Asn Ala Leu Gly Asp Pro Val Ala Val Arg Glu Phe
                90                  95                  100

att cgc act att ttg acg ggc gat gat ggt gca gct cgt agc gat ggc   451
Ile Arg Thr Ile Leu Thr Gly Asp Asp Gly Ala Ala Arg Ser Asp Gly
            105                 110                 115

gtg aag ggc tat ctg gat att aaa ggt tcc ggc gat gct               490
Val Lys Gly Tyr Leu Asp Ile Lys Gly Ser Gly Asp Ala
        120                 125                 130


<210> 1090
<211> 130
<212> PRT
<213> Corynebacterium glutamicum

<400> 1090
Met Ser Gly Thr Ala Ile Met Tyr Asp Thr Thr Val Val Pro Ser Lys
  1               5                  10                  15

Lys Glu Ile Ala Gln Ala Trp Thr Gly Tyr Val Asp Leu Gln Gly Ser
            20                  25                  30

Tyr Arg Leu Val Asp Thr Val Asp Gly Glu Val Gly Val Glu Val Leu
        35                  40                  45

Ile Ser Lys Asp Arg Glu Gly Arg Leu Leu Gln Ile Pro Phe Ser Tyr
    50                  55                  60

Arg Ser Ala Glu Ile Asn Pro Glu Gln Thr Leu Ser Thr Leu Glu His
65                  70                  75                  80

Gly Val Leu Gly Lys Arg Trp Val Thr Asn Ala Leu Gly Asp Pro Val
                85                  90                  95

Ala Val Arg Glu Phe Ile Arg Thr Ile Leu Thr Gly Asp Asp Gly Ala
            100                 105                 110

Ala Arg Ser Asp Gly Val Lys Gly Tyr Leu Asp Ile Lys Gly Ser Gly
        115                 120                 125
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Asp Ala
130

<210> 1091
<211> 564
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(541)
<223> RXN02314

<400> 1091
tgataccacc gaagtatccg gattcaccat tattgaagct tcgaccgtcc gagatacccg 60

ccgtgcacaa cagcaagctc tcatggacac ggtgcactaa atg gag tgg tac caa 115
Met Glu Trp Tyr Gln
1 5

gtg cgc cga cgg gcc cga caa ctg ctc att gtc ctt ttt ata gca gcg 163
Val Arg Arg Arg Ala Arg Gln Leu Leu Ile Val Leu Phe Ile Ala Ala
10 15 20

atg ctc gga gca gcc tcc atg gtg atc ggg cca ttc ctt aac gac cgc 211
Met Leu Gly Ala Ala Ser Met Val Ile Gly Pro Phe Leu Asn Asp Arg
25 30 35

act atc gaa ggc aac tcc ggg cgc gcc ttg gca caa gta acc aac gtc 259
Thr Ile Glu Gly Asn Ser Gly Arg Ala Leu Ala Gln Val Thr Asn Val
40 45 50

ggc agc tac cgc aca acg gtg gat ttc caa gat gaa aac ggc atc tat 307
Gly Ser Tyr Arg Thr Thr Val Asp Phe Gln Asp Glu Asn Gly Ile Tyr
55 60 65

cac tca cca gcc acc ggc ctg ttg ttc ccc acg gga ctg ggc gag ggg 355
His Ser Pro Ala Thr Gly Leu Leu Phe Pro Thr Gly Leu Gly Glu Gly
70 75 80 85

caa cgc gtg tgg gtg aac tac gcc aaa tca gat cca gac ctg gtc aaa 403
Gln Arg Val Trp Val Asn Tyr Ala Lys Ser Asp Pro Asp Leu Val Lys
90 95 100

gta gaa ggc cgc aag tgg aca ctg tcc atc atc cca gcg ctt agt gtc 451
Val Glu Gly Arg Lys Trp Thr Leu Ser Ile Ile Pro Ala Leu Ser Val
105 110 115

gca gct gtc gcc acc gct acc tgg tca gta cta tgg ctg gga gtg ggc 499
Ala Ala Val Ala Thr Ala Thr Trp Ser Val Leu Trp Leu Gly Val Gly
120 125 130

aga ttc gga aga cga tcc gac gac gcc aac gaa acc aca gtg 541
Arg Phe Gly Arg Arg Ser Asp Asp Ala Asn Glu Thr Thr Val
135 140 145

taaagctcta tgccgggagc att 564

<210> 1092

<211> 147
<212> PRT
<213> Corynebacterium glutamicum

<400> 1092
Met Glu Trp Tyr Gln Val Arg Arg Arg Ala Arg Gln Leu Leu Ile Val
1 5 10 15

Leu Phe Ile Ala Ala Met Leu Gly Ala Ala Ser Met Val Ile Gly Pro
20 25 30

Phe Leu Asn Asp Arg Thr Ile Glu Gly Asn Ser Gly Arg Ala Leu Ala
35 40 45

Gln Val Thr Asn Val Gly Ser Tyr Arg Thr Thr Val Asp Phe Gln Asp
50 55 60

Glu Asn Gly Ile Tyr His Ser Pro Ala Thr Gly Leu Leu Phe Pro Thr
65 70 75 80

Gly Leu Gly Glu Gly Gln Arg Val Trp Val Asn Tyr Ala Lys Ser Asp
85 90 95

Pro Asp Leu Val Lys Val Glu Gly Arg Lys Trp Thr Leu Ser Ile Ile
100 105 110

Pro Ala Leu Ser Val Ala Ala Val Ala Thr Ala Thr Trp Ser Val Leu
115 120 125

Trp Leu Gly Val Gly Arg Phe Gly Arg Arg Ser Asp Asp Ala Asn Glu
130 135 140

Thr Thr Val
145

<210> 1093
<211> 564
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(541)
<223> FRXA02314

<400> 1093
tgataccacc gaagtatccg gattcaccat tattgaagct tcgaccgtcc gagatacccg 60

ccgtgcacaa cagcaagctc tcatggacac ggtgcactaa atg gag tgg tac caa 115
Met Glu Trp Tyr Gln
1 5

gtg cgc cga cgg gcc cga caa ctg ctc att gtc ctt ttt ata gca gcg 163
Val Arg Arg Arg Ala Arg Gln Leu Leu Ile Val Leu Phe Ile Ala Ala
10 15 20

atg ctc gga gca gcc tcc atg gtg atc ggg cca ttc ctt aac gac cgc 211
Met Leu Gly Ala Ala Ser Met Val Ile Gly Pro Phe Leu Asn Asp Arg
25 30 35

```
act atc gaa ggc aac tcc ggg cgc gcc ttg gca caa gta acc aac gtc   259
Thr Ile Glu Gly Asn Ser Gly Arg Ala Leu Ala Gln Val Thr Asn Val
         40                  45                  50

ggc agc tac cgc aca acg gtg gat ttc caa gat gaa aac ggc atc tat   307
Gly Ser Tyr Arg Thr Thr Val Asp Phe Gln Asp Glu Asn Gly Ile Tyr
     55                  60                  65

cac tca cca gcc acc ggc ctg ttg ttc ccc acg gga ctg ggc gag ggg   355
His Ser Pro Ala Thr Gly Leu Leu Phe Pro Thr Gly Leu Gly Glu Gly
 70                  75                  80                  85

caa cgc gtg tgg gtg aac tac gcc aaa tca gat cca gac ctg gtc aaa   403
Gln Arg Val Trp Val Asn Tyr Ala Lys Ser Asp Pro Asp Leu Val Lys
                 90                  95                 100

gta gaa ggc cgc aag tgg aca ctg tcc atc atc cca gcg ctt agt gtc   451
Val Glu Gly Arg Lys Trp Thr Leu Ser Ile Ile Pro Ala Leu Ser Val
            105                 110                 115

gca gct gtc gcc acc gct acc tgg tca gta cta tgg ctg gga gtg ggc   499
Ala Ala Val Ala Thr Ala Thr Trp Ser Val Leu Trp Leu Gly Val Gly
        120                 125                 130

aga ttc gga aga cga tcc gac gac gcc aac gaa acc aca gtg           541
Arg Phe Gly Arg Arg Ser Asp Asp Ala Asn Glu Thr Thr Val
    135                 140                 145

taaagctcta tgccgggagc att                                        564


<210> 1094
<211> 147
<212> PRT
<213> Corynebacterium glutamicum

<400> 1094
Met Glu Trp Tyr Gln Val Arg Arg Arg Ala Arg Gln Leu Leu Ile Val
  1               5                  10                  15

Leu Phe Ile Ala Ala Met Leu Gly Ala Ala Ser Met Val Ile Gly Pro
             20                  25                  30

Phe Leu Asn Asp Arg Thr Ile Glu Gly Asn Ser Gly Arg Ala Leu Ala
         35                  40                  45

Gln Val Thr Asn Val Gly Ser Tyr Arg Thr Thr Val Asp Phe Gln Asp
     50                  55                  60

Glu Asn Gly Ile Tyr His Ser Pro Ala Thr Gly Leu Leu Phe Pro Thr
 65                  70                  75                  80

Gly Leu Gly Glu Gly Gln Arg Val Trp Val Asn Tyr Ala Lys Ser Asp
                 85                  90                  95

Pro Asp Leu Val Lys Val Glu Gly Arg Lys Trp Thr Leu Ser Ile Ile
            100                 105                 110

Pro Ala Leu Ser Val Ala Ala Val Ala Thr Ala Thr Trp Ser Val Leu
        115                 120                 125
```

```
Trp Leu Gly Val Gly Arg Phe Gly Arg Arg Ser Asp Asp Ala Asn Glu
    130                 135                 140

Thr Thr Val
145
```

<210> 1095
<211> 1446
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1423)
<223> RXN02337

<400> 1095

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cacaaggtaa aatttgtgta attgtgtcgt gtggatttga aggtttttgt aaatctagtt 60

aaatcatgag gtcataagct tttcgggagg ttgtcaaagg atg tcg aag ctt tac   115
                                              Met Ser Lys Leu Tyr
                                                1               5

gcg ggg gca agg atc aat gca ctg cgc cga acc cat cag ctc acc caa   163
Ala Gly Ala Arg Ile Asn Ala Leu Arg Arg Thr His Gln Leu Thr Gln
                10                  15                  20

tca gca ttg gcc gac aag ctt gat ctc tcc acc agc tat ctc aac cag   211
Ser Ala Leu Ala Asp Lys Leu Asp Leu Ser Thr Ser Tyr Leu Asn Gln
            25                  30                  35

ttg gaa aat gac gga cgg cca ctc act gcc acg gtg ctt ctg cag ctg   259
Leu Glu Asn Asp Gly Arg Pro Leu Thr Ala Thr Val Leu Leu Gln Leu
        40                  45                  50

atg aaa gtg ttc gat gtt gag gcc agt tac ttc tcc cct gac cgg ggt   307
Met Lys Val Phe Asp Val Glu Ala Ser Tyr Phe Ser Pro Asp Arg Gly
    55                  60                  65

acg gcc act gct acc cga ctg gct gaa acc ttg gcg atg aat cag ggt   355
Thr Ala Thr Ala Thr Arg Leu Ala Glu Thr Leu Ala Met Asn Gln Gly
70                  75                  80                  85

ccg acg atg tcg atg gat gat ctt tta gat ttc gcg gat cgt ttc cct   403
Pro Thr Met Ser Met Asp Asp Leu Leu Asp Phe Ala Asp Arg Phe Pro
                90                  95                 100

cag tta gcg cag cat att atc cag cct gct gag gtt gat ccc acg cat   451
Gln Leu Ala Gln His Ile Ile Gln Pro Ala Glu Val Asp Pro Thr His
            105                 110                 115

agt tct gcg cat gat ttt gtt cgg gat tat ttt gcc acc cac aaa aac   499
Ser Ser Ala His Asp Phe Val Arg Asp Tyr Phe Ala Thr His Lys Asn
        120                 125                 130

tac att gat tcg ctc gat cgc ctt gga gag gag ttg gca act gcc att   547
Tyr Ile Asp Ser Leu Asp Arg Leu Gly Glu Glu Leu Ala Thr Ala Ile
    135                 140                 145

ggt cag ccg gga ctt cgg gtt act agg ctc gcg cag ttg ctt gat gcg   595
```

```
Gly Gln Pro Gly Leu Arg Val Thr Arg Leu Ala Gln Leu Leu Asp Ala
150                 155                 160                 165

gag tac aac atc acg gtg cgt ttc cgg gcg ccg gat att act ggc cgg   643
Glu Tyr Asn Ile Thr Val Arg Phe Arg Ala Pro Asp Ile Thr Gly Arg
                170                 175                 180

agg cac ttt gat ccc caa tcg cgt cag att ctg ctg cgg caa gat ctc   691
Arg His Phe Asp Pro Gln Ser Arg Gln Ile Leu Leu Arg Gln Asp Leu
            185                 190                 195

agc gag gcg cag cag tgt ttc cag ttg gcg gag gaa ttg acg ttt ctt   739
Ser Glu Ala Gln Gln Cys Phe Gln Leu Ala Glu Glu Leu Thr Phe Leu
        200                 205                 210

gct cat gca gag ctc ttg gat acc ctg acc aca gat caa ccg gat ctc   787
Ala His Ala Glu Leu Leu Asp Thr Leu Thr Thr Asp Gln Pro Asp Leu
    215                 220                 225

cct tct gag gca gct atc cgc ctg gct aag gtg ggt ctc tcc caa tat   835
Pro Ser Glu Ala Ala Ile Arg Leu Ala Lys Val Gly Leu Ser Gln Tyr
230                 235                 240                 245

ttc gcg gct gct gtt gtc atg ccg tac acc cgc ttt ttg gaa ttc gcc   883
Phe Ala Ala Ala Val Val Met Pro Tyr Thr Arg Phe Leu Glu Phe Ala
                250                 255                 260

cag gat aag cac tat gac atc gag ttg atc tct gag gcg ttt gga gtg   931
Gln Asp Lys His Tyr Asp Ile Glu Leu Ile Ser Glu Ala Phe Gly Val
            265                 270                 275

tct ttc gag tct gca tgc cac cgc ctg tct act ctg cag cgt tcg ggg   979
Ser Phe Glu Ser Ala Cys His Arg Leu Ser Thr Leu Gln Arg Ser Gly
        280                 285                 290

gcg tca ggg gtg ccg ttt ttc ttt gtg cgc tcg gat cgt gca gga aat   1027
Ala Ser Gly Val Pro Phe Phe Phe Val Arg Ser Asp Arg Ala Gly Asn
    295                 300                 305

atc tcc aag cgg caa tct gca gct acg ttc cac ttc tcg cga aca gac   1075
Ile Ser Lys Arg Gln Ser Ala Ala Thr Phe His Phe Ser Arg Thr Asp
310                 315                 320                 325

ggc act tgt cct ttg tgg gcg ctg cat cgt gct ttt gaa cgt cag gga   1123
Gly Thr Cys Pro Leu Trp Ala Leu His Arg Ala Phe Glu Arg Gln Gly
                330                 335                 340

aac atc acc cgc cag gtt gct cgc atg ccg gat ggc cgg acc tat ttg   1171
Asn Ile Thr Arg Gln Val Ala Arg Met Pro Asp Gly Arg Thr Tyr Leu
            345                 350                 355

tgg ctc gca cgc gcg gtg aaa ggt cga act cat ggt ttc ggg tat cct   1219
Trp Leu Ala Arg Ala Val Lys Gly Arg Thr His Gly Phe Gly Tyr Pro
        360                 365                 370

gct gcg gaa ttc gcc atc ggc ctg ggc tgc gat atc agc gag gca cca   1267
Ala Ala Glu Phe Ala Ile Gly Leu Gly Cys Asp Ile Ser Glu Ala Pro
    375                 380                 385

ggc ttg gtg tat tcc caa ggc ctt aat ttg gat ccc gag tcc gcc gca   1315
Gly Leu Val Tyr Ser Gln Gly Leu Asn Leu Asp Pro Glu Ser Ala Ala
```

```
390                 395                 400                 405

gag atc ggc cct ggt tgt cgg atc tgt cct cgg gag aac tgt gtg cag   1363
Glu Ile Gly Pro Gly Cys Arg Ile Cys Pro Arg Glu Asn Cys Val Gln
                410                 415                 420

cgt gca ttc cca cca tcg ggt caa gaa tct atc cgc cca gcc cct gtc   1411
Arg Ala Phe Pro Pro Ser Gly Gln Glu Ser Ile Arg Pro Ala Pro Val
            425                 430                 435

caa ctc ctc aac taaaaaggca gcacttaaaa aac                        1446
Gln Leu Leu Asn
        440
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<210> 1096
<211> 441
<212> PRT
<213> Corynebacterium glutamicum

<400> 1096

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Met Ser Lys Leu Tyr Ala Gly Ala Arg Ile Asn Ala Leu Arg Arg Thr
  1               5                  10                  15

His Gln Leu Thr Gln Ser Ala Leu Ala Asp Lys Leu Asp Leu Ser Thr
             20                  25                  30

Ser Tyr Leu Asn Gln Leu Glu Asn Asp Gly Arg Pro Leu Thr Ala Thr
         35                  40                  45

Val Leu Leu Gln Leu Met Lys Val Phe Asp Val Glu Ala Ser Tyr Phe
     50                  55                  60

Ser Pro Asp Arg Gly Thr Ala Thr Ala Thr Arg Leu Ala Glu Thr Leu
 65                  70                  75                  80

Ala Met Asn Gln Gly Pro Thr Met Ser Met Asp Asp Leu Leu Asp Phe
                 85                  90                  95

Ala Asp Arg Phe Pro Gln Leu Ala Gln His Ile Ile Gln Pro Ala Glu
            100                 105                 110

Val Asp Pro Thr His Ser Ser Ala His Asp Phe Val Arg Asp Tyr Phe
        115                 120                 125

Ala Thr His Lys Asn Tyr Ile Asp Ser Leu Asp Arg Leu Gly Glu Glu
    130                 135                 140

Leu Ala Thr Ala Ile Gly Gln Pro Gly Leu Arg Val Thr Arg Leu Ala
145                 150                 155                 160

Gln Leu Leu Asp Ala Glu Tyr Asn Ile Thr Val Arg Phe Arg Ala Pro
                165                 170                 175

Asp Ile Thr Gly Arg Arg His Phe Asp Pro Gln Ser Arg Gln Ile Leu
            180                 185                 190

Leu Arg Gln Asp Leu Ser Glu Ala Gln Gln Cys Phe Gln Leu Ala Glu
        195                 200                 205

Glu Leu Thr Phe Leu Ala His Ala Glu Leu Leu Asp Thr Leu Thr Thr
```

```
    210                 215                 220

Asp Gln Pro Asp Leu Pro Ser Glu Ala Ala Ile Arg Leu Ala Lys Val
225                 230                 235                 240

Gly Leu Ser Gln Tyr Phe Ala Ala Ala Val Val Met Pro Tyr Thr Arg
                245                 250                 255

Phe Leu Glu Phe Ala Gln Asp Lys His Tyr Asp Ile Glu Leu Ile Ser
            260                 265                 270

Glu Ala Phe Gly Val Ser Phe Glu Ser Ala Cys His Arg Leu Ser Thr
        275                 280                 285

Leu Gln Arg Ser Gly Ala Ser Gly Val Pro Phe Phe Phe Val Arg Ser
    290                 295                 300

Asp Arg Ala Gly Asn Ile Ser Lys Arg Gln Ser Ala Ala Thr Phe His
305                 310                 315                 320

Phe Ser Arg Thr Asp Gly Thr Cys Pro Leu Trp Ala Leu His Arg Ala
                325                 330                 335

Phe Glu Arg Gln Gly Asn Ile Thr Arg Gln Val Ala Arg Met Pro Asp
            340                 345                 350

Gly Arg Thr Tyr Leu Trp Leu Ala Arg Ala Val Lys Gly Arg Thr His
        355                 360                 365

Gly Phe Gly Tyr Pro Ala Ala Glu Phe Ala Ile Gly Leu Gly Cys Asp
    370                 375                 380

Ile Ser Glu Ala Pro Gly Leu Val Tyr Ser Gln Gly Leu Asn Leu Asp
385                 390                 395                 400

Pro Glu Ser Ala Ala Glu Ile Gly Pro Gly Cys Arg Ile Cys Pro Arg
                405                 410                 415

Glu Asn Cys Val Gln Arg Ala Phe Pro Pro Ser Gly Gln Glu Ser Ile
            420                 425                 430

Arg Pro Ala Pro Val Gln Leu Leu Asn
        435                 440


<210> 1097
<211> 1024
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1024)
<223> FRXA02337

<400> 1097
cacaaggtaa aatttgtgta attgtgtcgt gtggatttga aggtttttgt aaatctagtt 60

aaatcatgag gtcataagct tttcgggagg ttgtcaaagg atg tcg aag ctt tac   115
                                                Met Ser Lys Leu Tyr
                                                  1               5
```

```
gcg ggg gca agg atc aat gca ctg cgc cga acc cat cag ctc acc caa   163
Ala Gly Ala Arg Ile Asn Ala Leu Arg Arg Thr His Gln Leu Thr Gln
                10                  15                  20

tca gca ttg gcc gac aag ctt gat ctc tcc acc agc tat ctc aac cag   211
Ser Ala Leu Ala Asp Lys Leu Asp Leu Ser Thr Ser Tyr Leu Asn Gln
            25                  30                  35

ttg gaa aat gac gga cgg cca ctc act gcc acg gtg ctt ctg cag ctg   259
Leu Glu Asn Asp Gly Arg Pro Leu Thr Ala Thr Val Leu Leu Gln Leu
        40                  45                  50

atg aaa gtg ttc gat gtt gag gcc agt tac ttc tcc cct gac cgg ggt   307
Met Lys Val Phe Asp Val Glu Ala Ser Tyr Phe Ser Pro Asp Arg Gly
    55                  60                  65

acg gcc act gct acc cga ctg gct gaa acc ttg gcg atg aat cag ggt   355
Thr Ala Thr Ala Thr Arg Leu Ala Glu Thr Leu Ala Met Asn Gln Gly
70                  75                  80                  85

ccg acg atg tcg atg gat gat ctt tta gat ttc gcg gat cgt ttc cct   403
Pro Thr Met Ser Met Asp Asp Leu Leu Asp Phe Ala Asp Arg Phe Pro
                90                  95                  100

cag tta gcg cag cat att atc cag cct gct gag gtt gat ccc acg cat   451
Gln Leu Ala Gln His Ile Ile Gln Pro Ala Glu Val Asp Pro Thr His
            105                 110                 115

agt tct gcg cat gat ttt gtt cgg gat tat ttt gcc acc cac aaa aac   499
Ser Ser Ala His Asp Phe Val Arg Asp Tyr Phe Ala Thr His Lys Asn
        120                 125                 130

tac att gat tcg ctc gat cgc ctt gga gag gag ttg gca act gcc att   547
Tyr Ile Asp Ser Leu Asp Arg Leu Gly Glu Glu Leu Ala Thr Ala Ile
    135                 140                 145

ggt cag ccg gga ctt cgg gtt act agg ctc gcg cag ttg ctt gat gcg   595
Gly Gln Pro Gly Leu Arg Val Thr Arg Leu Ala Gln Leu Leu Asp Ala
150                 155                 160                 165

gag tac aac atc acg gtg cgt ttc cgg gcg ccg gat att act ggc cgg   643
Glu Tyr Asn Ile Thr Val Arg Phe Arg Ala Pro Asp Ile Thr Gly Arg
                170                 175                 180

agg cac ttt gat ccc caa tcg cgt cag att ctg ctg cgg caa gat ctc   691
Arg His Phe Asp Pro Gln Ser Arg Gln Ile Leu Leu Arg Gln Asp Leu
            185                 190                 195

agc gag gcg cag cag tgt ttc cag ttg gcg gag gaa ttg acg ttt ctt   739
Ser Glu Ala Gln Gln Cys Phe Gln Leu Ala Glu Glu Leu Thr Phe Leu
        200                 205                 210

gct cat gca gag ctc ttg gat acc ctg acc aca gat caa ccg gat ctc   787
Ala His Ala Glu Leu Leu Asp Thr Leu Thr Thr Asp Gln Pro Asp Leu
    215                 220                 225

cct tct gag gca gct atc cgc ctg gct aag gtg ggt ctc tcc caa tat   835
Pro Ser Glu Ala Ala Ile Arg Leu Ala Lys Val Gly Leu Ser Gln Tyr
230                 235                 240                 245
```

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ttc gcg gct gct gtt gtc atg ccg tac acc cgc ttt ttg gaa ttc gcc   883
Phe Ala Ala Ala Val Val Met Pro Tyr Thr Arg Phe Leu Glu Phe Ala
                250                 255                 260

cag gat aag cac tat gac atc gag ttg atc tct gag gcg ttt gga gtg   931
Gln Asp Lys His Tyr Asp Ile Glu Leu Ile Ser Glu Ala Phe Gly Val
            265                 270                 275

tct ttc gag tct gca tgc cac cgc ctg tct act ctg cag cgt tcg ggg   979
Ser Phe Glu Ser Ala Cys His Arg Leu Ser Thr Leu Gln Arg Ser Gly
        280                 285                 290

gcg tca ggg gtg ccg ttt ttc ttt gtg cgc tcg gat cgt gca gga       1024
Ala Ser Gly Val Pro Phe Phe Phe Val Arg Ser Asp Arg Ala Gly
    295                 300                 305


<210> 1098
<211> 308
<212> PRT
<213> Corynebacterium glutamicum

<400> 1098
Met Ser Lys Leu Tyr Ala Gly Ala Arg Ile Asn Ala Leu Arg Arg Thr
  1               5                  10                  15

His Gln Leu Thr Gln Ser Ala Leu Ala Asp Lys Leu Asp Leu Ser Thr
             20                  25                  30

Ser Tyr Leu Asn Gln Leu Glu Asn Asp Gly Arg Pro Leu Thr Ala Thr
         35                  40                  45

Val Leu Leu Gln Leu Met Lys Val Phe Asp Val Glu Ala Ser Tyr Phe
     50                  55                  60

Ser Pro Asp Arg Gly Thr Ala Thr Ala Thr Arg Leu Ala Glu Thr Leu
 65                  70                  75                  80

Ala Met Asn Gln Gly Pro Thr Met Ser Met Asp Asp Leu Leu Asp Phe
                 85                  90                  95

Ala Asp Arg Phe Pro Gln Leu Ala Gln His Ile Ile Gln Pro Ala Glu
            100                 105                 110

Val Asp Pro Thr His Ser Ser Ala His Asp Phe Val Arg Asp Tyr Phe
        115                 120                 125

Ala Thr His Lys Asn Tyr Ile Asp Ser Leu Asp Arg Leu Gly Glu Glu
    130                 135                 140

Leu Ala Thr Ala Ile Gly Gln Pro Gly Leu Arg Val Thr Arg Leu Ala
145                 150                 155                 160

Gln Leu Leu Asp Ala Glu Tyr Asn Ile Thr Val Arg Phe Arg Ala Pro
                165                 170                 175

Asp Ile Thr Gly Arg Arg His Phe Asp Pro Gln Ser Arg Gln Ile Leu
            180                 185                 190

Leu Arg Gln Asp Leu Ser Glu Ala Gln Gln Cys Phe Gln Leu Ala Glu
        195                 200                 205
```

```
Glu Leu Thr Phe Leu Ala His Ala Glu Leu Leu Asp Thr Leu Thr Thr
    210                 215                 220

Asp Gln Pro Asp Leu Pro Ser Glu Ala Ala Ile Arg Leu Ala Lys Val
225                 230                 235                 240

Gly Leu Ser Gln Tyr Phe Ala Ala Ala Val Val Met Pro Tyr Thr Arg
                245                 250                 255

Phe Leu Glu Phe Ala Gln Asp Lys His Tyr Asp Ile Glu Leu Ile Ser
            260                 265                 270

Glu Ala Phe Gly Val Ser Phe Glu Ser Ala Cys His Arg Leu Ser Thr
        275                 280                 285

Leu Gln Arg Ser Gly Ala Ser Gly Val Pro Phe Phe Phe Val Arg Ser
    290                 295                 300

Asp Arg Ala Gly
305
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<210> 1099
<211> 515
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(492)
<223> RXN02339

<400> 1099

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ccc acc gac aac ctc ttt tca tat cct gca caa cgc tat gat ctt ctc   48
Pro Thr Asp Asn Leu Phe Ser Tyr Pro Ala Gln Arg Tyr Asp Leu Leu
  1               5                  10                  15

aca ctt gcc ttt gaa gtt agg att ggg gac atg gtt caa att aat gac   96
Thr Leu Ala Phe Glu Val Arg Ile Gly Asp Met Val Gln Ile Asn Asp
             20                  25                  30

atg ctt gcc cct cct cca gta aaa ctt ccg gaa gat cct gcc ctc ggc   144
Met Leu Ala Pro Pro Pro Val Lys Leu Pro Glu Asp Pro Ala Leu Gly
         35                  40                  45

gcc gat cca act ttg acc tcg aca gcg att gcg cat cct gac agc cca   192
Ala Asp Pro Thr Leu Thr Ser Thr Ala Ile Ala His Pro Asp Ser Pro
     50                  55                  60

ttg gtg tgg gcg tac cga gct gaa aat ctt atc aaa tct gca tca aat   240
Leu Val Trp Ala Tyr Arg Ala Glu Asn Leu Ile Lys Ser Ala Ser Asn
 65                  70                  75                  80

gat gaa gag aag att cag gcc tac gct ttt gcg cgc acg ggt tac cac   288
Asp Glu Glu Lys Ile Gln Ala Tyr Ala Phe Ala Arg Thr Gly Tyr His
                 85                  90                  95

cgc agt ctc gat cgt ctg cgt gcc aat ggt tgg aag ggt tgg ggt cct   336
Arg Ser Leu Asp Arg Leu Arg Ala Asn Gly Trp Lys Gly Trp Gly Pro
            100                 105                 110
```

```
gtc ccc ttc tct cat gag cca aac cag gga gtg ttg cgg gct atc gct   384
Val Pro Phe Ser His Glu Pro Asn Gln Gly Val Leu Arg Ala Ile Ala
        115                 120                 125

tcc cta gct ctt gct gcg aag ctg att ggt gag gac aac gaa tac gat   432
Ser Leu Ala Leu Ala Ala Lys Leu Ile Gly Glu Asp Asn Glu Tyr Asp
    130                 135                 140

cgt tgc cgc cag atg ctc tct gat gcg gat cca gag tcc gtc gca gtc   480
Arg Cys Arg Gln Met Leu Ser Asp Ala Asp Pro Glu Ser Val Ala Val
145                 150                 155                 160

cta ctc gac aaa taaaccacca aaaataaaac aat                        515
Leu Leu Asp Lys
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<210> 1100
<211> 164
<212> PRT
<213> Corynebacterium glutamicum

<400> 1100

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Pro Thr Asp Asn Leu Phe Ser Tyr Pro Ala Gln Arg Tyr Asp Leu Leu
  1               5                  10                  15

Thr Leu Ala Phe Glu Val Arg Ile Gly Asp Met Val Gln Ile Asn Asp
             20                  25                  30

Met Leu Ala Pro Pro Pro Val Lys Leu Pro Glu Asp Pro Ala Leu Gly
         35                  40                  45

Ala Asp Pro Thr Leu Thr Ser Thr Ala Ile Ala His Pro Asp Ser Pro
     50                  55                  60

Leu Val Trp Ala Tyr Arg Ala Glu Asn Leu Ile Lys Ser Ala Ser Asn
 65                  70                  75                  80

Asp Glu Glu Lys Ile Gln Ala Tyr Ala Phe Ala Arg Thr Gly Tyr His
                 85                  90                  95

Arg Ser Leu Asp Arg Leu Arg Ala Asn Gly Trp Lys Gly Trp Gly Pro
            100                 105                 110

Val Pro Phe Ser His Glu Pro Asn Gln Gly Val Leu Arg Ala Ile Ala
        115                 120                 125

Ser Leu Ala Leu Ala Ala Lys Leu Ile Gly Glu Asp Asn Glu Tyr Asp
    130                 135                 140

Arg Cys Arg Gln Met Leu Ser Asp Ala Asp Pro Glu Ser Val Ala Val
145                 150                 155                 160

Leu Leu Asp Lys
```

<210> 1101
<211> 515
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(492)
<223> FRXA02339

<400> 1101

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ccc acc gac aac ctc ttt tca tat cct gca caa cgc tat gat ctt ctc   48
Pro Thr Asp Asn Leu Phe Ser Tyr Pro Ala Gln Arg Tyr Asp Leu Leu
  1               5                  10                  15

aca ctt gcc ttt gaa gtt agg att ggg gac atg gtt caa att aat gac   96
Thr Leu Ala Phe Glu Val Arg Ile Gly Asp Met Val Gln Ile Asn Asp
             20                  25                  30

atg ctt gcc cct cct cca gta aaa ctt ccg gaa gat cct gcc ctc ggc   144
Met Leu Ala Pro Pro Pro Val Lys Leu Pro Glu Asp Pro Ala Leu Gly
         35                  40                  45

gcc gat cca act ttg acc tcg aca gcg att gcg cat cct gac agc cca   192
Ala Asp Pro Thr Leu Thr Ser Thr Ala Ile Ala His Pro Asp Ser Pro
     50                  55                  60

ttg gtg tgg gcg tac cga gct gaa aat ctt atc aaa tct gca tca aat   240
Leu Val Trp Ala Tyr Arg Ala Glu Asn Leu Ile Lys Ser Ala Ser Asn
 65                  70                  75                  80

gat gaa gag aag att cag gcc tac gct ttt gcg cgc acg ggt tac cac   288
Asp Glu Glu Lys Ile Gln Ala Tyr Ala Phe Ala Arg Thr Gly Tyr His
                 85                  90                  95

cgc agt ctc gat cgt ctg cgt gcc aat ggt tgg aag ggt tgg ggt cct   336
Arg Ser Leu Asp Arg Leu Arg Ala Asn Gly Trp Lys Gly Trp Gly Pro
            100                 105                 110

gtc ccc ttc tct cat gag cca aac cag gga gtg ttg cgg gct atc gct   384
Val Pro Phe Ser His Glu Pro Asn Gln Gly Val Leu Arg Ala Ile Ala
        115                 120                 125

tcc cta gct ctt gct gcg aag ctg att ggt gag gac aac gaa tac gat   432
Ser Leu Ala Leu Ala Ala Lys Leu Ile Gly Glu Asp Asn Glu Tyr Asp
    130                 135                 140

cgt tgc cgc cag atg ctc tct gat gcg gat cca gag tcc gtc gca gtc   480
Arg Cys Arg Gln Met Leu Ser Asp Ala Asp Pro Glu Ser Val Ala Val
145                 150                 155                 160

cta ctc gac aaa taaaccacca aaaataaaac aat                        515
Leu Leu Asp Lys
```

<210> 1102
<211> 164
<212> PRT
<213> Corynebacterium glutamicum

<400> 1102

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Pro Thr Asp Asn Leu Phe Ser Tyr Pro Ala Gln Arg Tyr Asp Leu Leu
  1               5                  10                  15
```

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Thr Leu Ala Phe Glu Val Arg Ile Gly Asp Met Val Gln Ile Asn Asp
            20                  25                  30

Met Leu Ala Pro Pro Pro Val Lys Leu Pro Glu Asp Pro Ala Leu Gly
        35                  40                  45

Ala Asp Pro Thr Leu Thr Ser Thr Ala Ile Ala His Pro Asp Ser Pro
    50                  55                  60

Leu Val Trp Ala Tyr Arg Ala Glu Asn Leu Ile Lys Ser Ala Ser Asn
65                  70                  75                  80

Asp Glu Glu Lys Ile Gln Ala Tyr Ala Phe Ala Arg Thr Gly Tyr His
                85                  90                  95

Arg Ser Leu Asp Arg Leu Arg Ala Asn Gly Trp Lys Gly Trp Gly Pro
            100                 105                 110

Val Pro Phe Ser His Glu Pro Asn Gln Gly Val Leu Arg Ala Ile Ala
        115                 120                 125

Ser Leu Ala Leu Ala Ala Lys Leu Ile Gly Glu Asp Asn Glu Tyr Asp
    130                 135                 140

Arg Cys Arg Gln Met Leu Ser Asp Ala Asp Pro Glu Ser Val Ala Val
145                 150                 155                 160

Leu Leu Asp Lys
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<210> 1103
<211> 1188
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1165)
<223> RXN02340

<400> 1103

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aaaacgtgtc taaaaattca gtttttattg ctgctgatca cctcttgaag aactcaaccc 60

aaaagtgctt caagttatga gaaagtgaaa tccaacaccc atg aaa aag agc atc   115
                                            Met Lys Lys Ser Ile
                                              1               5

gtt gta ttt gaa gtc gaa ggc ggc tcc gac aag cac ttc gac ggt cac   163
Val Val Phe Glu Val Glu Gly Gly Ser Asp Lys His Phe Asp Gly His
                10                  15                  20

cgt aaa gac acc atg cct atc gtc aac tcc ata aat gat gct ggc tgg   211
Arg Lys Asp Thr Met Pro Ile Val Asn Ser Ile Asn Asp Ala Gly Trp
            25                  30                  35

cag gca gag gtt gtg tac tac cgc cca gag tgg acc gaa ggt ctc ttt   259
Gln Ala Glu Val Val Tyr Tyr Arg Pro Glu Trp Thr Glu Gly Leu Phe
        40                  45                  50
```

```
gag tac gta tct gaa aac ttc gac ggc tac atc tca cgt gtc aac cca   307
Glu Tyr Val Ser Glu Asn Phe Asp Gly Tyr Ile Ser Arg Val Asn Pro
     55                  60                  65

ggc aac atc cca ggc ggc gag cgc ggc tac ttt gac ctg ctc acc cgc   355
Gly Asn Ile Pro Gly Gly Glu Arg Gly Tyr Phe Asp Leu Leu Thr Arg
 70                  75                  80                  85

ctg tcc gaa gca ggg ctc gtg ggc atg tcc acc cct gag gaa atg atg   403
Leu Ser Glu Ala Gly Leu Val Gly Met Ser Thr Pro Glu Glu Met Met
                 90                  95                 100

gca tac ggc gcg aaa gat gcg ctg gtc aag cta tcc caa acc gac ctg   451
Ala Tyr Gly Ala Lys Asp Ala Leu Val Lys Leu Ser Gln Thr Asp Leu
            105                 110                 115

gtg cca tcc gac acc gag gcg tac tac gac gtg gag acc ttc cac aag   499
Val Pro Ser Asp Thr Glu Ala Tyr Tyr Asp Val Glu Thr Phe His Lys
        120                 125                 130

gtt ttc cca acc tcc ctg tcc ttc ggt gag cgc gtg ctc aag caa aac   547
Val Phe Pro Thr Ser Leu Ser Phe Gly Glu Arg Val Leu Lys Gln Asn
    135                 140                 145

cgt ggc tcc acc ggc tcc ggc att tgg cgc gtc cag ttg gta gac aag   595
Arg Gly Ser Thr Gly Ser Gly Ile Trp Arg Val Gln Leu Val Asp Lys
150                 155                 160                 165

gaa ctg gct gca tcc atc gag cca ggc acc gca ctg cca ttg gac act   643
Glu Leu Ala Ala Ser Ile Glu Pro Gly Thr Ala Leu Pro Leu Asp Thr
                170                 175                 180

gaa atc aag tgc acc gaa gca gtc gac aac cac act gaa gtc cgc aag   691
Glu Ile Lys Cys Thr Glu Ala Val Asp Asn His Thr Glu Val Arg Lys
            185                 190                 195

ctc ggc gag ttc atg gat ttc tgt gac cag tac atc atc ggc gac aac   739
Leu Gly Glu Phe Met Asp Phe Cys Asp Gln Tyr Ile Ile Gly Asp Asn
        200                 205                 210

ggc atg ctc gtt gat atg cgt ttc atg cca cgc atc gtc gaa ggc gaa   787
Gly Met Leu Val Asp Met Arg Phe Met Pro Arg Ile Val Glu Gly Glu
    215                 220                 225

atc cgc atc ctt ctc gtc gga cca cac cca gtg ttc gtc gtg cac aag   835
Ile Arg Ile Leu Leu Val Gly Pro His Pro Val Phe Val Val His Lys
230                 235                 240                 245

aag cca gca gaa ggc ggc gac aac ttc tcc gca acc ctg ttc tcc ggc   883
Lys Pro Ala Glu Gly Gly Asp Asn Phe Ser Ala Thr Leu Phe Ser Gly
                250                 255                 260

gcg aag tac acc tac gac aag cca gag cag tgg cag gaa ctg att gac   931
Ala Lys Tyr Thr Tyr Asp Lys Pro Glu Gln Trp Gln Glu Leu Ile Asp
            265                 270                 275

ctc ttc gca gac gct cgc cca gtc atc gca gaa aag ctc ggc ggc gac   979
Leu Phe Ala Asp Ala Arg Pro Val Ile Ala Glu Lys Leu Gly Gly Asp
        280                 285                 290

aac atc cca ttg atc tgg acc gca gac ttc atg ctc ggc gat gtc gtt   1027
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Asn Ile Pro Leu Ile Trp Thr Ala Asp Phe Met Leu Gly Asp Val Val
    295                 300                 305

gac ggc aag gac acc tac gtg ctc ggt gaa atc aac tgc tcc tgc gtc   1075
Asp Gly Lys Asp Thr Tyr Val Leu Gly Glu Ile Asn Cys Ser Cys Val
310                 315                 320                 325

ggc ttc acc tcc gag ctg gac atg ggc atc cag cag ctt gtg gca tca   1123
Gly Phe Thr Ser Glu Leu Asp Met Gly Ile Gln Gln Leu Val Ala Ser
                330                 335                 340

gag gcc atc aag cgc atc gag gaa ttc gcg cag ctt act gtt           1165
Glu Ala Ile Lys Arg Ile Glu Glu Phe Ala Gln Leu Thr Val
            345                 350                 355

taaaactttg cttctcgacg tct                                        1188


<210> 1104
<211> 355
<212> PRT
<213> Corynebacterium glutamicum

<400> 1104
Met Lys Lys Ser Ile Val Val Phe Glu Val Glu Gly Gly Ser Asp Lys
  1               5                  10                  15

His Phe Asp Gly His Arg Lys Asp Thr Met Pro Ile Val Asn Ser Ile
             20                  25                  30

Asn Asp Ala Gly Trp Gln Ala Glu Val Val Tyr Tyr Arg Pro Glu Trp
         35                  40                  45

Thr Glu Gly Leu Phe Glu Tyr Val Ser Glu Asn Phe Asp Gly Tyr Ile
     50                  55                  60

Ser Arg Val Asn Pro Gly Asn Ile Pro Gly Gly Glu Arg Gly Tyr Phe
 65                  70                  75                  80

Asp Leu Leu Thr Arg Leu Ser Glu Ala Gly Leu Val Gly Met Ser Thr
                 85                  90                  95

Pro Glu Glu Met Met Ala Tyr Gly Ala Lys Asp Ala Leu Val Lys Leu
            100                 105                 110

Ser Gln Thr Asp Leu Val Pro Ser Asp Thr Glu Ala Tyr Tyr Asp Val
        115                 120                 125

Glu Thr Phe His Lys Val Phe Pro Thr Ser Leu Ser Phe Gly Glu Arg
    130                 135                 140

Val Leu Lys Gln Asn Arg Gly Ser Thr Gly Ser Gly Ile Trp Arg Val
145                 150                 155                 160

Gln Leu Val Asp Lys Glu Leu Ala Ala Ser Ile Glu Pro Gly Thr Ala
                165                 170                 175

Leu Pro Leu Asp Thr Glu Ile Lys Cys Thr Glu Ala Val Asp Asn His
            180                 185                 190

Thr Glu Val Arg Lys Leu Gly Glu Phe Met Asp Phe Cys Asp Gln Tyr
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        195                 200                 205

Ile Ile Gly Asp Asn Gly Met Leu Val Asp Met Arg Phe Met Pro Arg
    210                 215                 220

Ile Val Glu Gly Glu Ile Arg Ile Leu Leu Val Gly Pro His Pro Val
225                 230                 235                 240

Phe Val Val His Lys Lys Pro Ala Glu Gly Gly Asp Asn Phe Ser Ala
                245                 250                 255

Thr Leu Phe Ser Gly Ala Lys Tyr Thr Tyr Asp Lys Pro Glu Gln Trp
            260                 265                 270

Gln Glu Leu Ile Asp Leu Phe Ala Asp Ala Arg Pro Val Ile Ala Glu
        275                 280                 285

Lys Leu Gly Gly Asp Asn Ile Pro Leu Ile Trp Thr Ala Asp Phe Met
    290                 295                 300

Leu Gly Asp Val Val Asp Gly Lys Asp Thr Tyr Val Leu Gly Glu Ile
305                 310                 315                 320

Asn Cys Ser Cys Val Gly Phe Thr Ser Glu Leu Asp Met Gly Ile Gln
                325                 330                 335

Gln Leu Val Ala Ser Glu Ala Ile Lys Arg Ile Glu Glu Phe Ala Gln
            340                 345                 350

Leu Thr Val
        355


<210> 1105
<211> 580
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(580)
<223> FRXA02338

<400> 1105
aaaacgtgtc taaaaattca gtttttattg ctgctgatca cctcttgaag aactcaaccc 60

aaaagtgctt caagttatga gaaagtgaaa tccaacaccc atg aaa aag agc atc   115
                                              Met Lys Lys Ser Ile
                                                1               5

gtt gta ttt gaa gtc gaa ggc ggc tcc gac aag cac ttc gac ggt cac   163
Val Val Phe Glu Val Glu Gly Gly Ser Asp Lys His Phe Asp Gly His
                10                  15                  20

cgt aaa gac acc atg cct atc gtc aac tcc ata aat gat gct ggc tgg   211
Arg Lys Asp Thr Met Pro Ile Val Asn Ser Ile Asn Asp Ala Gly Trp
            25                  30                  35

cag gca gag gtt gtg tac tac cgc cca gag tgg acc gaa ggt ctc ttt   259
Gln Ala Glu Val Val Tyr Tyr Arg Pro Glu Trp Thr Glu Gly Leu Phe
        40                  45                  50
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gag tac gta tct gaa aac ttc gac ggc tac atc tca cgt gtc aac cca   307
Glu Tyr Val Ser Glu Asn Phe Asp Gly Tyr Ile Ser Arg Val Asn Pro
     55                  60                  65

ggc aac atc cca ggc ggc gag cgc ggc tac ttt gac ctg ctc acc cgc   355
Gly Asn Ile Pro Gly Gly Glu Arg Gly Tyr Phe Asp Leu Leu Thr Arg
 70                  75                  80                  85

ctg tcc gaa gca ggg ctc gtg ggc atg tcc acc cct gag gaa atg atg   403
Leu Ser Glu Ala Gly Leu Val Gly Met Ser Thr Pro Glu Glu Met Met
                90                  95                 100

gca tac ggc gcg aaa gat gcg ctg gtc aag cta tcc caa acc gac ctg   451
Ala Tyr Gly Ala Lys Asp Ala Leu Val Lys Leu Ser Gln Thr Asp Leu
            105                 110                 115

gtg cca tcc gac acc gag gcg tac tac gac gtg gag acc ttc cac aag   499
Val Pro Ser Asp Thr Glu Ala Tyr Tyr Asp Val Glu Thr Phe His Lys
        120                 125                 130

gtt ttc cca acc tcc ctg tcc ttc ggt gaa gcg cgt gct caa gca aaa   547
Val Phe Pro Thr Ser Leu Ser Phe Gly Glu Ala Arg Ala Gln Ala Lys
    135                 140                 145

acc tgg ctt cac cgg ctt ccg cat ttg gcg cgt                      580
Thr Trp Leu His Arg Leu Pro His Leu Ala Arg
150                 155                 160


<210> 1106
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 1106
Met Lys Lys Ser Ile Val Val Phe Glu Val Glu Gly Gly Ser Asp Lys
  1               5                  10                  15

His Phe Asp Gly His Arg Lys Asp Thr Met Pro Ile Val Asn Ser Ile
             20                  25                  30

Asn Asp Ala Gly Trp Gln Ala Glu Val Val Tyr Tyr Arg Pro Glu Trp
         35                  40                  45

Thr Glu Gly Leu Phe Glu Tyr Val Ser Glu Asn Phe Asp Gly Tyr Ile
     50                  55                  60

Ser Arg Val Asn Pro Gly Asn Ile Pro Gly Gly Glu Arg Gly Tyr Phe
 65                  70                  75                  80

Asp Leu Leu Thr Arg Leu Ser Glu Ala Gly Leu Val Gly Met Ser Thr
                 85                  90                  95

Pro Glu Glu Met Met Ala Tyr Gly Ala Lys Asp Ala Leu Val Lys Leu
            100                 105                 110

Ser Gln Thr Asp Leu Val Pro Ser Asp Thr Glu Ala Tyr Tyr Asp Val
        115                 120                 125

Glu Thr Phe His Lys Val Phe Pro Thr Ser Leu Ser Phe Gly Glu Ala
```

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    130                 135                 140

Arg Ala Gln Ala Lys Thr Trp Leu His Arg Leu Pro His Leu Ala Arg
145                 150                 155                 160
```

<210> 1107
<211> 662
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(639)
<223> FRXA02340

<400> 1107

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gag cgc gtg ctc aag caa aac cgt ggc tcc acc ggc tcc ggc att tgg   48
Glu Arg Val Leu Lys Gln Asn Arg Gly Ser Thr Gly Ser Gly Ile Trp
  1               5                  10                  15

cgc gtc cag ttg gta gac aag gaa ctg gct gca tcc atc gag cca ggc   96
Arg Val Gln Leu Val Asp Lys Glu Leu Ala Ala Ser Ile Glu Pro Gly
             20                  25                  30

acc gca ctg cca ttg gac act gaa atc aag tgc acc gaa gca gtc gac   144
Thr Ala Leu Pro Leu Asp Thr Glu Ile Lys Cys Thr Glu Ala Val Asp
         35                  40                  45

aac cac act gaa gtc cgc aag ctc ggc gag ttc atg gat ttc tgt gac   192
Asn His Thr Glu Val Arg Lys Leu Gly Glu Phe Met Asp Phe Cys Asp
     50                  55                  60

cag tac atc atc ggc gac aac ggc atg ctc gtt gat atg cgt ttc atg   240
Gln Tyr Ile Ile Gly Asp Asn Gly Met Leu Val Asp Met Arg Phe Met
 65                  70                  75                  80

cca cgc atc gtc gaa ggc gaa atc cgc atc ctt ctc gtc gga cca cac   288
Pro Arg Ile Val Glu Gly Glu Ile Arg Ile Leu Leu Val Gly Pro His
                 85                  90                  95

cca gtg ttc gtc gtg cac aag aag cca gca gaa ggc ggc gac aac ttc   336
Pro Val Phe Val Val His Lys Lys Pro Ala Glu Gly Gly Asp Asn Phe
            100                 105                 110

tcc gca acc ctg ttc tcc ggc gcg aag tac acc tac gac aag cca gag   384
Ser Ala Thr Leu Phe Ser Gly Ala Lys Tyr Thr Tyr Asp Lys Pro Glu
        115                 120                 125

cag tgg cag gaa ctg att gac ctc ttc gca gac gct cgc cca gtc atc   432
Gln Trp Gln Glu Leu Ile Asp Leu Phe Ala Asp Ala Arg Pro Val Ile
    130                 135                 140

gca gaa aag ctc ggc ggc gac aac atc cca ttg atc tgg acc gca gac   480
Ala Glu Lys Leu Gly Gly Asp Asn Ile Pro Leu Ile Trp Thr Ala Asp
145                 150                 155                 160

ttc atg ctc ggc gat gtc gtt gac ggc aag gac acc tac gtg ctc ggt   528
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```
Phe Met Leu Gly Asp Val Val Asp Gly Lys Asp Thr Tyr Val Leu Gly
                165                 170                 175

gaa atc aac tgc tcc tgc gtc ggc ttc acc tcc gag ctg gac atg ggc   576
Glu Ile Asn Cys Ser Cys Val Gly Phe Thr Ser Glu Leu Asp Met Gly
            180                 185                 190

atc cag cag ctt gtg gca tca gag gcc atc aag cgc atc gag gaa ttc   624
Ile Gln Gln Leu Val Ala Ser Glu Ala Ile Lys Arg Ile Glu Glu Phe
        195                 200                 205

gcg cag ctt act gtt taaaactttg cttctcgacg tct                     662
Ala Gln Leu Thr Val
    210


<210> 1108
<211> 213
<212> PRT
<213> Corynebacterium glutamicum

<400> 1108
Glu Arg Val Leu Lys Gln Asn Arg Gly Ser Thr Gly Ser Gly Ile Trp
  1               5                  10                  15

Arg Val Gln Leu Val Asp Lys Glu Leu Ala Ala Ser Ile Glu Pro Gly
             20                  25                  30

Thr Ala Leu Pro Leu Asp Thr Glu Ile Lys Cys Thr Glu Ala Val Asp
         35                  40                  45

Asn His Thr Glu Val Arg Lys Leu Gly Glu Phe Met Asp Phe Cys Asp
     50                  55                  60

Gln Tyr Ile Ile Gly Asp Asn Gly Met Leu Val Asp Met Arg Phe Met
 65                  70                  75                  80

Pro Arg Ile Val Glu Gly Glu Ile Arg Ile Leu Leu Val Gly Pro His
                 85                  90                  95

Pro Val Phe Val Val His Lys Lys Pro Ala Glu Gly Gly Asp Asn Phe
            100                 105                 110

Ser Ala Thr Leu Phe Ser Gly Ala Lys Tyr Thr Tyr Asp Lys Pro Glu
        115                 120                 125

Gln Trp Gln Glu Leu Ile Asp Leu Phe Ala Asp Ala Arg Pro Val Ile
    130                 135                 140

Ala Glu Lys Leu Gly Gly Asp Asn Ile Pro Leu Ile Trp Thr Ala Asp
145                 150                 155                 160

Phe Met Leu Gly Asp Val Val Asp Gly Lys Asp Thr Tyr Val Leu Gly
                165                 170                 175

Glu Ile Asn Cys Ser Cys Val Gly Phe Thr Ser Glu Leu Asp Met Gly
            180                 185                 190

Ile Gln Gln Leu Val Ala Ser Glu Ala Ile Lys Arg Ile Glu Glu Phe
        195                 200                 205
```

```
Ala Gln Leu Thr Val
    210


<210> 1109
<211> 609
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(586)
<223> RXN02341

<400> 1109
cgcgactggc ggagaaattc gtgttcgcga tgcttcgggc accgttcaca ccctcaacgc 60

cggtgaaatt acgcaccttc gcctgcagta aggtgacggt atg ggg aat tca ctt   115
                                            Met Gly Asn Ser Leu
                                              1               5

gag aaa cat att gca gag gga gac cgg atc cac gtc gat ctg aca tct   163
Glu Lys His Ile Ala Glu Gly Asp Arg Ile His Val Asp Leu Thr Ser
                 10                  15                  20

cct tta tcc gca atg ttg ttc ccc att ttt gaa ctc att gtg att act   211
Pro Leu Ser Ala Met Leu Phe Pro Ile Phe Glu Leu Ile Val Ile Thr
             25                  30                  35

gga atc tgt tgg atg ggc atc ggc ttt ttg gat cag ctt cca gga atc   259
Gly Ile Cys Trp Met Gly Ile Gly Phe Leu Asp Gln Leu Pro Gly Ile
         40                  45                  50

gat ggc acc aac ccc gcc gat agc ttc ccc gaa ggc acc cgc aat ctt   307
Asp Gly Thr Asn Pro Ala Asp Ser Phe Pro Glu Gly Thr Arg Asn Leu
     55                  60                  65

cta gtg ggt gtg tgg gca gta ctt gct gca tgg cgt ttc ggt ctt cct   355
Leu Val Gly Val Trp Ala Val Leu Ala Ala Trp Arg Phe Gly Leu Pro
 70                  75                  80                  85

tta ata agg caa cgt cga ctc cgc gtg atc ttg agc gac cgc aaa ctg   403
Leu Ile Arg Gln Arg Arg Leu Arg Val Ile Leu Ser Asp Arg Lys Leu
                 90                  95                 100

ctg gtc cga cgc gcg ggt ctg cgc acc ggg ttc gat tcc att cca ctg   451
Leu Val Arg Arg Ala Gly Leu Arg Thr Gly Phe Asp Ser Ile Pro Leu
            105                 110                 115

agc tac att cag cga gtc caa cgt cgg cga aac acc ctg gtc tta ggt   499
Ser Tyr Ile Gln Arg Val Gln Arg Arg Arg Asn Thr Leu Val Leu Gly
        120                 125                 130

gtt ggt gga cac cac cga ccc tat gta atc aac cag gtt ccc aag gct   547
Val Gly Gly His His Arg Pro Tyr Val Ile Asn Gln Val Pro Lys Ala
    135                 140                 145

cga aaa gtg gaa gcg ctg ctc aaa gat ctt aca ttt tgg tgaaggcgtt    596
Arg Lys Val Glu Ala Leu Leu Lys Asp Leu Thr Phe Trp
150                 155                 160
```

atagttagga ctt 609

<210> 1110
<211> 162
<212> PRT
<213> Corynebacterium glutamicum

<400> 1110

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Met Gly Asn Ser Leu Glu Lys His Ile Ala Glu Gly Asp Arg Ile His
  1               5                  10                  15

Val Asp Leu Thr Ser Pro Leu Ser Ala Met Leu Phe Pro Ile Phe Glu
             20                  25                  30

Leu Ile Val Ile Thr Gly Ile Cys Trp Met Gly Ile Gly Phe Leu Asp
         35                  40                  45

Gln Leu Pro Gly Ile Asp Gly Thr Asn Pro Ala Asp Ser Phe Pro Glu
     50                  55                  60

Gly Thr Arg Asn Leu Leu Val Gly Val Trp Ala Val Leu Ala Ala Trp
 65                  70                  75                  80

Arg Phe Gly Leu Pro Leu Ile Arg Gln Arg Arg Leu Arg Val Ile Leu
                 85                  90                  95

Ser Asp Arg Lys Leu Leu Val Arg Arg Ala Gly Leu Arg Thr Gly Phe
            100                 105                 110

Asp Ser Ile Pro Leu Ser Tyr Ile Gln Arg Val Gln Arg Arg Arg Asn
        115                 120                 125

Thr Leu Val Leu Gly Val Gly Gly His His Arg Pro Tyr Val Ile Asn
    130                 135                 140

Gln Val Pro Lys Ala Arg Lys Val Glu Ala Leu Leu Lys Asp Leu Thr
145                 150                 155                 160

Phe Trp
```

<210> 1111
<211> 511
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(511)
<223> FRXA02341

<400> 1111

cgcgactggc ggagaaattc gtgttcgcga tgcttcgggc accgttcaca ccctcaacgc 60

cggtgaaatt acgcaccttc gcctgcagta aggtgacggt atg ggg aat tca ctt 115
Met Gly Asn Ser Leu
1 5

gag aaa cat att gca gag gga gac cgg atc cac gtc gat ctg aca tct 163

```
Glu Lys His Ile Ala Glu Gly Asp Arg Ile His Val Asp Leu Thr Ser
                10                  15                  20

cct tta tcc gca atg ttg ttc ccc att ttt gaa ctc att gtg att act   211
Pro Leu Ser Ala Met Leu Phe Pro Ile Phe Glu Leu Ile Val Ile Thr
            25                  30                  35

gga atc tgt tgg atg ggc atc ggc ttt ttg gat cag ctt cca gga atc   259
Gly Ile Cys Trp Met Gly Ile Gly Phe Leu Asp Gln Leu Pro Gly Ile
        40                  45                  50

gat ggc acc aac ccc gcc gat agc ttc ccc gaa ggc acc cgc aat ctt   307
Asp Gly Thr Asn Pro Ala Asp Ser Phe Pro Glu Gly Thr Arg Asn Leu
    55                  60                  65

cta gtg ggt gtg tgg gca gta ctt gct gca tgg cgt ttc ggt ctt cct   355
Leu Val Gly Val Trp Ala Val Leu Ala Ala Trp Arg Phe Gly Leu Pro
70                  75                  80                  85

tta ata agg caa cgt cga ctc cgc gtg atc ttg agc gac cgc aaa ctg   403
Leu Ile Arg Gln Arg Arg Leu Arg Val Ile Leu Ser Asp Arg Lys Leu
                90                  95                  100

ctg gtc cga cgc gcg ggt ctg cgc acc ggg ttc gat tcc att cca ctg   451
Leu Val Arg Arg Ala Gly Leu Arg Thr Gly Phe Asp Ser Ile Pro Leu
            105                 110                 115

agc tac att cag cga gtc caa cgt cgg cga aac acc ctg gtc tta ggt   499
Ser Tyr Ile Gln Arg Val Gln Arg Arg Arg Asn Thr Leu Val Leu Gly
        120                 125                 130

gtt ggt gga cac                                                  511
Val Gly Gly His
    135


<210> 1112
<211> 137
<212> PRT
<213> Corynebacterium glutamicum

<400> 1112
Met Gly Asn Ser Leu Glu Lys His Ile Ala Glu Gly Asp Arg Ile His
  1               5                  10                  15

Val Asp Leu Thr Ser Pro Leu Ser Ala Met Leu Phe Pro Ile Phe Glu
            20                  25                  30

Leu Ile Val Ile Thr Gly Ile Cys Trp Met Gly Ile Gly Phe Leu Asp
        35                  40                  45

Gln Leu Pro Gly Ile Asp Gly Thr Asn Pro Ala Asp Ser Phe Pro Glu
    50                  55                  60

Gly Thr Arg Asn Leu Leu Val Gly Val Trp Ala Val Leu Ala Ala Trp
65                  70                  75                  80

Arg Phe Gly Leu Pro Leu Ile Arg Gln Arg Arg Leu Arg Val Ile Leu
                85                  90                  95

Ser Asp Arg Lys Leu Leu Val Arg Arg Ala Gly Leu Arg Thr Gly Phe
```

```
            100                 105                 110

Asp Ser Ile Pro Leu Ser Tyr Ile Gln Arg Val Gln Arg Arg Arg Asn
        115                 120                 125

Thr Leu Val Leu Gly Val Gly Gly His
    130                 135


<210> 1113
<211> 2556
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2533)
<223> RXN02360

<400> 1113
aagtaactaa agttcgaaag tatttccgaa cggtgtcggc ctctgcgcat acactgtatt 60

tttaaagaaa attcttctca attctaaggg tgaatatcca atg cgt ggt gac gtt   115
                                            Met Arg Gly Asp Val
                                              1               5

caa aaa ata acc aag gtt tat gac ggc aag cac cga acc ttg gaa atc   163
Gln Lys Ile Thr Lys Val Tyr Asp Gly Lys His Arg Thr Leu Glu Ile
                10                  15                  20

ccg gtt tat caa cgc aat tac gac tgg act gaa aag caa tgt tca cgc   211
Pro Val Tyr Gln Arg Asn Tyr Asp Trp Thr Glu Lys Gln Cys Ser Arg
            25                  30                  35

ctc ttt gat gac ctc agc gaa gtg gtc aaa gaa aac cac cgt caa cat   259
Leu Phe Asp Asp Leu Ser Glu Val Val Lys Glu Asn His Arg Gln His
        40                  45                  50

ttt ttt gga gct gtg gtt ggt aag cct caa ggc agc tgg acc tgg gtt   307
Phe Phe Gly Ala Val Val Gly Lys Pro Gln Gly Ser Trp Thr Trp Val
    55                  60                  65

gtc atc gat gga cag cag cgt ctt aca aca atc agc ttg ttc atg ctt   355
Val Ile Asp Gly Gln Gln Arg Leu Thr Thr Ile Ser Leu Phe Met Leu
70                  75                  80                  85

gcg ctg gta cat tcc ttg cgc gca tct gaa gtt gaa gaa ggt gag ttt   403
Ala Leu Val His Ser Leu Arg Ala Ser Glu Val Glu Glu Gly Glu Phe
                90                  95                  100

aat gct ggc tac aac att gat cta gcc aca ttg att gag gat gac tac   451
Asn Ala Gly Tyr Asn Ile Asp Leu Ala Thr Leu Ile Glu Asp Asp Tyr
            105                 110                 115

ctc cga tcc ggc aat gag gga aac ctc aag ttc aag ctc aag cca gtt   499
Leu Arg Ser Gly Asn Glu Gly Asn Leu Lys Phe Lys Leu Lys Pro Val
        120                 125                 130

aaa aac gat aat gag gct tat caa aag ctc ttc ggc cca gaa tct gaa   547
Lys Asn Asp Asn Glu Ala Tyr Gln Lys Leu Phe Gly Pro Glu Ser Glu
    135                 140                 145
```

```
ttc ata gag tcc tca aac ctc act gct aat tat cgc tac ttc cgc aat   595
Phe Ile Glu Ser Ser Asn Leu Thr Ala Asn Tyr Arg Tyr Phe Arg Asn
150                 155                 160                 165

gtc ctt aag gca acc gat ctc acc gca gct caa cta tgg gaa gct atc   643
Val Leu Lys Ala Thr Asp Leu Thr Ala Ala Gln Leu Trp Glu Ala Ile
                170                 175                 180

gag aaa ctc agg gtc atg tat ctt gac ctt gag gaa ttt gat gat ccg   691
Glu Lys Leu Arg Val Met Tyr Leu Asp Leu Glu Glu Phe Asp Asp Pro
            185                 190                 195

cag cga atc ttt gaa agt ctc aac tcc acg gga tta gag ctc agt gaa   739
Gln Arg Ile Phe Glu Ser Leu Asn Ser Thr Gly Leu Glu Leu Ser Glu
        200                 205                 210

gct gat aag gta cgc aac ttg gtt ctt atg gat cag gag ctc aaa acc   787
Ala Asp Lys Val Arg Asn Leu Val Leu Met Asp Gln Glu Leu Lys Thr
    215                 220                 225

caa gaa aag ctc tat gag cag cgt tgg aat ccc att gaa gtc tgc gtg   835
Gln Glu Lys Leu Tyr Glu Gln Arg Trp Asn Pro Ile Glu Val Cys Val
230                 235                 240                 245

aaa ttt gat acc gac aat ttc att cgc tgg tac tta act ctc aaa acc   883
Lys Phe Asp Thr Asp Asn Phe Ile Arg Trp Tyr Leu Thr Leu Lys Thr
                250                 255                 260

gcg cgc acc cca aga aag caa gat gtt tat gag gaa ttc aag aaa ttc   931
Ala Arg Thr Pro Arg Lys Gln Asp Val Tyr Glu Glu Phe Lys Lys Phe
            265                 270                 275

atc cgt aac tcc aag ctc ccg gtc gaa ttc atc ctc gac gat atg tac   979
Ile Arg Asn Ser Lys Leu Pro Val Glu Phe Ile Leu Asp Asp Met Tyr
        280                 285                 290

gag tac gcg aag ctg tac cga gat ctc tta ggt gcc act act ggg ttt   1027
Glu Tyr Ala Lys Leu Tyr Arg Asp Leu Leu Gly Ala Thr Thr Gly Phe
    295                 300                 305

ata gct gcc gat agg tgt ctt aag cgt ttt gtc cct gtc atg ggc gat   1075
Ile Ala Ala Asp Arg Cys Leu Lys Arg Phe Val Pro Val Met Gly Asp
310                 315                 320                 325

gtg gtt ttg cct ttt ctg ctg cct gtt ctc aaa gat gct aaa gac ggc   1123
Val Val Leu Pro Phe Leu Leu Pro Val Leu Lys Asp Ala Lys Asp Gly
                330                 335                 340

atc atc acc gaa tca gac ttc ctc gga gtt cta aaa gtt ctg gaa tcc   1171
Ile Ile Thr Glu Ser Asp Phe Leu Gly Val Leu Lys Val Leu Glu Ser
            345                 350                 355

tat tta ttc cgc cgt ttt gca gtc ggg gtt gct agt aac gcc tta agc   1219
Tyr Leu Phe Arg Arg Phe Ala Val Gly Val Ala Ser Asn Ala Leu Ser
        360                 365                 370

aag atc ttc tcc act gct tat agc gac atc aag aaa ttc tgg act cca   1267
Lys Ile Phe Ser Thr Ala Tyr Ser Asp Ile Lys Lys Phe Trp Thr Pro
    375                 380                 385
```

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ggg caa agt tat agc tca ctg ctg gcc tac att ctg aaa cgt cgc gat   1315
Gly Gln Ser Tyr Ser Ser Leu Leu Ala Tyr Ile Leu Lys Arg Arg Asp
390                 395                 400                 405

ggt tcc ggg cgt ttt ccc tcc gac agt gaa ttc cgt gag aac ttc gca   1363
Gly Ser Gly Arg Phe Pro Ser Asp Ser Glu Phe Arg Glu Asn Phe Ala
                410                 415                 420

acc aaa aat ttc tgg aat att cat aac gaa aac agg cgt tac tta ttt   1411
Thr Lys Asn Phe Trp Asn Ile His Asn Glu Asn Arg Arg Tyr Leu Phe
            425                 430                 435

gat tgt cta gaa aat gcc gat tcc aat gat gtt cgt gac atc caa aca   1459
Asp Cys Leu Glu Asn Ala Asp Ser Asn Asp Val Arg Asp Ile Gln Thr
        440                 445                 450

agt ctg gat gaa gga tct ctc tcc att gaa cac atc atg cca cgt agc   1507
Ser Leu Asp Glu Gly Ser Leu Ser Ile Glu His Ile Met Pro Arg Ser
    455                 460                 465

cta aac gat cag tgg aga gct gaa ctc ggc cct gaa tat gct cga att   1555
Leu Asn Asp Gln Trp Arg Ala Glu Leu Gly Pro Glu Tyr Ala Arg Ile
470                 475                 480                 485

cat gag act tgg att aat aga att ggt aac ctc acc atc acc ggc tac   1603
His Glu Thr Trp Ile Asn Arg Ile Gly Asn Leu Thr Ile Thr Gly Tyr
                490                 495                 500

aac tcc gcc tat tca aat tct tcc tat gag cgc aag cgg acg atg gaa   1651
Asn Ser Ala Tyr Ser Asn Ser Ser Tyr Glu Arg Lys Arg Thr Met Glu
            505                 510                 515

aat gga ttt ttg gta tcc ccc tat cgc atc aat aat ttc atc aaa aag   1699
Asn Gly Phe Leu Val Ser Pro Tyr Arg Ile Asn Asn Phe Ile Lys Lys
        520                 525                 530

cag aag cat tgg tct gaa gaa cag cta att gag cga acc gag ctg ctc   1747
Gln Lys His Trp Ser Glu Glu Gln Leu Ile Glu Arg Thr Glu Leu Leu
    535                 540                 545

act caa gca gcg ctg gac tac tgg ccc ctt cca aaa gaa acc ttc cag   1795
Thr Gln Ala Ala Leu Asp Tyr Trp Pro Leu Pro Lys Glu Thr Phe Gln
550                 555                 560                 565

cca cca caa gct gtg ctt cct aca gaa tcc tta gat agt gat ctt tct   1843
Pro Pro Gln Ala Val Leu Pro Thr Glu Ser Leu Asp Ser Asp Leu Ser
                570                 575                 580

ttc cgc gga cgc gaa att gtc gcc ttt gaa tat gag gac tac aag gaa   1891
Phe Arg Gly Arg Glu Ile Val Ala Phe Glu Tyr Glu Asp Tyr Lys Glu
            585                 590                 595

acg gta acg tcc tgg gca gac atg ctc cag agc gtt cta aaa gtc ttg   1939
Thr Val Thr Ser Trp Ala Asp Met Leu Gln Ser Val Leu Lys Val Leu
        600                 605                 610

aac caa tcc ttc cgc cag gaa ctc ata gct ttg acc aat gaa gaa atc   1987
Asn Gln Ser Phe Arg Gln Glu Leu Ile Ala Leu Thr Asn Glu Glu Ile
    615                 620                 625

tgc ctg gca act tca aac aac agt aac agc agt ctc cgt gaa att gac   2035
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Cys Leu Ala Thr Ser Asn Asn Ser Asn Ser Ser Leu Arg Glu Ile Asp
630                 635                 640                 645

cac ggg ctt ttt gta gac act ggc tct agt acg agt gta aag att ggc   2083
His Gly Leu Phe Val Asp Thr Gly Ser Ser Thr Ser Val Lys Ile Gly
                650                 655                 660

ttc ctc cgc aga gtt ttt act caa ctg ggg cta gag cag gaa gca ttg   2131
Phe Leu Arg Arg Val Phe Thr Gln Leu Gly Leu Glu Gln Glu Ala Leu
            665                 670                 675

gtt ttc acc ctt cga cca ctg gca aat gat gta gaa ccc cga gat gat   2179
Val Phe Thr Leu Arg Pro Leu Ala Asn Asp Val Glu Pro Arg Asp Asp
        680                 685                 690

gaa ctc gag gta gag gta gaa aag aaa tat tcc gat ttg act aaa ttc   2227
Glu Leu Glu Val Glu Val Glu Lys Lys Tyr Ser Asp Leu Thr Lys Phe
    695                 700                 705

atc cca cag tta gaa gaa gct gag aat ctc gag ggg gcg gat aca gag   2275
Ile Pro Gln Leu Glu Glu Ala Glu Asn Leu Glu Gly Ala Asp Thr Glu
710                 715                 720                 725

gtt att cct ctc ctc tca aag ctc aag gaa caa ctg aca gcc ttt agc   2323
Val Ile Pro Leu Leu Ser Lys Leu Lys Glu Gln Leu Thr Ala Phe Ser
                730                 735                 740

ccg gag aat cct caa gca gcc cta ggg ggc cta cct gtt cca gaa ttc   2371
Pro Glu Asn Pro Gln Ala Ala Leu Gly Gly Leu Pro Val Pro Glu Phe
            745                 750                 755

ctc aaa caa aat gtg att gaa caa cta agc gca gag cac atc ctt gct   2419
Leu Lys Gln Asn Val Ile Glu Gln Leu Ser Ala Glu His Ile Leu Ala
        760                 765                 770

gta ctc act caa cac ttt aat atc gca tcc atg atg ggt gat gac tat   2467
Val Leu Thr Gln His Phe Asn Ile Ala Ser Met Met Gly Asp Asp Tyr
    775                 780                 785

ttg ctc gaa gag ctc agg tca ggc cgc tta agg gaa tta ctg cag cgt   2515
Leu Leu Glu Glu Leu Arg Ser Gly Arg Leu Arg Glu Leu Leu Gln Arg
790                 795                 800                 805

tta gag gaa ttg gat agc taatagccgt agtcggtggt caa                 2556
Leu Glu Glu Leu Asp Ser
                810
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<210> 1114
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<212> PRT
<213> Corynebacterium glutamicum

<400> 1114

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Arg Thr Leu Glu Ile Pro Val Tyr Gln Arg Asn Tyr Asp Trp Thr Glu
             20                  25                  30

Lys Gln Cys Ser Arg Leu Phe Asp Asp Leu Ser Glu Val Val Lys Glu
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         35                  40                  45

Asn His Arg Gln His Phe Phe Gly Ala Val Val Gly Lys Pro Gln Gly
     50                  55                  60

Ser Trp Thr Trp Val Val Ile Asp Gly Gln Gln Arg Leu Thr Thr Ile
 65                  70                  75                  80

Ser Leu Phe Met Leu Ala Leu Val His Ser Leu Arg Ala Ser Glu Val
                85                  90                  95

Glu Glu Gly Glu Phe Asn Ala Gly Tyr Asn Ile Asp Leu Ala Thr Leu
            100                 105                 110

Ile Glu Asp Asp Tyr Leu Arg Ser Gly Asn Glu Gly Asn Leu Lys Phe
        115                 120                 125

Lys Leu Lys Pro Val Lys Asn Asp Asn Glu Ala Tyr Gln Lys Leu Phe
    130                 135                 140

Gly Pro Glu Ser Glu Phe Ile Glu Ser Ser Asn Leu Thr Ala Asn Tyr
145                 150                 155                 160

Arg Tyr Phe Arg Asn Val Leu Lys Ala Thr Asp Leu Thr Ala Ala Gln
                165                 170                 175

Leu Trp Glu Ala Ile Glu Lys Leu Arg Val Met Tyr Leu Asp Leu Glu
            180                 185                 190

Glu Phe Asp Asp Pro Gln Arg Ile Phe Glu Ser Leu Asn Ser Thr Gly
        195                 200                 205

Leu Glu Leu Ser Glu Ala Asp Lys Val Arg Asn Leu Val Leu Met Asp
    210                 215                 220

Gln Glu Leu Lys Thr Gln Glu Lys Leu Tyr Glu Gln Arg Trp Asn Pro
225                 230                 235                 240

Ile Glu Val Cys Val Lys Phe Asp Thr Asp Asn Phe Ile Arg Trp Tyr
                245                 250                 255

Leu Thr Leu Lys Thr Ala Arg Thr Pro Arg Lys Gln Asp Val Tyr Glu
            260                 265                 270

Glu Phe Lys Lys Phe Ile Arg Asn Ser Lys Leu Pro Val Glu Phe Ile
        275                 280                 285

Leu Asp Asp Met Tyr Glu Tyr Ala Lys Leu Tyr Arg Asp Leu Leu Gly
    290                 295                 300

Ala Thr Thr Gly Phe Ile Ala Ala Asp Arg Cys Leu Lys Arg Phe Val
305                 310                 315                 320

Pro Val Met Gly Asp Val Val Leu Pro Phe Leu Leu Pro Val Leu Lys
                325                 330                 335

Asp Ala Lys Asp Gly Ile Ile Thr Glu Ser Asp Phe Leu Gly Val Leu
            340                 345                 350

Lys Val Leu Glu Ser Tyr Leu Phe Arg Arg Phe Ala Val Gly Val Ala
        355                 360                 365
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Ser Asn Ala Leu Ser Lys Ile Phe Ser Thr Ala Tyr Ser Asp Ile Lys
    370                 375                 380

Lys Phe Trp Thr Pro Gly Gln Ser Tyr Ser Ser Leu Leu Ala Tyr Ile
385                 390                 395                 400

Leu Lys Arg Arg Asp Gly Ser Gly Arg Phe Pro Ser Asp Ser Glu Phe
                405                 410                 415

Arg Glu Asn Phe Ala Thr Lys Asn Phe Trp Asn Ile His Asn Glu Asn
            420                 425                 430

Arg Arg Tyr Leu Phe Asp Cys Leu Glu Asn Ala Asp Ser Asn Asp Val
        435                 440                 445

Arg Asp Ile Gln Thr Ser Leu Asp Glu Gly Ser Leu Ser Ile Glu His
    450                 455                 460

Ile Met Pro Arg Ser Leu Asn Asp Gln Trp Arg Ala Glu Leu Gly Pro
465                 470                 475                 480

Glu Tyr Ala Arg Ile His Glu Thr Trp Ile Asn Arg Ile Gly Asn Leu
                485                 490                 495

Thr Ile Thr Gly Tyr Asn Ser Ala Tyr Ser Asn Ser Ser Tyr Glu Arg
            500                 505                 510

Lys Arg Thr Met Glu Asn Gly Phe Leu Val Ser Pro Tyr Arg Ile Asn
        515                 520                 525

Asn Phe Ile Lys Lys Gln Lys His Trp Ser Glu Glu Gln Leu Ile Glu
    530                 535                 540

Arg Thr Glu Leu Leu Thr Gln Ala Ala Leu Asp Tyr Trp Pro Leu Pro
545                 550                 555                 560

Lys Glu Thr Phe Gln Pro Pro Gln Ala Val Leu Pro Thr Glu Ser Leu
                565                 570                 575

Asp Ser Asp Leu Ser Phe Arg Gly Arg Glu Ile Val Ala Phe Glu Tyr
            580                 585                 590

Glu Asp Tyr Lys Glu Thr Val Thr Ser Trp Ala Asp Met Leu Gln Ser
        595                 600                 605

Val Leu Lys Val Leu Asn Gln Ser Phe Arg Gln Glu Leu Ile Ala Leu
    610                 615                 620

Thr Asn Glu Glu Ile Cys Leu Ala Thr Ser Asn Asn Ser Asn Ser Ser
625                 630                 635                 640

Leu Arg Glu Ile Asp His Gly Leu Phe Val Asp Thr Gly Ser Ser Thr
                645                 650                 655

Ser Val Lys Ile Gly Phe Leu Arg Arg Val Phe Thr Gln Leu Gly Leu
            660                 665                 670

Glu Gln Glu Ala Leu Val Phe Thr Leu Arg Pro Leu Ala Asn Asp Val
        675                 680                 685
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Glu Pro Arg Asp Asp Glu Leu Glu Val Glu Val Glu Lys Lys Tyr Ser
    690                 695                 700

Asp Leu Thr Lys Phe Ile Pro Gln Leu Glu Glu Ala Glu Asn Leu Glu
705                 710                 715                 720

Gly Ala Asp Thr Glu Val Ile Pro Leu Leu Ser Lys Leu Lys Glu Gln
                725                 730                 735

Leu Thr Ala Phe Ser Pro Glu Asn Pro Gln Ala Ala Leu Gly Gly Leu
            740                 745                 750

Pro Val Pro Glu Phe Leu Lys Gln Asn Val Ile Glu Gln Leu Ser Ala
        755                 760                 765

Glu His Ile Leu Ala Val Leu Thr Gln His Phe Asn Ile Ala Ser Met
    770                 775                 780

Met Gly Asp Asp Tyr Leu Leu Glu Glu Leu Arg Ser Gly Arg Leu Arg
785                 790                 795                 800

Glu Leu Leu Gln Arg Leu Glu Glu Leu Asp Ser
                805                 810
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Do not enter any text in this area

<210> 1115
<211> 2556
<212> DNA
<213> Corynebacterium glutamicum

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<221> CDS
<222> (101)..(2533)
<223> FRXA02360

<400> 1115

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tttaaagaaa attcttctca attctaaggg tgaatatcca atg cgt ggt gac gtt   115
                                            Met Arg Gly Asp Val
                                              1               5

caa aaa ata acc aag gtt tat gac ggc aag cac cga acc ttg gaa atc   163
Gln Lys Ile Thr Lys Val Tyr Asp Gly Lys His Arg Thr Leu Glu Ile
                 10                  15                  20

ccg gtt tat caa cgc aat tac gac tgg act gaa aag caa tgt tca cgc   211
Pro Val Tyr Gln Arg Asn Tyr Asp Trp Thr Glu Lys Gln Cys Ser Arg
             25                  30                  35

ctc ttt gat gac ctc agc gaa gtg gtc aaa gaa aac cac cgt caa cat   259
Leu Phe Asp Asp Leu Ser Glu Val Val Lys Glu Asn His Arg Gln His
         40                  45                  50

ttt ttt gga gct gtg gtt ggt aag cct caa ggc agc tgg acc tgg gtt   307
Phe Phe Gly Ala Val Val Gly Lys Pro Gln Gly Ser Trp Thr Trp Val
     55                  60                  65

gtc atc gat gga cag cag cgt ctt aca aca atc agc ttg ttc atg ctt   355
Val Ile Asp Gly Gln Gln Arg Leu Thr Thr Ile Ser Leu Phe Met Leu
 70                  75                  80                  85
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gcg ctg gta cat tcc ttg cgc gca tct gaa gtt gaa gaa ggt gag ttt   403
Ala Leu Val His Ser Leu Arg Ala Ser Glu Val Glu Glu Gly Glu Phe
                 90                  95                 100

aat gct ggc tac aac att gat cta gcc aca ttg att gag gat gac tac   451
Asn Ala Gly Tyr Asn Ile Asp Leu Ala Thr Leu Ile Glu Asp Asp Tyr
            105                 110                 115

ctc cga tcc ggc aat gag gga aac ctc aag ttc aag ctc aag cca gtt   499
Leu Arg Ser Gly Asn Glu Gly Asn Leu Lys Phe Lys Leu Lys Pro Val
        120                 125                 130

aaa aac gat aat gag gct tat caa aag ctc ttc ggc cca gaa tct gaa   547
Lys Asn Asp Asn Glu Ala Tyr Gln Lys Leu Phe Gly Pro Glu Ser Glu
    135                 140                 145

ttc ata gag tcc tca aac ctc act gct aat tat cgc tac ttc cgc aat   595
Phe Ile Glu Ser Ser Asn Leu Thr Ala Asn Tyr Arg Tyr Phe Arg Asn
150                 155                 160                 165

gtc ctt aag gca acc gat ctc acc gca gct caa cta tgg gaa gct atc   643
Val Leu Lys Ala Thr Asp Leu Thr Ala Ala Gln Leu Trp Glu Ala Ile
                170                 175                 180

gag aaa ctc agg gtc atg tat ctt gac ctt gag gaa ttt gat gat ccg   691
Glu Lys Leu Arg Val Met Tyr Leu Asp Leu Glu Glu Phe Asp Asp Pro
            185                 190                 195

cag cga atc ttt gaa agt ctc aac tcc acg gga tta gag ctc agt gaa   739
Gln Arg Ile Phe Glu Ser Leu Asn Ser Thr Gly Leu Glu Leu Ser Glu
        200                 205                 210

gct gat aag gta cgc aac ttg gtt ctt atg gat cag gag ctc aaa acc   787
Ala Asp Lys Val Arg Asn Leu Val Leu Met Asp Gln Glu Leu Lys Thr
    215                 220                 225

caa gaa aag ctc tat gag cag cgt tgg aat ccc att gaa gtc tgc gtg   835
Gln Glu Lys Leu Tyr Glu Gln Arg Trp Asn Pro Ile Glu Val Cys Val
230                 235                 240                 245

aaa ttt gat acc gac aat ttc att cgc tgg tac tta act ctc aaa acc   883
Lys Phe Asp Thr Asp Asn Phe Ile Arg Trp Tyr Leu Thr Leu Lys Thr
                250                 255                 260

gcg cgc acc cca aga aag caa gat gtt tat gag gaa ttc aag aaa ttc   931
Ala Arg Thr Pro Arg Lys Gln Asp Val Tyr Glu Glu Phe Lys Lys Phe
            265                 270                 275

atc cgt aac tcc aag ctc ccg gtc gaa ttc atc ctc gac gat atg tac   979
Ile Arg Asn Ser Lys Leu Pro Val Glu Phe Ile Leu Asp Asp Met Tyr
        280                 285                 290

gag tac gcg aag ctg tac cga gat ctc tta ggt gcc act act ggg ttt   1027
Glu Tyr Ala Lys Leu Tyr Arg Asp Leu Leu Gly Ala Thr Thr Gly Phe
    295                 300                 305

ata gct gcc gat agg tgt ctt aag cgt ttt gtc cct gtc atg ggc gat   1075
Ile Ala Ala Asp Arg Cys Leu Lys Arg Phe Val Pro Val Met Gly Asp
310                 315                 320                 325
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gtg gtt ttg cct ttt ctg ctg cct gtt ctc aaa gat gct aaa gac ggc   1123
Val Val Leu Pro Phe Leu Leu Pro Val Leu Lys Asp Ala Lys Asp Gly
                330                 335                 340

atc atc acc gaa tca gac ttc ctc gga gtt cta aaa gtt ctg gaa tcc   1171
Ile Ile Thr Glu Ser Asp Phe Leu Gly Val Leu Lys Val Leu Glu Ser
            345                 350                 355

tat tta ttc cgc cgt ttt gca gtc ggg gtt gct agt aac gcc tta agc   1219
Tyr Leu Phe Arg Arg Phe Ala Val Gly Val Ala Ser Asn Ala Leu Ser
        360                 365                 370

aag atc ttc tcc act gct tat agc gac atc aag aaa ttc tgg act cca   1267
Lys Ile Phe Ser Thr Ala Tyr Ser Asp Ile Lys Lys Phe Trp Thr Pro
    375                 380                 385

ggg caa agt tat agc tca ctg ctg gcc tac att ctg aaa cgt cgc gat   1315
Gly Gln Ser Tyr Ser Ser Leu Leu Ala Tyr Ile Leu Lys Arg Arg Asp
390                 395                 400                 405

ggt tcc ggg cgt ttt ccc tcc gac agt gaa ttc cgt gag aac ttc gca   1363
Gly Ser Gly Arg Phe Pro Ser Asp Ser Glu Phe Arg Glu Asn Phe Ala
                410                 415                 420

acc aaa aat ttc tgg aat att cat aac gaa aac agg cgt tac tta ttt   1411
Thr Lys Asn Phe Trp Asn Ile His Asn Glu Asn Arg Arg Tyr Leu Phe
            425                 430                 435

gat tgt cta gaa aat gcc gat tcc aat gat gtt cgt gac atc caa aca   1459
Asp Cys Leu Glu Asn Ala Asp Ser Asn Asp Val Arg Asp Ile Gln Thr
        440                 445                 450

agt ctg gat gaa gga tct ctc tcc att gaa cac atc atg cca cgt agc   1507
Ser Leu Asp Glu Gly Ser Leu Ser Ile Glu His Ile Met Pro Arg Ser
    455                 460                 465

cta aac gat cag tgg aga gct gaa ctc ggc cct gaa tat gct cga att   1555
Leu Asn Asp Gln Trp Arg Ala Glu Leu Gly Pro Glu Tyr Ala Arg Ile
470                 475                 480                 485

cat gag act tgg att aat aga att ggt aac ctc acc atc acc ggc tac   1603
His Glu Thr Trp Ile Asn Arg Ile Gly Asn Leu Thr Ile Thr Gly Tyr
                490                 495                 500

aac tcc gcc tat tca aat tct tcc tat gag cgc aag cgg acg atg gaa   1651
Asn Ser Ala Tyr Ser Asn Ser Ser Tyr Glu Arg Lys Arg Thr Met Glu
            505                 510                 515

aat gga ttt ttg gta tcc ccc tat cgc atc aat aat ttc atc aaa aag   1699
Asn Gly Phe Leu Val Ser Pro Tyr Arg Ile Asn Asn Phe Ile Lys Lys
        520                 525                 530

cag aag cat tgg tct gaa gaa cag cta att gag cga acc gag ctg ctc   1747
Gln Lys His Trp Ser Glu Glu Gln Leu Ile Glu Arg Thr Glu Leu Leu
    535                 540                 545

act caa gca gcg ctg gac tac tgg ccc ctt cca aaa gaa acc ttc cag   1795
Thr Gln Ala Ala Leu Asp Tyr Trp Pro Leu Pro Lys Glu Thr Phe Gln
550                 555                 560                 565

cca cca caa gct gtg ctt cct aca gaa tcc tta gat agt gat ctt tct   1843
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Pro Pro Gln Ala Val Leu Pro Thr Glu Ser Leu Asp Ser Asp Leu Ser
                570                 575                 580

ttc cgc gga cgc gaa att gtc gcc ttt gaa tat gag gac tac aag gaa   1891
Phe Arg Gly Arg Glu Ile Val Ala Phe Glu Tyr Glu Asp Tyr Lys Glu
            585                 590                 595

acg gta acg tcc tgg gca gac atg ctc cag agc gtt cta aaa gtc ttg   1939
Thr Val Thr Ser Trp Ala Asp Met Leu Gln Ser Val Leu Lys Val Leu
        600                 605                 610

aac caa tcc ttc cgc cag gaa ctc ata gct ttg acc aat gaa gaa atc   1987
Asn Gln Ser Phe Arg Gln Glu Leu Ile Ala Leu Thr Asn Glu Glu Ile
    615                 620                 625

tgc ctg gca act tca aac aac agt aac agc agt ctc cgt gaa att gac   2035
Cys Leu Ala Thr Ser Asn Asn Ser Asn Ser Ser Leu Arg Glu Ile Asp
630                 635                 640                 645

cac ggg ctt ttt gta gac act ggc tct agt acg agt gta aag att ggc   2083
His Gly Leu Phe Val Asp Thr Gly Ser Ser Thr Ser Val Lys Ile Gly
                650                 655                 660

ttc ctc cgc aga gtt ttt act caa ctg ggg cta gag cag gaa gca ttg   2131
Phe Leu Arg Arg Val Phe Thr Gln Leu Gly Leu Glu Gln Glu Ala Leu
            665                 670                 675

gtt ttc acc ctt cga cca ctg gca aat gat gta gaa ccc cga gat gat   2179
Val Phe Thr Leu Arg Pro Leu Ala Asn Asp Val Glu Pro Arg Asp Asp
        680                 685                 690

gaa ctc gag gta gag gta gaa aag aaa tat tcc gat ttg act aaa ttc   2227
Glu Leu Glu Val Glu Val Glu Lys Lys Tyr Ser Asp Leu Thr Lys Phe
    695                 700                 705

atc cca cag tta gaa gaa gct gag aat ctc gag ggg gcg gat aca gag   2275
Ile Pro Gln Leu Glu Glu Ala Glu Asn Leu Glu Gly Ala Asp Thr Glu
710                 715                 720                 725

gtt att cct ctc ctc tca aag ctc aag gaa caa ctg aca gcc ttt agc   2323
Val Ile Pro Leu Leu Ser Lys Leu Lys Glu Gln Leu Thr Ala Phe Ser
                730                 735                 740

ccg gag aat cct caa gca gcc cta ggg ggc cta cct gtt cca gaa ttc   2371
Pro Glu Asn Pro Gln Ala Ala Leu Gly Gly Leu Pro Val Pro Glu Phe
            745                 750                 755

ctc aaa caa aat gtg att gaa caa cta agc gca gag cac atc ctt gct   2419
Leu Lys Gln Asn Val Ile Glu Gln Leu Ser Ala Glu His Ile Leu Ala
        760                 765                 770

gta ctc act caa cac ttt aat atc gca tcc atg atg ggt gat gac tat   2467
Val Leu Thr Gln His Phe Asn Ile Ala Ser Met Met Gly Asp Asp Tyr
    775                 780                 785

ttg ctc gaa gag ctc agg tca ggc cgc tta agg gaa tta ctg cag cgt   2515
Leu Leu Glu Glu Leu Arg Ser Gly Arg Leu Arg Glu Leu Leu Gln Arg
790                 795                 800                 805

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Leu Glu Glu Leu Asp Ser
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810

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Arg Thr Leu Glu Ile Pro Val Tyr Gln Arg Asn Tyr Asp Trp Thr Glu
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Lys Gln Cys Ser Arg Leu Phe Asp Asp Leu Ser Glu Val Val Lys Glu
         35                  40                  45

Asn His Arg Gln His Phe Phe Gly Ala Val Val Gly Lys Pro Gln Gly
     50                  55                  60

Ser Trp Thr Trp Val Val Ile Asp Gly Gln Gln Arg Leu Thr Thr Ile
 65                  70                  75                  80

Ser Leu Phe Met Leu Ala Leu Val His Ser Leu Arg Ala Ser Glu Val
                 85                  90                  95

Glu Glu Gly Glu Phe Asn Ala Gly Tyr Asn Ile Asp Leu Ala Thr Leu
            100                 105                 110

Ile Glu Asp Asp Tyr Leu Arg Ser Gly Asn Glu Gly Asn Leu Lys Phe
        115                 120                 125

Lys Leu Lys Pro Val Lys Asn Asp Asn Glu Ala Tyr Gln Lys Leu Phe
    130                 135                 140

Gly Pro Glu Ser Glu Phe Ile Glu Ser Ser Asn Leu Thr Ala Asn Tyr
145                 150                 155                 160

Arg Tyr Phe Arg Asn Val Leu Lys Ala Thr Asp Leu Thr Ala Ala Gln
                165                 170                 175

Leu Trp Glu Ala Ile Glu Lys Leu Arg Val Met Tyr Leu Asp Leu Glu
            180                 185                 190

Glu Phe Asp Asp Pro Gln Arg Ile Phe Glu Ser Leu Asn Ser Thr Gly
        195                 200                 205

Leu Glu Leu Ser Glu Ala Asp Lys Val Arg Asn Leu Val Leu Met Asp
    210                 215                 220

Gln Glu Leu Lys Thr Gln Glu Lys Leu Tyr Glu Gln Arg Trp Asn Pro
225                 230                 235                 240

Ile Glu Val Cys Val Lys Phe Asp Thr Asp Asn Phe Ile Arg Trp Tyr
                245                 250                 255

Leu Thr Leu Lys Thr Ala Arg Thr Pro Arg Lys Gln Asp Val Tyr Glu
            260                 265                 270

Glu Phe Lys Lys Phe Ile Arg Asn Ser Lys Leu Pro Val Glu Phe Ile
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        275                 280                 285

Leu Asp Asp Met Tyr Glu Tyr Ala Lys Leu Tyr Arg Asp Leu Leu Gly
    290                 295                 300

Ala Thr Thr Gly Phe Ile Ala Ala Asp Arg Cys Leu Lys Arg Phe Val
305                 310                 315                 320

Pro Val Met Gly Asp Val Val Leu Pro Phe Leu Leu Pro Val Leu Lys
                325                 330                 335

Asp Ala Lys Asp Gly Ile Ile Thr Glu Ser Asp Phe Leu Gly Val Leu
            340                 345                 350

Lys Val Leu Glu Ser Tyr Leu Phe Arg Arg Phe Ala Val Gly Val Ala
        355                 360                 365

Ser Asn Ala Leu Ser Lys Ile Phe Ser Thr Ala Tyr Ser Asp Ile Lys
    370                 375                 380

Lys Phe Trp Thr Pro Gly Gln Ser Tyr Ser Ser Leu Leu Ala Tyr Ile
385                 390                 395                 400

Leu Lys Arg Arg Asp Gly Ser Gly Arg Phe Pro Ser Asp Ser Glu Phe
                405                 410                 415

Arg Glu Asn Phe Ala Thr Lys Asn Phe Trp Asn Ile His Asn Glu Asn
            420                 425                 430

Arg Arg Tyr Leu Phe Asp Cys Leu Glu Asn Ala Asp Ser Asn Asp Val
        435                 440                 445

Arg Asp Ile Gln Thr Ser Leu Asp Glu Gly Ser Leu Ser Ile Glu His
    450                 455                 460

Ile Met Pro Arg Ser Leu Asn Asp Gln Trp Arg Ala Glu Leu Gly Pro
465                 470                 475                 480

Glu Tyr Ala Arg Ile His Glu Thr Trp Ile Asn Arg Ile Gly Asn Leu
                485                 490                 495

Thr Ile Thr Gly Tyr Asn Ser Ala Tyr Ser Asn Ser Ser Tyr Glu Arg
            500                 505                 510

Lys Arg Thr Met Glu Asn Gly Phe Leu Val Ser Pro Tyr Arg Ile Asn
        515                 520                 525

Asn Phe Ile Lys Lys Gln Lys His Trp Ser Glu Glu Gln Leu Ile Glu
    530                 535                 540

Arg Thr Glu Leu Leu Thr Gln Ala Ala Leu Asp Tyr Trp Pro Leu Pro
545                 550                 555                 560

Lys Glu Thr Phe Gln Pro Pro Gln Ala Val Leu Pro Thr Glu Ser Leu
                565                 570                 575

Asp Ser Asp Leu Ser Phe Arg Gly Arg Glu Ile Val Ala Phe Glu Tyr
            580                 585                 590

Glu Asp Tyr Lys Glu Thr Val Thr Ser Trp Ala Asp Met Leu Gln Ser
        595                 600                 605
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Val Leu Lys Val Leu Asn Gln Ser Phe Arg Gln Glu Leu Ile Ala Leu
    610                 615                 620

Thr Asn Glu Glu Ile Cys Leu Ala Thr Ser Asn Asn Ser Asn Ser Ser
625                 630                 635                 640

Leu Arg Glu Ile Asp His Gly Leu Phe Val Asp Thr Gly Ser Ser Thr
                645                 650                 655

Ser Val Lys Ile Gly Phe Leu Arg Arg Val Phe Thr Gln Leu Gly Leu
            660                 665                 670

Glu Gln Glu Ala Leu Val Phe Thr Leu Arg Pro Leu Ala Asn Asp Val
        675                 680                 685

Glu Pro Arg Asp Asp Glu Leu Glu Val Glu Val Glu Lys Lys Tyr Ser
    690                 695                 700

Asp Leu Thr Lys Phe Ile Pro Gln Leu Glu Glu Ala Glu Asn Leu Glu
705                 710                 715                 720

Gly Ala Asp Thr Glu Val Ile Pro Leu Leu Ser Lys Leu Lys Glu Gln
                725                 730                 735

Leu Thr Ala Phe Ser Pro Glu Asn Pro Gln Ala Ala Leu Gly Gly Leu
            740                 745                 750

Pro Val Pro Glu Phe Leu Lys Gln Asn Val Ile Glu Gln Leu Ser Ala
        755                 760                 765

Glu His Ile Leu Ala Val Leu Thr Gln His Phe Asn Ile Ala Ser Met
    770                 775                 780

Met Gly Asp Asp Tyr Leu Leu Glu Glu Leu Arg Ser Gly Arg Leu Arg
785                 790                 795                 800

Glu Leu Leu Gln Arg Leu Glu Glu Leu Asp Ser
                805                 810
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Sequence Listing as filed with the application

<210> 1117
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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(751)
<223> RXN02361

<400> 1117

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tagaggaatt ggatagctaa tagccgtagt cggtggtcaa actttgacca ccggactccc 60

ctttaagcac aatctctagc ttttatttag gcttggagtt atg gaa ctt ctc tcc   115
                                              Met Glu Leu Leu Ser
                                                1               5

cac ttg ctt gct ctt gat cct gcc tcc cct cgt ttg act gtt tat aac   163
His Leu Leu Ala Leu Asp Pro Ala Ser Pro Arg Leu Thr Val Tyr Asn
                10                  15                  20
```

```
gag tcc acg ggt gcg cgt ttg gat ttc tcc gcc atc act ctt gat aac   211
Glu Ser Thr Gly Ala Arg Leu Asp Phe Ser Ala Ile Thr Leu Asp Asn
            25                  30                  35

tgg gcg tcc aag gtt ggc aat atg ctc ctt gag gaa ttg gat ctg gag   259
Trp Ala Ser Lys Val Gly Asn Met Leu Leu Glu Glu Leu Asp Leu Glu
         40                  45                  50

gaa ggc tcg ctc atc act att gat ttg ccg gtg agc tgg cag gcc gca   307
Glu Gly Ser Leu Ile Thr Ile Asp Leu Pro Val Ser Trp Gln Ala Ala
     55                  60                  65

atg att atg ctc ggc gct tta gca act agt gtt gag gtc tct ttt gat   355
Met Ile Met Leu Gly Ala Leu Ala Thr Ser Val Glu Val Ser Phe Asp
 70                  75                  80                  85

gat ccc gag gca gat gcc atc ttt acc tcc ctc gat aga ttt tcc cac   403
Asp Pro Glu Ala Asp Ala Ile Phe Thr Ser Leu Asp Arg Phe Ser His
                90                  95                 100

tac aag ggc cat agt gat gtg ctg att gtc agc gag gat cct ttt ggt   451
Tyr Lys Gly His Ser Asp Val Leu Ile Val Ser Glu Asp Pro Phe Gly
            105                 110                 115

cgt gga gtt gtt gaa ggt ggc ggt gaa ctg cct aat ggt gcc atc gat   499
Arg Gly Val Val Glu Gly Gly Gly Glu Leu Pro Asn Gly Ala Ile Asp
        120                 125                 130

ttt ggc ccc aca gtg cgt ttt tat ggc gat caa ttc ttc cag cct acc   547
Phe Gly Pro Thr Val Arg Phe Tyr Gly Asp Gln Phe Phe Gln Pro Thr
    135                 140                 145

cgc aca ttg ccg gaa atc atc cag cat tct gat gtt ccg gtt ggc gcc   595
Arg Thr Leu Pro Glu Ile Ile Gln His Ser Asp Val Pro Val Gly Ala
150                 155                 160                 165

aga gtt ctt gca act ggt tgg tca gat atc gag tcc ttc aat cac cag   643
Arg Val Leu Ala Thr Gly Trp Ser Asp Ile Glu Ser Phe Asn His Gln
                170                 175                 180

gtt tta gaa cca ctc gca gtg ggt ggc tct gca gta att gtg acc gga   691
Val Leu Glu Pro Leu Ala Val Gly Gly Ser Ala Val Ile Val Thr Gly
            185                 190                 195

ctg gct gat att gag cgt tta aac cag att gca acc aat gag aag aca   739
Leu Ala Asp Ile Glu Arg Leu Asn Gln Ile Ala Thr Asn Glu Lys Thr
        200                 205                 210

acc cac cgt atc taggcaaatt tcggttacta cta                        774
Thr His Arg Ile
    215
```

<210> 1118
<211> 217
<212> PRT
<213> Corynebacterium glutamicum

<400> 1118

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Met Glu Leu Leu Ser His Leu Leu Ala Leu Asp Pro Ala Ser Pro Arg
```

```
  1               5                  10                  15

Leu Thr Val Tyr Asn Glu Ser Thr Gly Ala Arg Leu Asp Phe Ser Ala
            20                  25                  30

Ile Thr Leu Asp Asn Trp Ala Ser Lys Val Gly Asn Met Leu Leu Glu
        35                  40                  45

Glu Leu Asp Leu Glu Glu Gly Ser Leu Ile Thr Ile Asp Leu Pro Val
    50                  55                  60

Ser Trp Gln Ala Ala Met Ile Met Leu Gly Ala Leu Ala Thr Ser Val
65                  70                  75                  80

Glu Val Ser Phe Asp Asp Pro Glu Ala Asp Ala Ile Phe Thr Ser Leu
                85                  90                  95

Asp Arg Phe Ser His Tyr Lys Gly His Ser Asp Val Leu Ile Val Ser
            100                 105                 110

Glu Asp Pro Phe Gly Arg Gly Val Val Glu Gly Gly Gly Glu Leu Pro
        115                 120                 125

Asn Gly Ala Ile Asp Phe Gly Pro Thr Val Arg Phe Tyr Gly Asp Gln
    130                 135                 140

Phe Phe Gln Pro Thr Arg Thr Leu Pro Glu Ile Ile Gln His Ser Asp
145                 150                 155                 160

Val Pro Val Gly Ala Arg Val Leu Ala Thr Gly Trp Ser Asp Ile Glu
                165                 170                 175

Ser Phe Asn His Gln Val Leu Glu Pro Leu Ala Val Gly Gly Ser Ala
            180                 185                 190

Val Ile Val Thr Gly Leu Ala Asp Ile Glu Arg Leu Asn Gln Ile Ala
        195                 200                 205

Thr Asn Glu Lys Thr Thr His Arg Ile
    210                 215
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Date Recue/Date Received 2020-12-22

<210> 1119
<211> 774
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(751)
<223> FRXA02361

<400> 1119
tagaggaatt ggatagctaa tagccgtagt cggtggtcaa actttgacca ccggactccc 60

ctttaagcac aatctctagc ttttatttag gcttggagtt atg gaa ctt ctc tcc 115
                                                Met Glu Leu Leu Ser
                                                  1   5

cac ttg ctt gct ctt gat cct gcc tcc cct cgt ttg act gtt tat aac 163
His Leu Leu Ala Leu Asp Pro Ala Ser Pro Arg Leu Thr Val Tyr Asn

```
                10                  15                  20

gag tcc acg ggt gcg cgt ttg gat ttc tcc gcc atc act ctt gat aac   211
Glu Ser Thr Gly Ala Arg Leu Asp Phe Ser Ala Ile Thr Leu Asp Asn
            25                  30                  35

tgg gcg tcc aag gtt ggc aat atg ctc ctt gag gaa ttg gat ctg gag   259
Trp Ala Ser Lys Val Gly Asn Met Leu Leu Glu Glu Leu Asp Leu Glu
        40                  45                  50

gaa ggc tcg ctc atc act att gat ttg ccg gtg agc tgg cag gcc gca   307
Glu Gly Ser Leu Ile Thr Ile Asp Leu Pro Val Ser Trp Gln Ala Ala
    55                  60                  65

atg att atg ctc ggc gct tta gca act agt gtt gag gtc tct ttt gat   355
Met Ile Met Leu Gly Ala Leu Ala Thr Ser Val Glu Val Ser Phe Asp
70                  75                  80                  85

gat ccc gag gca gat gcc atc ttt acc tcc ctc gat aga ttt tcc cac   403
Asp Pro Glu Ala Asp Ala Ile Phe Thr Ser Leu Asp Arg Phe Ser His
                90                  95                  100

tac aag ggc cat agt gat gtg ctg att gtc agc gag gat cct ttt ggt   451
Tyr Lys Gly His Ser Asp Val Leu Ile Val Ser Glu Asp Pro Phe Gly
            105                 110                 115

cgt gga gtt gtt gaa ggt ggc ggt gaa ctg cct aat ggt gcc atc gat   499
Arg Gly Val Val Glu Gly Gly Gly Glu Leu Pro Asn Gly Ala Ile Asp
        120                 125                 130

ttt ggc ccc aca gtg cgt ttt tat ggc gat caa ttc ttc cag cct acc   547
Phe Gly Pro Thr Val Arg Phe Tyr Gly Asp Gln Phe Phe Gln Pro Thr
    135                 140                 145

cgc aca ttg ccg gaa atc atc cag cat tct gat gtt ccg gtt ggc gcc   595
Arg Thr Leu Pro Glu Ile Ile Gln His Ser Asp Val Pro Val Gly Ala
150                 155                 160                 165

aga gtt ctt gca act ggt tgg tca gat atc gag tcc ttc aat cac cag   643
Arg Val Leu Ala Thr Gly Trp Ser Asp Ile Glu Ser Phe Asn His Gln
                170                 175                 180

gtt tta gaa cca ctc gca gtg ggt ggc tct gca gta att gtg acc gga   691
Val Leu Glu Pro Leu Ala Val Gly Gly Ser Ala Val Ile Val Thr Gly
            185                 190                 195

ctg gct gat att gag cgt tta aac cag att gca acc aat gag aag aca   739
Leu Ala Asp Ile Glu Arg Leu Asn Gln Ile Ala Thr Asn Glu Lys Thr
        200                 205                 210

acc cac cgt atc taggcaaatt tcggttacta cta                        774
Thr His Arg Ile
    215
```

<210> 1120
<211> 217
<212> PRT
<213> Corynebacterium glutamicum

<400> 1120

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Met Glu Leu Leu Ser His Leu Leu Ala Leu Asp Pro Ala Ser Pro Arg
  1               5                  10                  15

Leu Thr Val Tyr Asn Glu Ser Thr Gly Ala Arg Leu Asp Phe Ser Ala
            20                  25                  30

Ile Thr Leu Asp Asn Trp Ala Ser Lys Val Gly Asn Met Leu Leu Glu
         35                  40                  45

Glu Leu Asp Leu Glu Glu Gly Ser Leu Ile Thr Ile Asp Leu Pro Val
     50                  55                  60

Ser Trp Gln Ala Ala Met Ile Met Leu Gly Ala Leu Ala Thr Ser Val
 65                  70                  75                  80

Glu Val Ser Phe Asp Asp Pro Glu Ala Asp Ala Ile Phe Thr Ser Leu
                85                  90                  95

Asp Arg Phe Ser His Tyr Lys Gly His Ser Asp Val Leu Ile Val Ser
            100                 105                 110

Glu Asp Pro Phe Gly Arg Gly Val Val Glu Gly Gly Gly Glu Leu Pro
        115                 120                 125

Asn Gly Ala Ile Asp Phe Gly Pro Thr Val Arg Phe Tyr Gly Asp Gln
    130                 135                 140

Phe Phe Gln Pro Thr Arg Thr Leu Pro Glu Ile Ile Gln His Ser Asp
145                 150                 155                 160

Val Pro Val Gly Ala Arg Val Leu Ala Thr Gly Trp Ser Asp Ile Glu
                165                 170                 175

Ser Phe Asn His Gln Val Leu Glu Pro Leu Ala Val Gly Gly Ser Ala
            180                 185                 190

Val Ile Val Thr Gly Leu Ala Asp Ile Glu Arg Leu Asn Gln Ile Ala
        195                 200                 205

Thr Asn Glu Lys Thr Thr His Arg Ile
    210                 215
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Date Recue/Date Received 2020-07-27

<210> 1121
<211> 732
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(709)
<223> RXN02367

<400> 1121
ggcacttgaa tccggacgct aagttgttga tacatcaact tatttcttgg ctatacttga 60

ggtcacgttt cctcagctca ggagaagttc ggagaagtcc atg tca aac gca gaa 115
Met Ser Asn Ala Glu
1 5

att aat ccc gtt gaa tat gaa atc aac aac cac gcc cct ggt acc gcg 163

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Ile Asn Pro Val Glu Tyr Glu Ile Asn Asn His Ala Pro Gly Thr Ala
                10                  15                  20

cta aac cca cag tgc gaa gac ggc gcc aac gta gaa atc atc acc tcc   211
Leu Asn Pro Gln Cys Glu Asp Gly Ala Asn Val Glu Ile Ile Thr Ser
            25                  30                  35

cgt gaa gtc ccc ctc ggc gga cca cgc gcc atg acc gtg cac cgc aca   259
Arg Glu Val Pro Leu Gly Gly Pro Arg Ala Met Thr Val His Arg Thr
        40                  45                  50

ctc ccc caa cgc cag cgc tcc ctc atc ggt gcc tgg tgt ttt gtg gat   307
Leu Pro Gln Arg Gln Arg Ser Leu Ile Gly Ala Trp Cys Phe Val Asp
    55                  60                  65

cat tac ggc ccc gat gat gtc tca cta acc ggt ggc atg gat atg gcc   355
His Tyr Gly Pro Asp Asp Val Ser Leu Thr Gly Gly Met Asp Met Ala
70                  75                  80                  85

tcc cac ccg cac acc gga ttg caa aca gtc acg tgg ctt ttt gaa ggc   403
Ser His Pro His Thr Gly Leu Gln Thr Val Thr Trp Leu Phe Glu Gly
                90                  95                  100

gaa gtc acc cac cat gat tcc ggc gga aat cac gca gtc gtg ctt cct   451
Glu Val Thr His His Asp Ser Gly Gly Asn His Ala Val Val Leu Pro
            105                 110                 115

ggc gaa gtc aac ctc atg acc gcc ggc gca ggc atc tgt cac acc gaa   499
Gly Glu Val Asn Leu Met Thr Ala Gly Ala Gly Ile Cys His Thr Glu
        120                 125                 130

gtt tcc gcc acc tcc acc acg att ctg cat ggt ctg cag ttg tgg aca   547
Val Ser Ala Thr Ser Thr Thr Ile Leu His Gly Leu Gln Leu Trp Thr
    135                 140                 145

gtt ctt ccc gac aaa gac cgc gaa gga cca cgc cgc ttt gat cac tac   595
Val Leu Pro Asp Lys Asp Arg Glu Gly Pro Arg Arg Phe Asp His Tyr
150                 155                 160                 165

gct cca gaa gaa atc aca ctc gaa ggc gga agt gca cgc gtt ttc cta   643
Ala Pro Glu Glu Ile Thr Leu Glu Gly Gly Ser Ala Arg Val Phe Leu
                170                 175                 180

ggt tcg cta ttt ggt caa acc tcc cct gtt cat acg ttt act ggc tct   691
Gly Ser Leu Phe Gly Gln Thr Ser Pro Val His Thr Phe Thr Gly Ser
            185                 190                 195

tcc tgt ttt aga gtg cat tgatcttatg gaccaactgc cct                732
Ser Cys Phe Arg Val His
        200
```

<210> 1122
<211> 203
<212> PRT
<213> Corynebacterium glutamicum

<400> 1122

```
Met Ser Asn Ala Glu Ile Asn Pro Val Glu Tyr Glu Ile Asn Asn His
  1               5                  10                  15
```

```
Ala Pro Gly Thr Ala Leu Asn Pro Gln Cys Glu Asp Gly Ala Asn Val
            20                  25                  30

Glu Ile Ile Thr Ser Arg Glu Val Pro Leu Gly Gly Pro Arg Ala Met
        35                  40                  45

Thr Val His Arg Thr Leu Pro Gln Arg Gln Arg Ser Leu Ile Gly Ala
    50                  55                  60

Trp Cys Phe Val Asp His Tyr Gly Pro Asp Asp Val Ser Leu Thr Gly
65                  70                  75                  80

Gly Met Asp Met Ala Ser His Pro His Thr Gly Leu Gln Thr Val Thr
                85                  90                  95

Trp Leu Phe Glu Gly Glu Val Thr His His Asp Ser Gly Gly Asn His
            100                 105                 110

Ala Val Val Leu Pro Gly Glu Val Asn Leu Met Thr Ala Gly Ala Gly
        115                 120                 125

Ile Cys His Thr Glu Val Ser Ala Thr Ser Thr Thr Ile Leu His Gly
    130                 135                 140

Leu Gln Leu Trp Thr Val Leu Pro Asp Lys Asp Arg Glu Gly Pro Arg
145                 150                 155                 160

Arg Phe Asp His Tyr Ala Pro Glu Glu Ile Thr Leu Glu Gly Gly Ser
                165                 170                 175

Ala Arg Val Phe Leu Gly Ser Leu Phe Gly Gln Thr Ser Pro Val His
            180                 185                 190

Thr Phe Thr Gly Ser Ser Cys Phe Arg Val His
        195                 200
```

<210> 1123
<211> 732
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(709)
<223> FRXA02367

<400> 1123
ggcacttgaa tccggacgct aagttgttga tacatcaact tatttcttgg ctatacttga 60

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ggtcacgttt cctcagctca ggagaagttc ggagaagtcc atg tca aac gca gaa   115
                                              Met Ser Asn Ala Glu
                                                1               5

att aat ccc gtt gaa tat gaa atc aac aac cac gcc cct ggt acc gcg   163
Ile Asn Pro Val Glu Tyr Glu Ile Asn Asn His Ala Pro Gly Thr Ala
                10                  15                  20

cta aac cca cag tgc gaa gac ggc gcc aac gta gaa atc atc acc tcc   211
Leu Asn Pro Gln Cys Glu Asp Gly Ala Asn Val Glu Ile Ile Thr Ser
            25                  30                  35
```

```
cgt gaa gtc ccc ctc ggc gga cca cgc gcc atg acc gtg cac cgc aca   259
Arg Glu Val Pro Leu Gly Gly Pro Arg Ala Met Thr Val His Arg Thr
         40                  45                  50

ctc ccc caa cgc cag cgc tcc ctc atc ggt gcc tgg tgt ttt gtg gat   307
Leu Pro Gln Arg Gln Arg Ser Leu Ile Gly Ala Trp Cys Phe Val Asp
     55                  60                  65

cat tac ggc ccc gat gat gtc tca cta acc ggt ggc atg gat atg gcc   355
His Tyr Gly Pro Asp Asp Val Ser Leu Thr Gly Gly Met Asp Met Ala
 70                  75                  80                  85

tcc cac ccg cac acc gga ttg caa aca gtc acg tgg ctt ttt gaa ggc   403
Ser His Pro His Thr Gly Leu Gln Thr Val Thr Trp Leu Phe Glu Gly
                90                  95                 100

gaa gtc acc cac cat gat tcc ggc gga aat cac gca gtc gtg ctt cct   451
Glu Val Thr His His Asp Ser Gly Gly Asn His Ala Val Val Leu Pro
            105                 110                 115

ggc gaa gtc aac ctc atg acc gcc ggc gca ggc atc tgt cac acc gaa   499
Gly Glu Val Asn Leu Met Thr Ala Gly Ala Gly Ile Cys His Thr Glu
        120                 125                 130

gtt tcc gcc acc tcc acc acg att ctg cat ggt ctg cag ttg tgg aca   547
Val Ser Ala Thr Ser Thr Thr Ile Leu His Gly Leu Gln Leu Trp Thr
    135                 140                 145

gtt ctt ccc gac aaa gac cgc gaa gga cca cgc cgc ttt gat cac tac   595
Val Leu Pro Asp Lys Asp Arg Glu Gly Pro Arg Arg Phe Asp His Tyr
150                 155                 160                 165

gct cca gaa gaa atc aca ctc gaa ggc gga agt gca cgc gtt ttc cta   643
Ala Pro Glu Glu Ile Thr Leu Glu Gly Gly Ser Ala Arg Val Phe Leu
                170                 175                 180

ggt tcg cta ttt ggt caa acc tcc cct gtt cat acg ttt act ggc tct   691
Gly Ser Leu Phe Gly Gln Thr Ser Pro Val His Thr Phe Thr Gly Ser
            185                 190                 195

tcc tgt ttt aga gtg cat tgatcttatg gaccaactgc cct                732
Ser Cys Phe Arg Val His
        200
```

<210> 1124
<211> 203
<212> PRT
<213> Corynebacterium glutamicum

<400> 1124

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Met Ser Asn Ala Glu Ile Asn Pro Val Glu Tyr Glu Ile Asn Asn His
  1               5                  10                  15

Ala Pro Gly Thr Ala Leu Asn Pro Gln Cys Glu Asp Gly Ala Asn Val
             20                  25                  30

Glu Ile Ile Thr Ser Arg Glu Val Pro Leu Gly Gly Pro Arg Ala Met
         35                  40                  45
```

```
Thr Val His Arg Thr Leu Pro Gln Arg Gln Arg Ser Leu Ile Gly Ala
     50                  55                  60

Trp Cys Phe Val Asp His Tyr Gly Pro Asp Asp Val Ser Leu Thr Gly
 65                  70                  75                  80

Gly Met Asp Met Ala Ser His Pro His Thr Gly Leu Gln Thr Val Thr
                85                  90                  95

Trp Leu Phe Glu Gly Glu Val Thr His His Asp Ser Gly Gly Asn His
            100                 105                 110

Ala Val Val Leu Pro Gly Glu Val Asn Leu Met Thr Ala Gly Ala Gly
        115                 120                 125

Ile Cys His Thr Glu Val Ser Ala Thr Ser Thr Thr Ile Leu His Gly
    130                 135                 140

Leu Gln Leu Trp Thr Val Leu Pro Asp Lys Asp Arg Glu Gly Pro Arg
145                 150                 155                 160

Arg Phe Asp His Tyr Ala Pro Glu Glu Ile Thr Leu Glu Gly Gly Ser
                165                 170                 175

Ala Arg Val Phe Leu Gly Ser Leu Phe Gly Gln Thr Ser Pro Val His
            180                 185                 190

Thr Phe Thr Gly Ser Ser Cys Phe Arg Val His
        195                 200
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Sequence Listing

<210> 1125
<211> 798
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(775)
<223> RXN02368

<400> 1125

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cttaggtcaa gcttgcattt attggctagt gtcggaaatc atgggagatt tagcaaagca 60

catgggcagt gaaccaccag catggtggaa gtttttaccg atg att gtc ctc gct   115
                                            Met Ile Val Leu Ala
                                              1               5

gga gcc act cga gtt acc tat gaa gta gaa cct tgg ctg gcg atc cca   163
Gly Ala Thr Arg Val Thr Tyr Glu Val Glu Pro Trp Leu Ala Ile Pro
                10                  15                  20

tta ttc att ttg gct ttt gca tcg ata ttg atc cca ttc ccg atc tct   211
Leu Phe Ile Leu Ala Phe Ala Ser Ile Leu Ile Pro Phe Pro Ile Ser
            25                  30                  35

aag aca aaa gga ctc cgt gat atc gat gcc tgg aaa atc cac acc acg   259
Lys Thr Lys Gly Leu Arg Asp Ile Asp Ala Trp Lys Ile His Thr Thr
        40                  45                  50

caa ggc gat aaa aag cgt gcc atc cgc caa ctg atc att ccg gct acg   307
```

```
Gln Gly Asp Lys Lys Arg Ala Ile Arg Gln Leu Ile Ile Pro Ala Thr
     55                  60                  65

gct ttg gcc atc gac atc att ggg ctg ccg aca tta ttt aat gcc cct   355
Ala Leu Ala Ile Asp Ile Ile Gly Leu Pro Thr Leu Phe Asn Ala Pro
 70                  75                  80                  85

ccc ctt gct tcc gct gca ctt ttt ggc ggt gtt tac ggc gct tcc cta   403
Pro Leu Ala Ser Ala Ala Leu Phe Gly Gly Val Tyr Gly Ala Ser Leu
                90                  95                 100

gct tgg gct gcg tac aga gct gat cag ctt cca cgc att cga acg aag   451
Ala Trp Ala Ala Tyr Arg Ala Asp Gln Leu Pro Arg Ile Arg Thr Lys
            105                 110                 115

gaa cgc ctc gca gaa ctt tca caa aat gca tct ctg gat gat gtg cgc   499
Glu Arg Leu Ala Glu Leu Ser Gln Asn Ala Ser Leu Asp Asp Val Arg
        120                 125                 130

tca gat gac tta gat gtt cta gag cag ccg gaa tcc cgt gaa tta gtg   547
Ser Asp Asp Leu Asp Val Leu Glu Gln Pro Glu Ser Arg Glu Leu Val
    135                 140                 145

cgc tgt ctg ctt gcc cac ggt gcg atg gat ggc act cgg gtg atg gcc   595
Arg Cys Leu Leu Ala His Gly Ala Met Asp Gly Thr Arg Val Met Ala
150                 155                 160                 165

aga cag gtc gcg cga gta ctg gat acc gag gta gac gaa gta cat cag   643
Arg Gln Val Ala Arg Val Leu Asp Thr Glu Val Asp Glu Val His Gln
                170                 175                 180

gta gca cgc tca cta gaa cag cat ggt ttg gtt agt cgc tcc acc atc   691
Val Ala Arg Ser Leu Glu Gln His Gly Leu Val Ser Arg Ser Thr Ile
            185                 190                 195

atg ccg ggt ggg gat cca gga aaa gta ttc atc gaa gtt tcc ctg aaa   739
Met Pro Gly Gly Asp Pro Gly Lys Val Phe Ile Glu Val Ser Leu Lys
        200                 205                 210

ggg atc tca gcc atc aag gca ctt gaa tcc gga cgc taagttgttg        785
Gly Ile Ser Ala Ile Lys Ala Leu Glu Ser Gly Arg
    215                 220                 225

atacatcaac tta                                                   798


<210> 1126
<211> 225
<212> PRT
<213> Corynebacterium glutamicum

<400> 1126
Met Ile Val Leu Ala Gly Ala Thr Arg Val Thr Tyr Glu Val Glu Pro
  1               5                  10                  15

Trp Leu Ala Ile Pro Leu Phe Ile Leu Ala Phe Ala Ser Ile Leu Ile
             20                  25                  30

Pro Phe Pro Ile Ser Lys Thr Lys Gly Leu Arg Asp Ile Asp Ala Trp
         35                  40                  45
```

```
Lys Ile His Thr Thr Gln Gly Asp Lys Lys Arg Ala Ile Arg Gln Leu
     50                  55                  60

Ile Ile Pro Ala Thr Ala Leu Ala Ile Asp Ile Ile Gly Leu Pro Thr
 65                  70                  75                  80

Leu Phe Asn Ala Pro Pro Leu Ala Ser Ala Ala Leu Phe Gly Gly Val
                 85                  90                  95

Tyr Gly Ala Ser Leu Ala Trp Ala Ala Tyr Arg Ala Asp Gln Leu Pro
            100                 105                 110

Arg Ile Arg Thr Lys Glu Arg Leu Ala Glu Leu Ser Gln Asn Ala Ser
        115                 120                 125

Leu Asp Asp Val Arg Ser Asp Asp Leu Asp Val Leu Glu Gln Pro Glu
    130                 135                 140

Ser Arg Glu Leu Val Arg Cys Leu Leu Ala His Gly Ala Met Asp Gly
145                 150                 155                 160

Thr Arg Val Met Ala Arg Gln Val Ala Arg Val Leu Asp Thr Glu Val
                165                 170                 175

Asp Glu Val His Gln Val Ala Arg Ser Leu Glu Gln His Gly Leu Val
            180                 185                 190

Ser Arg Ser Thr Ile Met Pro Gly Gly Asp Pro Gly Lys Val Phe Ile
        195                 200                 205

Glu Val Ser Leu Lys Gly Ile Ser Ala Ile Lys Ala Leu Glu Ser Gly
    210                 215                 220

Arg
225
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US 20090246829 A1

<210> 1127
<211> 798
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(775)
<223> FRXA02368

<400> 1127
cttaggtcaa gcttgcattt attggctagt gtcggaaatc atgggagatt tagcaaagca 60

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catgggcagt gaaccaccag catggtggaa gtttttaccg atg att gtc ctc gct   115
                                            Met Ile Val Leu Ala
                                              1               5

gga gcc act cga gtt acc tat gaa gta gaa cct tgg ctg gcg atc cca   163
Gly Ala Thr Arg Val Thr Tyr Glu Val Glu Pro Trp Leu Ala Ile Pro
                 10                  15                  20

tta ttc att ttg gct ttt gca tcg ata ttg atc cca ttc ccg atc tct   211
Leu Phe Ile Leu Ala Phe Ala Ser Ile Leu Ile Pro Phe Pro Ile Ser
             25                  30                  35
```

```
aag aca aaa gga ctc cgt gat atc gat gcc tgg aaa atc cac acc acg   259
Lys Thr Lys Gly Leu Arg Asp Ile Asp Ala Trp Lys Ile His Thr Thr
         40                  45                  50

caa ggc gat aaa aag cgt gcc atc cgc caa ctg atc att ccg gct acg   307
Gln Gly Asp Lys Lys Arg Ala Ile Arg Gln Leu Ile Ile Pro Ala Thr
     55                  60                  65

gct ttg gcc atc gac atc att ggg ctg ccg aca tta ttt aat gcc cct   355
Ala Leu Ala Ile Asp Ile Ile Gly Leu Pro Thr Leu Phe Asn Ala Pro
 70                  75                  80                  85

ccc ctt gct tcc gct gca ctt ttt ggc ggt gtt tac ggc gct tcc cta   403
Pro Leu Ala Ser Ala Ala Leu Phe Gly Gly Val Tyr Gly Ala Ser Leu
                 90                  95                 100

gct tgg gct gcg tac aga gct gat cag ctt cca cgc att cga acg aag   451
Ala Trp Ala Ala Tyr Arg Ala Asp Gln Leu Pro Arg Ile Arg Thr Lys
            105                 110                 115

gaa cgc ctc gca gaa ctt tca caa aat gca tct ctg gat gat gtg cgc   499
Glu Arg Leu Ala Glu Leu Ser Gln Asn Ala Ser Leu Asp Asp Val Arg
        120                 125                 130

tca gat gac tta gat gtt cta gag cag ccg gaa tcc cgt gaa tta gtg   547
Ser Asp Asp Leu Asp Val Leu Glu Gln Pro Glu Ser Arg Glu Leu Val
    135                 140                 145

cgc tgt ctg ctt gcc cac ggt gcg atg gat ggc act cgg gtg atg gcc   595
Arg Cys Leu Leu Ala His Gly Ala Met Asp Gly Thr Arg Val Met Ala
150                 155                 160                 165

aga cag gtc gcg cga gta ctg gat acc gag gta gac gaa gta cat cag   643
Arg Gln Val Ala Arg Val Leu Asp Thr Glu Val Asp Glu Val His Gln
                170                 175                 180

gta gca cgc tca cta gaa cag cat ggt ttg gtt agt cgc tcc acc atc   691
Val Ala Arg Ser Leu Glu Gln His Gly Leu Val Ser Arg Ser Thr Ile
            185                 190                 195

atg ccg ggt ggg gat cca gga aaa gta ttc atc gaa gtt tcc ctg aaa   739
Met Pro Gly Gly Asp Pro Gly Lys Val Phe Ile Glu Val Ser Leu Lys
        200                 205                 210

ggg atc tca gcc atc aag gca ctt gaa tcc gga cgc taagttgttg        785
Gly Ile Ser Ala Ile Lys Ala Leu Glu Ser Gly Arg
    215                 220                 225

atacatcaac tta                                                   798
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<210> 1128
<211> 225
<212> PRT
<213> Corynebacterium glutamicum

<400> 1128

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Met Ile Val Leu Ala Gly Ala Thr Arg Val Thr Tyr Glu Val Glu Pro
  1               5                  10                  15
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```
Trp Leu Ala Ile Pro Leu Phe Ile Leu Ala Phe Ala Ser Ile Leu Ile
            20                  25                  30

Pro Phe Pro Ile Ser Lys Thr Lys Gly Leu Arg Asp Ile Asp Ala Trp
        35                  40                  45

Lys Ile His Thr Thr Gln Gly Asp Lys Lys Arg Ala Ile Arg Gln Leu
    50                  55                  60

Ile Ile Pro Ala Thr Ala Leu Ala Ile Asp Ile Ile Gly Leu Pro Thr
65                  70                  75                  80

Leu Phe Asn Ala Pro Pro Leu Ala Ser Ala Ala Leu Phe Gly Gly Val
                85                  90                  95

Tyr Gly Ala Ser Leu Ala Trp Ala Ala Tyr Arg Ala Asp Gln Leu Pro
            100                 105                 110

Arg Ile Arg Thr Lys Glu Arg Leu Ala Glu Leu Ser Gln Asn Ala Ser
        115                 120                 125

Leu Asp Asp Val Arg Ser Asp Asp Leu Asp Val Leu Glu Gln Pro Glu
    130                 135                 140

Ser Arg Glu Leu Val Arg Cys Leu Leu Ala His Gly Ala Met Asp Gly
145                 150                 155                 160

Thr Arg Val Met Ala Arg Gln Val Ala Arg Val Leu Asp Thr Glu Val
                165                 170                 175

Asp Glu Val His Gln Val Ala Arg Ser Leu Glu Gln His Gly Leu Val
            180                 185                 190

Ser Arg Ser Thr Ile Met Pro Gly Gly Asp Pro Gly Lys Val Phe Ile
        195                 200                 205

Glu Val Ser Leu Lys Gly Ile Ser Ala Ile Lys Ala Leu Glu Ser Gly
    210                 215                 220

Arg
225
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<210> 1129
<211> 1146
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1123)
<223> RXN02381

<400> 1129
aagtttgaag aagtaatcaa gctcccctgt gaggactcgt tgtagtcttt tatttagtta 60

ataaaagatt tcataccaac ttgtcagcag gggagctttc atg tct gtc aca aac 115
                                                Met Ser Val Thr Asn
                                                  1   5

ttc cgt cgg ttt ctt gct ggc ata gcg gtc atc gcg gcg tgt gtt gct 163

```
Phe Arg Arg Phe Leu Ala Gly Ile Ala Val Ile Ala Ala Cys Val Ala
                10                  15                  20

gcg act cca aca gct cag gca caa agc agt ggc tct tct gga tcc tct   211
Ala Thr Pro Thr Ala Gln Ala Gln Ser Ser Gly Ser Ser Gly Ser Ser
            25                  30                  35

ggt tct tca gcg gga tct agc ggg ctg tgg gat tta ctt ttt cca gaa   259
Gly Ser Ser Ala Gly Ser Ser Gly Leu Trp Asp Leu Leu Phe Pro Glu
        40                  45                  50

tcc cat gag tct ttt atc gag cgg ctt ctt gat cct ttg gat gac agc   307
Ser His Glu Ser Phe Ile Glu Arg Leu Leu Asp Pro Leu Asp Asp Ser
    55                  60                  65

cat ata tct att cac cct gac ctc acc cca gac ctg tat gaa gag gtg   355
His Ile Ser Ile His Pro Asp Leu Thr Pro Asp Leu Tyr Glu Glu Val
70                  75                  80                  85

ttt gat cca ccg caa att ggt gaa tgc cca gcc gtt gtt gct gtg gtc   403
Phe Asp Pro Pro Gln Ile Gly Glu Cys Pro Ala Val Val Ala Val Val
                90                  95                  100

gca cga ggc agt gaa caa aac ctt caa atc cga ccc gcg cga tac agc   451
Ala Arg Gly Ser Glu Gln Asn Leu Gln Ile Arg Pro Ala Arg Tyr Ser
            105                 110                 115

gag gaa tct cca tgg aca tcc aat gga ttt gag gaa aaa aac ttt cgt   499
Glu Glu Ser Pro Trp Thr Ser Asn Gly Phe Glu Glu Lys Asn Phe Arg
        120                 125                 130

agt ttc ttt ggc cga atg gaa aaa cac tac cgt gaa tcg act ggc gag   547
Ser Phe Phe Gly Arg Met Glu Lys His Tyr Arg Glu Ser Thr Gly Glu
    135                 140                 145

tcg ttg atg aaa gac gtc tac gtg atg ggt ctg aat aat atc gaa tac   595
Ser Leu Met Lys Asp Val Tyr Val Met Gly Leu Asn Asn Ile Glu Tyr
150                 155                 160                 165

cct gct tct ttg cca ctg tct tcg gag gga agc agc gcc att gaa ttg   643
Pro Ala Ser Leu Pro Leu Ser Ser Glu Gly Ser Ser Ala Ile Glu Leu
                170                 175                 180

ggc act tcc att tct agt ggt cgc gac aat gtc atc agc gcg att gat   691
Gly Thr Ser Ile Ser Ser Gly Arg Asp Asn Val Ile Ser Ala Ile Asp
            185                 190                 195

cgc ttt gaa tca gcg aca ggg tgc acg ccg aag tac ctg ttg gcg ggt   739
Arg Phe Glu Ser Ala Thr Gly Cys Thr Pro Lys Tyr Leu Leu Ala Gly
        200                 205                 210

tat tct caa ggt gtc ctc atc gtt gat ggc tat gaa gag gag ttg att   787
Tyr Ser Gln Gly Val Leu Ile Val Asp Gly Tyr Glu Glu Glu Leu Ile
    215                 220                 225

gcg agg gat cag tac ctc ggc acc ctg cac atc gcg aat cca gcg caa   835
Ala Arg Asp Gln Tyr Leu Gly Thr Leu His Ile Ala Asn Pro Ala Gln
230                 235                 240                 245

caa gtt gat gat cca aca ctt gtt ggg cat gaa gta acc acg gga ggc   883
Gln Val Asp Asp Pro Thr Leu Val Gly His Glu Val Thr Thr Gly Gly
```

```
                250                 255                 260

ttg gct agt tcc gtg gag ccc gtc gag gac aat cct ttc aag gtg agc   931
Leu Ala Ser Ser Val Glu Pro Val Glu Asp Asn Pro Phe Lys Val Ser
            265                 270                 275

tac tgc ctg cct gga gac atc gtg tgc gat cgt tct ttt gaa cag ttc   979
Tyr Cys Leu Pro Gly Asp Ile Val Cys Asp Arg Ser Phe Glu Gln Phe
        280                 285                 290

tct gct gcg gga tcc tct ata gca gct gcg caa ttg agc acc gga aat   1027
Ser Ala Ala Gly Ser Ser Ile Ala Ala Ala Gln Leu Ser Thr Gly Asn
    295                 300                 305

atc cgt cca ggt cga gta cac gtg caa tac ttc gtt acc acc caa ccg   1075
Ile Arg Pro Gly Arg Val His Val Gln Tyr Phe Val Thr Thr Gln Pro
310                 315                 320                 325

tgg gat gag cag att ttt gac gaa gtc gca tcg tgg att gaa gct gcc   1123
Trp Asp Glu Gln Ile Phe Asp Glu Val Ala Ser Trp Ile Glu Ala Ala
                330                 335                 340

taaaaactcg cgaggacgca tgc                                       1146


<210> 1130
<211> 341
<212> PRT
<213> Corynebacterium glutamicum

<400> 1130
Met Ser Val Thr Asn Phe Arg Arg Phe Leu Ala Gly Ile Ala Val Ile
  1               5                  10                  15

Ala Ala Cys Val Ala Ala Thr Pro Thr Ala Gln Ala Gln Ser Ser Gly
             20                  25                  30

Ser Ser Gly Ser Ser Gly Ser Ser Ala Gly Ser Ser Gly Leu Trp Asp
         35                  40                  45

Leu Leu Phe Pro Glu Ser His Glu Ser Phe Ile Glu Arg Leu Leu Asp
     50                  55                  60

Pro Leu Asp Asp Ser His Ile Ser Ile His Pro Asp Leu Thr Pro Asp
 65                  70                  75                  80

Leu Tyr Glu Glu Val Phe Asp Pro Pro Gln Ile Gly Glu Cys Pro Ala
                 85                  90                  95

Val Val Ala Val Val Ala Arg Gly Ser Glu Gln Asn Leu Gln Ile Arg
            100                 105                 110

Pro Ala Arg Tyr Ser Glu Glu Ser Pro Trp Thr Ser Asn Gly Phe Glu
        115                 120                 125

Glu Lys Asn Phe Arg Ser Phe Phe Gly Arg Met Glu Lys His Tyr Arg
    130                 135                 140

Glu Ser Thr Gly Glu Ser Leu Met Lys Asp Val Tyr Val Met Gly Leu
145                 150                 155                 160
```

```
Asn Asn Ile Glu Tyr Pro Ala Ser Leu Pro Leu Ser Ser Glu Gly Ser
                165                 170                 175

Ser Ala Ile Glu Leu Gly Thr Ser Ile Ser Ser Gly Arg Asp Asn Val
            180                 185                 190

Ile Ser Ala Ile Asp Arg Phe Glu Ser Ala Thr Gly Cys Thr Pro Lys
        195                 200                 205

Tyr Leu Leu Ala Gly Tyr Ser Gln Gly Val Leu Ile Val Asp Gly Tyr
    210                 215                 220

Glu Glu Glu Leu Ile Ala Arg Asp Gln Tyr Leu Gly Thr Leu His Ile
225                 230                 235                 240

Ala Asn Pro Ala Gln Gln Val Asp Asp Pro Thr Leu Val Gly His Glu
                245                 250                 255

Val Thr Thr Gly Gly Leu Ala Ser Ser Val Glu Pro Val Glu Asp Asn
            260                 265                 270

Pro Phe Lys Val Ser Tyr Cys Leu Pro Gly Asp Ile Val Cys Asp Arg
        275                 280                 285

Ser Phe Glu Gln Phe Ser Ala Ala Gly Ser Ser Ile Ala Ala Ala Gln
    290                 295                 300

Leu Ser Thr Gly Asn Ile Arg Pro Gly Arg Val His Val Gln Tyr Phe
305                 310                 315                 320

Val Thr Thr Gln Pro Trp Asp Glu Gln Ile Phe Asp Glu Val Ala Ser
                325                 330                 335

Trp Ile Glu Ala Ala
            340
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<210> 1131
<211> 1146
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1123)
<223> FRXA02381

<400> 1131
aagtttgaag aagtaatcaa gctcccctgt gaggactcgt tgtagtcttt tatttagtta 60

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ataaaagatt tcataccaac ttgtcagcag gggagctttc atg tct gtc aca aac   115
                                             Met Ser Val Thr Asn
                                               1               5

ttc cgt cgg ttt ctt gct ggc ata gcg gtc atc gcg gcg tgt gtt gct   163
Phe Arg Arg Phe Leu Ala Gly Ile Ala Val Ile Ala Ala Cys Val Ala
                 10                  15                  20

gcg act cca aca gct cag gca caa agc agt ggc tct tct gga tcc tct   211
Ala Thr Pro Thr Ala Gln Ala Gln Ser Ser Gly Ser Ser Gly Ser Ser
             25                  30                  35
```

```
ggt tct tca gcg gga tct agc ggg ctg tgg gat tta ctt ttt cca gaa   259
Gly Ser Ser Ala Gly Ser Ser Gly Leu Trp Asp Leu Leu Phe Pro Glu
         40                  45                  50

tcc cat gag tct ttt atc gag cgg ctt ctt gat cct ttg gat gac agc   307
Ser His Glu Ser Phe Ile Glu Arg Leu Leu Asp Pro Leu Asp Asp Ser
     55                  60                  65

cat ata tct att cac cct gac ctc acc cca gac ctg tat gaa gag gtg   355
His Ile Ser Ile His Pro Asp Leu Thr Pro Asp Leu Tyr Glu Glu Val
 70                  75                  80                  85

ttt gat cca ccg caa att ggt gaa tgc cca gcc gtt gtt gct gtg gtc   403
Phe Asp Pro Pro Gln Ile Gly Glu Cys Pro Ala Val Val Ala Val Val
                 90                  95                 100

gca cga ggc agt gaa caa aac ctt caa atc cga ccc gcg cga tac agc   451
Ala Arg Gly Ser Glu Gln Asn Leu Gln Ile Arg Pro Ala Arg Tyr Ser
            105                 110                 115

gag gaa tct cca tgg aca tcc aat gga ttt gag gaa aaa aac ttt cgt   499
Glu Glu Ser Pro Trp Thr Ser Asn Gly Phe Glu Glu Lys Asn Phe Arg
        120                 125                 130

agt ttc ttt ggc cga atg gaa aaa cac tac cgt gaa tcg act ggc gag   547
Ser Phe Phe Gly Arg Met Glu Lys His Tyr Arg Glu Ser Thr Gly Glu
    135                 140                 145

tcg ttg atg aaa gac gtc tac gtg atg ggt ctg aat aat atc gaa tac   595
Ser Leu Met Lys Asp Val Tyr Val Met Gly Leu Asn Asn Ile Glu Tyr
150                 155                 160                 165

cct gct tct ttg cca ctg tct tcg gag gga agc agc gcc att gaa ttg   643
Pro Ala Ser Leu Pro Leu Ser Ser Glu Gly Ser Ser Ala Ile Glu Leu
                170                 175                 180

ggc act tcc att tct agt ggt cgc gac aat gtc atc agc gcg att gat   691
Gly Thr Ser Ile Ser Ser Gly Arg Asp Asn Val Ile Ser Ala Ile Asp
            185                 190                 195

cgc ttt gaa tca gcg aca ggg tgc acg ccg aag tac ctg ttg gcg ggt   739
Arg Phe Glu Ser Ala Thr Gly Cys Thr Pro Lys Tyr Leu Leu Ala Gly
        200                 205                 210

tat tct caa ggt gtc ctc atc gtt gat ggc tat gaa gag gag ttg att   787
Tyr Ser Gln Gly Val Leu Ile Val Asp Gly Tyr Glu Glu Glu Leu Ile
    215                 220                 225

gcg agg gat cag tac ctc ggc acc ctg cac atc gcg aat cca gcg caa   835
Ala Arg Asp Gln Tyr Leu Gly Thr Leu His Ile Ala Asn Pro Ala Gln
230                 235                 240                 245

caa gtt gat gat cca aca ctt gtt ggg cat gaa gta acc acg gga ggc   883
Gln Val Asp Asp Pro Thr Leu Val Gly His Glu Val Thr Thr Gly Gly
                250                 255                 260

ttg gct agt tcc gtg gag ccc gtc gag gac aat cct ttc aag gtg agc   931
Leu Ala Ser Ser Val Glu Pro Val Glu Asp Asn Pro Phe Lys Val Ser
            265                 270                 275
```

```
tac tgc ctg cct gga gac atc gtg tgc gat cgt tct ttt gaa cag ttc   979
Tyr Cys Leu Pro Gly Asp Ile Val Cys Asp Arg Ser Phe Glu Gln Phe
        280                 285                 290

tct gct gcg gga tcc tct ata gca gct gcg caa ttg agc acc gga aat   1027
Ser Ala Ala Gly Ser Ser Ile Ala Ala Ala Gln Leu Ser Thr Gly Asn
    295                 300                 305

atc cgt cca ggt cga gta cac gtg caa tac ttc gtt acc acc caa ccg   1075
Ile Arg Pro Gly Arg Val His Val Gln Tyr Phe Val Thr Thr Gln Pro
310                 315                 320                 325

tgg gat gag cag att ttt gac gaa gtc gca tcg tgg att gaa gct gcc   1123
Trp Asp Glu Gln Ile Phe Asp Glu Val Ala Ser Trp Ile Glu Ala Ala
                330                 335                 340

taaaaactcg cgaggacgca tgc                                        1146
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<210> 1132
<211> 341
<212> PRT
<213> Corynebacterium glutamicum

<400> 1132

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Met Ser Val Thr Asn Phe Arg Arg Phe Leu Ala Gly Ile Ala Val Ile
  1               5                  10                  15

Ala Ala Cys Val Ala Ala Thr Pro Thr Ala Gln Ala Gln Ser Ser Gly
             20                  25                  30

Ser Ser Gly Ser Ser Gly Ser Ser Ala Gly Ser Ser Gly Leu Trp Asp
         35                  40                  45

Leu Leu Phe Pro Glu Ser His Glu Ser Phe Ile Glu Arg Leu Leu Asp
     50                  55                  60

Pro Leu Asp Asp Ser His Ile Ser Ile His Pro Asp Leu Thr Pro Asp
 65                  70                  75                  80

Leu Tyr Glu Glu Val Phe Asp Pro Pro Gln Ile Gly Glu Cys Pro Ala
                85                  90                  95

Val Val Ala Val Val Ala Arg Gly Ser Glu Gln Asn Leu Gln Ile Arg
            100                 105                 110

Pro Ala Arg Tyr Ser Glu Glu Ser Pro Trp Thr Ser Asn Gly Phe Glu
        115                 120                 125

Glu Lys Asn Phe Arg Ser Phe Phe Gly Arg Met Glu Lys His Tyr Arg
    130                 135                 140

Glu Ser Thr Gly Glu Ser Leu Met Lys Asp Val Tyr Val Met Gly Leu
145                 150                 155                 160

Asn Asn Ile Glu Tyr Pro Ala Ser Leu Pro Leu Ser Ser Glu Gly Ser
                165                 170                 175

Ser Ala Ile Glu Leu Gly Thr Ser Ile Ser Ser Gly Arg Asp Asn Val
            180                 185                 190
```

```
Ile Ser Ala Ile Asp Arg Phe Glu Ser Ala Thr Gly Cys Thr Pro Lys
        195                 200                 205

Tyr Leu Leu Ala Gly Tyr Ser Gln Gly Val Leu Ile Val Asp Gly Tyr
    210                 215                 220

Glu Glu Glu Leu Ile Ala Arg Asp Gln Tyr Leu Gly Thr Leu His Ile
225                 230                 235                 240

Ala Asn Pro Ala Gln Gln Val Asp Asp Pro Thr Leu Val Gly His Glu
                245                 250                 255

Val Thr Thr Gly Gly Leu Ala Ser Ser Val Glu Pro Val Glu Asp Asn
            260                 265                 270

Pro Phe Lys Val Ser Tyr Cys Leu Pro Gly Asp Ile Val Cys Asp Arg
        275                 280                 285

Ser Phe Glu Gln Phe Ser Ala Ala Gly Ser Ser Ile Ala Ala Ala Gln
    290                 295                 300

Leu Ser Thr Gly Asn Ile Arg Pro Gly Arg Val His Val Gln Tyr Phe
305                 310                 315                 320

Val Thr Thr Gln Pro Trp Asp Glu Gln Ile Phe Asp Glu Val Ala Ser
                325                 330                 335

Trp Ile Glu Ala Ala
            340
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<210> 1133
<211> 736
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(736)
<223> RXN02383

<400> 1133
gggcaacaat gtggaaaacg cccagtggta tcttgacggc tggaacatgg gtgttacgca 60

gtaaagaaga tggcaataaa aatgtggagg agtaaaggcg atg cca gtt cgg gta   115
                                              Met Pro Val Arg Val
                                                1               5

att gtt gat tcc tcc gca tgc ttg cca acg cat gtg gcc gag gac ctc   163
Ile Val Asp Ser Ser Ala Cys Leu Pro Thr His Val Ala Glu Asp Leu
                10                  15                  20

gac atc acg gtg att aac ttg cac gtg atg aat aac ggt gaa gaa cgc   211
Asp Ile Thr Val Ile Asn Leu His Val Met Asn Asn Gly Glu Glu Arg
            25                  30                  35

agt aca tcc ggg ttg tcg tcg ttg gaa ctt gca gca agt tac gcc cgc   259
Ser Thr Ser Gly Leu Ser Ser Leu Glu Leu Ala Ala Ser Tyr Ala Arg
        40                  45                  50

cag ctt gaa cgc ggt ggc gat gac ggt gtg ctt gcg ctg cat att tct   307
```

```
Gln Leu Glu Arg Gly Gly Asp Asp Gly Val Leu Ala Leu His Ile Ser
     55                  60                  65

aaa gag ctc tcg tcc acg tgg tcc gca gcg gtg aca gca gcc gct gtg   355
Lys Glu Leu Ser Ser Thr Trp Ser Ala Ala Val Thr Ala Ala Ala Val
 70                  75                  80                  85

ttt gat gat gat tct gtg cgc gtg gtg gat acc agt tcg ctc ggt atg   403
Phe Asp Asp Asp Ser Val Arg Val Val Asp Thr Ser Ser Leu Gly Met
                90                  95                 100

gct gtg ggt gct gcc gcg atg gct gct gcc cgc atg gct aaa gat ggc   451
Ala Val Gly Ala Ala Ala Met Ala Ala Ala Arg Met Ala Lys Asp Gly
            105                 110                 115

gcg tct ttg cag gaa tgc tac gac atc gcg gtg gat acc ttg aag cgt   499
Ala Ser Leu Gln Glu Cys Tyr Asp Ile Ala Val Asp Thr Leu Lys Arg
        120                 125                 130

tca gaa acc tgg atc tac ctg cac cgc att gat gaa atc tgg aag tcg   547
Ser Glu Thr Trp Ile Tyr Leu His Arg Ile Asp Glu Ile Trp Lys Ser
    135                 140                 145

gga cgg att tcc act gca acc gcc atg gtg tca acg gct ctg gca acc   595
Gly Arg Ile Ser Thr Ala Thr Ala Met Val Ser Thr Ala Leu Ala Thr
150                 155                 160                 165

cgc ccc atc atg cgt ttc aac ggt ggt cgc atg gag atc gcc gct aag   643
Arg Pro Ile Met Arg Phe Asn Gly Gly Arg Met Glu Ile Ala Ala Lys
                170                 175                 180

acc cgc acc caa tct aaa gcg ttt gcc aaa ttg gtg gaa tta gcc cag   691
Thr Arg Thr Gln Ser Lys Ala Phe Ala Lys Leu Val Glu Leu Ala Gln
            185                 190                 195

atc agg gca gat ggt gaa ccc gta ttc att gcg att ggc caa aac       736
Ile Arg Ala Asp Gly Glu Pro Val Phe Ile Ala Ile Gly Gln Asn
        200                 205                 210


<210> 1134
<211> 212
<212> PRT
<213> Corynebacterium glutamicum

<400> 1134
Met Pro Val Arg Val Ile Val Asp Ser Ser Ala Cys Leu Pro Thr His
  1               5                  10                  15

Val Ala Glu Asp Leu Asp Ile Thr Val Ile Asn Leu His Val Met Asn
             20                  25                  30

Asn Gly Glu Glu Arg Ser Thr Ser Gly Leu Ser Ser Leu Glu Leu Ala
         35                  40                  45

Ala Ser Tyr Ala Arg Gln Leu Glu Arg Gly Gly Asp Asp Gly Val Leu
     50                  55                  60

Ala Leu His Ile Ser Lys Glu Leu Ser Ser Thr Trp Ser Ala Ala Val
 65                  70                  75                  80
```

```
Thr Ala Ala Ala Val Phe Asp Asp Asp Ser Val Arg Val Val Asp Thr
                 85                  90                  95

Ser Ser Leu Gly Met Ala Val Gly Ala Ala Ala Met Ala Ala Ala Arg
            100                 105                 110

Met Ala Lys Asp Gly Ala Ser Leu Gln Glu Cys Tyr Asp Ile Ala Val
        115                 120                 125

Asp Thr Leu Lys Arg Ser Glu Thr Trp Ile Tyr Leu His Arg Ile Asp
    130                 135                 140

Glu Ile Trp Lys Ser Gly Arg Ile Ser Thr Ala Thr Ala Met Val Ser
145                 150                 155                 160

Thr Ala Leu Ala Thr Arg Pro Ile Met Arg Phe Asn Gly Gly Arg Met
                165                 170                 175

Glu Ile Ala Ala Lys Thr Arg Thr Gln Ser Lys Ala Phe Ala Lys Leu
            180                 185                 190

Val Glu Leu Ala Gln Ile Arg Ala Asp Gly Glu Pro Val Phe Ile Ala
        195                 200                 205

Ile Gly Gln Asn
    210


<210> 1135
<211> 703
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(703)
<223> FRXA02383

<400> 1135
gggcaacaat gtggaaaacg cccagtggta tcttgacggc tggaacatgg gtgttacgca 60

gtaaagaaga tggcaataaa aatgtggagg agtaaaggcg atg cca gtt cgg gta   115
                                              Met Pro Val Arg Val
                                                1               5

att gtt gat tcc tcc gca tgc ttg cca acg cat gtg gcc gag gac ctc   163
Ile Val Asp Ser Ser Ala Cys Leu Pro Thr His Val Ala Glu Asp Leu
                10                  15                  20

gac atc acg gtg att aac ttg cac gtg atg aat aac ggt gaa gaa cgc   211
Asp Ile Thr Val Ile Asn Leu His Val Met Asn Asn Gly Glu Glu Arg
            25                  30                  35

agt aca tcc ggg ttg tcg tcg ttg gaa ctt gca gca agt tac gcc cgc   259
Ser Thr Ser Gly Leu Ser Ser Leu Glu Leu Ala Ala Ser Tyr Ala Arg
        40                  45                  50

cag ctt gaa cgc ggt ggc gat gac ggt gtg ctt gcg ctg cat att tct   307
Gln Leu Glu Arg Gly Gly Asp Asp Gly Val Leu Ala Leu His Ile Ser
    55                  60                  65
```

```
aaa gag ctc tcg tcc acg tgg tcc gca gcg gtg aca gca gcc gct gtg   355
Lys Glu Leu Ser Ser Thr Trp Ser Ala Ala Val Thr Ala Ala Ala Val
 70                  75                  80                  85

ttt gat gat gat tct gtg cgc gtg gtg gat acc agt tcg ctc ggt atg   403
Phe Asp Asp Asp Ser Val Arg Val Val Asp Thr Ser Ser Leu Gly Met
                 90                  95                 100

gct gtg ggt gct gcc gcg atg gct gct gcc cgc atg gct aaa gat ggc   451
Ala Val Gly Ala Ala Ala Met Ala Ala Ala Arg Met Ala Lys Asp Gly
            105                 110                 115

gcg tct ttg cag gaa tgc tac gac atc gcg gtg gat acc ttg aag cgt   499
Ala Ser Leu Gln Glu Cys Tyr Asp Ile Ala Val Asp Thr Leu Lys Arg
        120                 125                 130

tca gaa acc tgg atc tac ctg cac cgc att gat gaa atc tgg aag tcg   547
Ser Glu Thr Trp Ile Tyr Leu His Arg Ile Asp Glu Ile Trp Lys Ser
    135                 140                 145

gga cgg att tcc act gca acc gcc atg gtg tca acg gct ctg gca acc   595
Gly Arg Ile Ser Thr Ala Thr Ala Met Val Ser Thr Ala Leu Ala Thr
150                 155                 160                 165

cgc ccc atc atg cgt ttc aac ggt ggt cgc atg gag atc gcc gct aag   643
Arg Pro Ile Met Arg Phe Asn Gly Gly Arg Met Glu Ile Ala Ala Lys
                170                 175                 180

acc cgc acc caa tct aaa gcg ttt gcc aaa ttg gtg gaa tta gcc cag   691
Thr Arg Thr Gln Ser Lys Ala Phe Ala Lys Leu Val Glu Leu Ala Gln
            185                 190                 195

atc agg gca gat                                                  703
Ile Arg Ala Asp
        200
```

Sequence Listing.ST25.txt

<210> 1136
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 1136

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Met Pro Val Arg Val Ile Val Asp Ser Ser Ala Cys Leu Pro Thr His
  1               5                  10                  15

Val Ala Glu Asp Leu Asp Ile Thr Val Ile Asn Leu His Val Met Asn
             20                  25                  30

Asn Gly Glu Glu Arg Ser Thr Ser Gly Leu Ser Ser Leu Glu Leu Ala
         35                  40                  45

Ala Ser Tyr Ala Arg Gln Leu Glu Arg Gly Gly Asp Asp Gly Val Leu
     50                  55                  60

Ala Leu His Ile Ser Lys Glu Leu Ser Ser Thr Trp Ser Ala Ala Val
 65                  70                  75                  80

Thr Ala Ala Ala Val Phe Asp Asp Asp Ser Val Arg Val Val Asp Thr
                 85                  90                  95
```

```
Ser Ser Leu Gly Met Ala Val Gly Ala Ala Ala Met Ala Ala Ala Arg
            100                 105                 110

Met Ala Lys Asp Gly Ala Ser Leu Gln Glu Cys Tyr Asp Ile Ala Val
        115                 120                 125

Asp Thr Leu Lys Arg Ser Glu Thr Trp Ile Tyr Leu His Arg Ile Asp
    130                 135                 140

Glu Ile Trp Lys Ser Gly Arg Ile Ser Thr Ala Thr Ala Met Val Ser
145                 150                 155                 160

Thr Ala Leu Ala Thr Arg Pro Ile Met Arg Phe Asn Gly Gly Arg Met
                165                 170                 175

Glu Ile Ala Ala Lys Thr Arg Thr Gln Ser Lys Ala Phe Ala Lys Leu
            180                 185                 190

Val Glu Leu Ala Gln Ile Arg Ala Asp
        195                 200
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<210> 1137
<211> 885
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(862)
<223> RXN02387

<400> 1137

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gctagccccg attcgcttca ggtcaccacc ttgaaggcca gcgaaattac tcagggtgaa 60

ttgttggatg cgttaagccc atccttgttt gctgaagacc gtg tgg tgg tgc tta   115
                                            Val Trp Trp Cys Leu
                                              1               5

cca aca tgg atc aaa gca ggc caa gat gct gta gat cta gcc tta tcc   163
Pro Thr Trp Ile Lys Ala Gly Gln Asp Ala Val Asp Leu Ala Leu Ser
                 10                  15                  20

gca gca gtt gat ccc agc cct ggt acc tac ttg atc gtc atg cac tct   211
Ala Ala Val Asp Pro Ser Pro Gly Thr Tyr Leu Ile Val Met His Ser
             25                  30                  35

ggc ggt gga cgc tct aag tcg atg gtg aag aag ctg gaa aaa gtc gcg   259
Gly Gly Gly Arg Ser Lys Ser Met Val Lys Lys Leu Glu Lys Val Ala
         40                  45                  50

gtg gtg cac gat gcc gca aag ctg aaa gac cgg gat cgt cca ggt tgg   307
Val Val His Asp Ala Ala Lys Leu Lys Asp Arg Asp Arg Pro Gly Trp
     55                  60                  65

gta aaa caa gag ttc aaa aac cac aaa gtc cag gtc acc cca gat gtc   355
Val Lys Gln Glu Phe Lys Asn His Lys Val Gln Val Thr Pro Asp Val
 70                  75                  80                  85

att cat gct ctt tta gag ggc gtg ggt tca gat ctt aga gag ctg gcg   403
Ile His Ala Leu Leu Glu Gly Val Gly Ser Asp Leu Arg Glu Leu Ala
```

```
                 90                  95                 100

tcc gcc gta tcc caa ttg gtt gag gac acc caa ggc aac gtg acg gtg   451
Ser Ala Val Ser Gln Leu Val Glu Asp Thr Gln Gly Asn Val Thr Val
            105                 110                 115

gaa aaa gtc cgt gcc tat tac gtg ggt gtt gct gag gta tcg ggt ttc   499
Glu Lys Val Arg Ala Tyr Tyr Val Gly Val Ala Glu Val Ser Gly Phe
        120                 125                 130

gac atc gcc gat tct gca tgc gcc ggt caa atg tca aag gcc gtg gcc   547
Asp Ile Ala Asp Ser Ala Cys Ala Gly Gln Met Ser Lys Ala Val Ala
    135                 140                 145

agc acc aga cgt gcc ctt caa ttg ggt acc agc ccg gtt gca ttg gca   595
Ser Thr Arg Arg Ala Leu Gln Leu Gly Thr Ser Pro Val Ala Leu Ala
150                 155                 160                 165

gct gcg ttg agt atg aaa gtt ggc cag atc gcc agg ctg tat tcc acc   643
Ala Ala Leu Ser Met Lys Val Gly Gln Ile Ala Arg Leu Tyr Ser Thr
                170                 175                 180

agg gga cgc atc aac ggt ttt gag ctg gcc aaa gaa ttg ggc atg ccg   691
Arg Gly Arg Ile Asn Gly Phe Glu Leu Ala Lys Glu Leu Gly Met Pro
            185                 190                 195

ccg ttc gtg gtg gag aag act gcg aaa gtg gcc cga aac tgg tcg gga   739
Pro Phe Val Val Glu Lys Thr Ala Lys Val Ala Arg Asn Trp Ser Gly
        200                 205                 210

gat gcg gtc agc gag gcc gtg att ttg atg gcc gat ctg gat gcc gct   787
Asp Ala Val Ser Glu Ala Val Ile Leu Met Ala Asp Leu Asp Ala Ala
    215                 220                 225

gta aaa gga caa agt ggc gat cct gaa ttt gcc atc gaa tct gcc gtg   835
Val Lys Gly Gln Ser Gly Asp Pro Glu Phe Ala Ile Glu Ser Ala Val
230                 235                 240                 245

aga aga gtt gca gag ctg gcg agg cgg taacgctgaa cggcggcggg         882
Arg Arg Val Ala Glu Leu Ala Arg Arg
                250

taa                                                              885


<210> 1138
<211> 254
<212> PRT
<213> Corynebacterium glutamicum

<400> 1138
Val Trp Trp Cys Leu Pro Thr Trp Ile Lys Ala Gly Gln Asp Ala Val
  1               5                  10                  15

Asp Leu Ala Leu Ser Ala Ala Val Asp Pro Ser Pro Gly Thr Tyr Leu
             20                  25                  30

Ile Val Met His Ser Gly Gly Gly Arg Ser Lys Ser Met Val Lys Lys
         35                  40                  45

Leu Glu Lys Val Ala Val Val His Asp Ala Ala Lys Leu Lys Asp Arg
```

```
     50                  55                  60

Asp Arg Pro Gly Trp Val Lys Gln Glu Phe Lys Asn His Lys Val Gln
 65                  70                  75                  80

Val Thr Pro Asp Val Ile His Ala Leu Leu Glu Gly Val Gly Ser Asp
                85                  90                  95

Leu Arg Glu Leu Ala Ser Ala Val Ser Gln Leu Val Glu Asp Thr Gln
            100                 105                 110

Gly Asn Val Thr Val Glu Lys Val Arg Ala Tyr Tyr Val Gly Val Ala
        115                 120                 125

Glu Val Ser Gly Phe Asp Ile Ala Asp Ser Ala Cys Ala Gly Gln Met
    130                 135                 140

Ser Lys Ala Val Ala Ser Thr Arg Arg Ala Leu Gln Leu Gly Thr Ser
145                 150                 155                 160

Pro Val Ala Leu Ala Ala Ala Leu Ser Met Lys Val Gly Gln Ile Ala
                165                 170                 175

Arg Leu Tyr Ser Thr Arg Gly Arg Ile Asn Gly Phe Glu Leu Ala Lys
            180                 185                 190

Glu Leu Gly Met Pro Pro Phe Val Val Glu Lys Thr Ala Lys Val Ala
        195                 200                 205

Arg Asn Trp Ser Gly Asp Ala Val Ser Glu Ala Val Ile Leu Met Ala
    210                 215                 220

Asp Leu Asp Ala Ala Val Lys Gly Gln Ser Gly Asp Pro Glu Phe Ala
225                 230                 235                 240

Ile Glu Ser Ala Val Arg Arg Val Ala Glu Leu Ala Arg Arg
                245                 250
```

<210> 1139
<211> 778
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(778)
<223> FRXA02387

<400> 1139
gctagccccg attcgcttca ggtcaccacc ttgaaggcca gcgaaattac tcagggtgaa 60

ttgttggatg cgttaagccc atccttgttt gctgaagacc gtg tgg tgg tgc tta 115
                                              Val Trp Trp Cys Leu
                                                1   5

cca aca tgg atc aaa gca ggc caa gat gct gta gat cta gcc tta tcc 163
Pro Thr Trp Ile Lys Ala Gly Gln Asp Ala Val Asp Leu Ala Leu Ser
                10   15   20

gca gca gtt gat ccc agc cct ggt acc tac ttg atc gtc atg cac tct 211

```
Ala Ala Val Asp Pro Ser Pro Gly Thr Tyr Leu Ile Val Met His Ser
            25                  30                  35

ggc ggt gga cgc tct aag tcg atg gtg aag aag ctg gaa aaa gtc gcg   259
Gly Gly Gly Arg Ser Lys Ser Met Val Lys Lys Leu Glu Lys Val Ala
         40                  45                  50

gtg gtg cac gat gcc gca aag ctg aaa gac cgg gat cgt cca ggt tgg   307
Val Val His Asp Ala Ala Lys Leu Lys Asp Arg Asp Arg Pro Gly Trp
     55                  60                  65

gta aaa caa gag ttc aaa aac cac aaa gtc cag gtc acc cca gat gtc   355
Val Lys Gln Glu Phe Lys Asn His Lys Val Gln Val Thr Pro Asp Val
 70                  75                  80                  85

att cat gct ctt tta gag ggc gtg ggt tca gat ctt aga gag ctg gcg   403
Ile His Ala Leu Leu Glu Gly Val Gly Ser Asp Leu Arg Glu Leu Ala
                 90                  95                 100

tcc gcc gta tcc caa ttg gtt gag gac acc caa ggc aac gtg acg gtg   451
Ser Ala Val Ser Gln Leu Val Glu Asp Thr Gln Gly Asn Val Thr Val
            105                 110                 115

gaa aaa gtc cgt gcc tat tac gtg ggt gtt gct gag gta tcg ggt ttc   499
Glu Lys Val Arg Ala Tyr Tyr Val Gly Val Ala Glu Val Ser Gly Phe
        120                 125                 130

gac atc gcc gat tct gca tgc gcc ggt caa atg tca aag gcc gtg gcc   547
Asp Ile Ala Asp Ser Ala Cys Ala Gly Gln Met Ser Lys Ala Val Ala
    135                 140                 145

agc acc aga cgt gcc ctt caa ttg ggt acc agc ccg gtt gca ttg gca   595
Ser Thr Arg Arg Ala Leu Gln Leu Gly Thr Ser Pro Val Ala Leu Ala
150                 155                 160                 165

gct gcg ttg agt atg aaa gtt ggc cag atc gcc agg ctg tat tcc acc   643
Ala Ala Leu Ser Met Lys Val Gly Gln Ile Ala Arg Leu Tyr Ser Thr
                170                 175                 180

agg gga cgc atc aac ggt ttt gag ctg gcc aaa gaa ttg ggc atg ccg   691
Arg Gly Arg Ile Asn Gly Phe Glu Leu Ala Lys Glu Leu Gly Met Pro
            185                 190                 195

ccg ttc gtg gtg gag aag act gcg aaa gtg gcc cga aac tgg tcg gga   739
Pro Phe Val Val Glu Lys Thr Ala Lys Val Ala Arg Asn Trp Ser Gly
        200                 205                 210

gat gcg gtc agc gag gcc gtg att ttg atg gcc gat ctg               778
Asp Ala Val Ser Glu Ala Val Ile Leu Met Ala Asp Leu
    215                 220                 225


<210> 1140
<211> 226
<212> PRT
<213> Corynebacterium glutamicum

<400> 1140
Val Trp Trp Cys Leu Pro Thr Trp Ile Lys Ala Gly Gln Asp Ala Val
  1               5                  10                  15
```

```
Asp Leu Ala Leu Ser Ala Ala Val Asp Pro Ser Pro Gly Thr Tyr Leu
            20                  25                  30

Ile Val Met His Ser Gly Gly Gly Arg Ser Lys Ser Met Val Lys Lys
        35                  40                  45

Leu Glu Lys Val Ala Val Val His Asp Ala Ala Lys Leu Lys Asp Arg
    50                  55                  60

Asp Arg Pro Gly Trp Val Lys Gln Glu Phe Lys Asn His Lys Val Gln
65                  70                  75                  80

Val Thr Pro Asp Val Ile His Ala Leu Leu Glu Gly Val Gly Ser Asp
                85                  90                  95

Leu Arg Glu Leu Ala Ser Ala Val Ser Gln Leu Val Glu Asp Thr Gln
            100                 105                 110

Gly Asn Val Thr Val Glu Lys Val Arg Ala Tyr Tyr Val Gly Val Ala
        115                 120                 125

Glu Val Ser Gly Phe Asp Ile Ala Asp Ser Ala Cys Ala Gly Gln Met
    130                 135                 140

Ser Lys Ala Val Ala Ser Thr Arg Arg Ala Leu Gln Leu Gly Thr Ser
145                 150                 155                 160

Pro Val Ala Leu Ala Ala Ala Leu Ser Met Lys Val Gly Gln Ile Ala
                165                 170                 175

Arg Leu Tyr Ser Thr Arg Gly Arg Ile Asn Gly Phe Glu Leu Ala Lys
            180                 185                 190

Glu Leu Gly Met Pro Pro Phe Val Val Glu Lys Thr Ala Lys Val Ala
        195                 200                 205

Arg Asn Trp Ser Gly Asp Ala Val Ser Glu Ala Val Ile Leu Met Ala
    210                 215                 220

Asp Leu
225
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<210> 1141
<211> 1725
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1702)
<223> RXN02398

<400> 1141
gtgtccaatg aatgcgttca ataaatgccc tctttaagca tattctctga gtgcattcat 60

tacaggcgtt aattaaatgc gttcatagaa gaacttgaaa gtg gtt gaa gtg aag 115
Val Val Glu Val Lys
1 5

aag cgt aat ctc ctc gta gct ccc ctc act gct tcc ctg gtg ttc tgt 163

```
Lys Arg Asn Leu Leu Val Ala Pro Leu Thr Ala Ser Leu Val Phe Cys
                10                  15                  20

aac ttg gct gtt gca gca aac gcc gtt gaa gtt gag gcc gaa tca cca   211
Asn Leu Ala Val Ala Ala Asn Ala Val Glu Val Glu Ala Glu Ser Pro
            25                  30                  35

gtt gtc atc aat gaa gtt gaa tcc aac agc gac cca gtt ggt gac tgg   259
Val Val Ile Asn Glu Val Glu Ser Asn Ser Asp Pro Val Gly Asp Trp
        40                  45                  50

gtg gag ttg gct aac acc gac aac aac aac tcc atc gac att tcc ggt   307
Val Glu Leu Ala Asn Thr Asp Asn Asn Asn Ser Ile Asp Ile Ser Gly
    55                  60                  65

tgg tcc tta gtc gat gac aag gaa gac ctg gaa aat gcc ctc gtc ctt   355
Trp Ser Leu Val Asp Asp Lys Glu Asp Leu Glu Asn Ala Leu Val Leu
70                  75                  80                  85

cct gaa ggc act gag att gag tcc ggt gga tac ttt gtt atc tac acc   403
Pro Glu Gly Thr Glu Ile Glu Ser Gly Gly Tyr Phe Val Ile Tyr Thr
                90                  95                  100

gac tct gct gat tac gtg cct acc aac aac acc ttt ggt ggc cag gaa   451
Asp Ser Ala Asp Tyr Val Pro Thr Asn Asn Thr Phe Gly Gly Gln Glu
            105                 110                 115

tac ttc ggc ctc ggc aaa gat gac act gtt act ctg cgc aac gct gaa   499
Tyr Phe Gly Leu Gly Lys Asp Asp Thr Val Thr Leu Arg Asn Ala Glu
        120                 125                 130

ggc gaa gta gtt gct acc tat tcc tgg aag gat ctg ggc gag cac gca   547
Gly Glu Val Val Ala Thr Tyr Ser Trp Lys Asp Leu Gly Glu His Ala
    135                 140                 145

gaa aac acc tat ggt cgc atc cca gat atg act ggt gat ttc gca aac   595
Glu Asn Thr Tyr Gly Arg Ile Pro Asp Met Thr Gly Asp Phe Ala Asn
150                 155                 160                 165

acc ggc gtt cca acc cca ggt gca aag aat gtt gct gct gaa ggc tcc   643
Thr Gly Val Pro Thr Pro Gly Ala Lys Asn Val Ala Ala Glu Gly Ser
                170                 175                 180

ggc gaa gaa gaa ggc gtt gtt gca aac gcc cag ctt cca ttc cac aac   691
Gly Glu Glu Glu Gly Val Val Ala Asn Ala Gln Leu Pro Phe His Asn
            185                 190                 195

gtt gaa atc acc cca att cac ctc ggt gga gat ttc acc ggt gaa gat   739
Val Glu Ile Thr Pro Ile His Leu Gly Gly Asp Phe Thr Gly Glu Asp
        200                 205                 210

atg tcc ggc gtt gat ttc gat gca aac agc acc gca tgg atc gcc aac   787
Met Ser Gly Val Asp Phe Asp Ala Asn Ser Thr Ala Trp Ile Ala Asn
    215                 220                 225

aat gac att gga aag atc tac tcc ctc gcc cac gac ata gct aac aac   835
Asn Asp Ile Gly Lys Ile Tyr Ser Leu Ala His Asp Ile Ala Asn Asn
230                 235                 240                 245

acc tac aag ctg act ggc gaa tgg gaa acc ggc tac cca gaa ggc ggc   883
Thr Tyr Lys Leu Thr Gly Glu Trp Glu Thr Gly Tyr Pro Glu Gly Gly
```

```
                  250                 255                 260

gga gag cca gac gct gaa ggc atc gtc gca gct acc aac ggt gac atc   931
Gly Glu Pro Asp Ala Glu Gly Ile Val Ala Ala Thr Asn Gly Asp Ile
            265                 270                 275

tac ctg tcc acc gag cgc aac aac gct gac aag aac gtc tct cgc cca   979
Tyr Leu Ser Thr Glu Arg Asn Asn Ala Asp Lys Asn Val Ser Arg Pro
        280                 285                 290

tcc atc ctg cgt ttt gct acc cca act ggc aag act ggc gta caa aac   1027
Ser Ile Leu Arg Phe Ala Thr Pro Thr Gly Lys Thr Gly Val Gln Asn
    295                 300                 305

gca gtt cag gaa tgg gac ctg tct gag ttc gtc ggc gac att cag ccc   1075
Ala Val Gln Glu Trp Asp Leu Ser Glu Phe Val Gly Asp Ile Gln Pro
310                 315                 320                 325

aat ggt ggt ctt gag gca atc gcg cag ctc gag gac aac atc ttc gtt   1123
Asn Gly Gly Leu Glu Ala Ile Ala Gln Leu Glu Asp Asn Ile Phe Val
                330                 335                 340

gtc ggt gtc gaa gag aca ggt gat gtc atc gtt gtt gat ctt tcc gct   1171
Val Gly Val Glu Glu Thr Gly Asp Val Ile Val Val Asp Leu Ser Ala
            345                 350                 355

gac cag cca gtt ctg gtt caa agg tac gaa tct tcc ttc gac ggt gtc   1219
Asp Gln Pro Val Leu Val Gln Arg Tyr Glu Ser Ser Phe Asp Gly Val
        360                 365                 370

atg tcg ctt gat tac aac gca gca acc aag cag ctc agc gtt gtg tgc   1267
Met Ser Leu Asp Tyr Asn Ala Ala Thr Lys Gln Leu Ser Val Val Cys
    375                 380                 385

gac gaa gca tgt gac ggc ttg tct gaa atc ctc gaa tgg gat ggc gag   1315
Asp Glu Ala Cys Asp Gly Leu Ser Glu Ile Leu Glu Trp Asp Gly Glu
390                 395                 400                 405

aag ctg tac aag tcc gac gac aag atc tac gag cgt cca gca aac ctg   1363
Lys Leu Tyr Lys Ser Asp Asp Lys Ile Tyr Glu Arg Pro Ala Asn Leu
                410                 415                 420

ggc aac tgg gct aac gaa ggc ttc ggc acc tac acc tca gag ctt aaa   1411
Gly Asn Trp Ala Asn Glu Gly Phe Gly Thr Tyr Thr Ser Glu Leu Lys
            425                 430                 435

tgc gag aac ggc aac acc gtt tct gtc acc agc tac ctc tgg gct gac   1459
Cys Glu Asn Gly Asn Thr Val Ser Val Thr Ser Tyr Leu Trp Ala Asp
        440                 445                 450

gat gca gca acc aac gaa ggc acc tcc ctc aac tcc gca cag gtc atc   1507
Asp Ala Ala Thr Asn Glu Gly Thr Ser Leu Asn Ser Ala Gln Val Ile
    455                 460                 465

aac gga gat tgc ggc gac gtc aac atc cct gga gag tcc tct tcc gac   1555
Asn Gly Asp Cys Gly Asp Val Asn Ile Pro Gly Glu Ser Ser Ser Asp
470                 475                 480                 485

aat tcc tct tct gac ttt gca acc ggc agc atc gca ggc gcc ttt gca   1603
Asn Ser Ser Ser Asp Phe Ala Thr Gly Ser Ile Ala Gly Ala Phe Ala
                490                 495                 500
```

```
acc gca gtg ctc gca gtc gta ggc att gcg ggc gca ctg ggt gga ttc   1651
Thr Ala Val Leu Ala Val Val Gly Ile Ala Gly Ala Leu Gly Gly Phe
            505                 510                 515

ttc cag cag atc ctc gca gcg ttc cca gca ttg cag cag gtc atc cgt   1699
Phe Gln Gln Ile Leu Ala Ala Phe Pro Ala Leu Gln Gln Val Ile Arg
        520                 525                 530

ttc taaacccact gcttgaaaca ctt                                     1725
Phe
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<210> 1142
<211> 534
<212> PRT
<213> Corynebacterium glutamicum

<400> 1142

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Val Val Glu Val Lys Lys Arg Asn Leu Leu Val Ala Pro Leu Thr Ala
  1               5                  10                  15

Ser Leu Val Phe Cys Asn Leu Ala Val Ala Ala Asn Ala Val Glu Val
             20                  25                  30

Glu Ala Glu Ser Pro Val Val Ile Asn Glu Val Glu Ser Asn Ser Asp
         35                  40                  45

Pro Val Gly Asp Trp Val Glu Leu Ala Asn Thr Asp Asn Asn Asn Ser
     50                  55                  60

Ile Asp Ile Ser Gly Trp Ser Leu Val Asp Asp Lys Glu Asp Leu Glu
 65                  70                  75                  80

Asn Ala Leu Val Leu Pro Glu Gly Thr Glu Ile Glu Ser Gly Gly Tyr
                 85                  90                  95

Phe Val Ile Tyr Thr Asp Ser Ala Asp Tyr Val Pro Thr Asn Asn Thr
            100                 105                 110

Phe Gly Gly Gln Glu Tyr Phe Gly Leu Gly Lys Asp Asp Thr Val Thr
        115                 120                 125

Leu Arg Asn Ala Glu Gly Glu Val Val Ala Thr Tyr Ser Trp Lys Asp
    130                 135                 140

Leu Gly Glu His Ala Glu Asn Thr Tyr Gly Arg Ile Pro Asp Met Thr
145                 150                 155                 160

Gly Asp Phe Ala Asn Thr Gly Val Pro Thr Pro Gly Ala Lys Asn Val
                165                 170                 175

Ala Ala Glu Gly Ser Gly Glu Glu Glu Gly Val Val Ala Asn Ala Gln
            180                 185                 190

Leu Pro Phe His Asn Val Glu Ile Thr Pro Ile His Leu Gly Gly Asp
        195                 200                 205

Phe Thr Gly Glu Asp Met Ser Gly Val Asp Phe Asp Ala Asn Ser Thr
    210                 215                 220
```

```
Ala Trp Ile Ala Asn Asn Asp Ile Gly Lys Ile Tyr Ser Leu Ala His
225                 230                 235                 240

Asp Ile Ala Asn Asn Thr Tyr Lys Leu Thr Gly Glu Trp Glu Thr Gly
                245                 250                 255

Tyr Pro Glu Gly Gly Gly Glu Pro Asp Ala Glu Gly Ile Val Ala Ala
            260                 265                 270

Thr Asn Gly Asp Ile Tyr Leu Ser Thr Glu Arg Asn Asn Ala Asp Lys
        275                 280                 285

Asn Val Ser Arg Pro Ser Ile Leu Arg Phe Ala Thr Pro Thr Gly Lys
    290                 295                 300

Thr Gly Val Gln Asn Ala Val Gln Glu Trp Asp Leu Ser Glu Phe Val
305                 310                 315                 320

Gly Asp Ile Gln Pro Asn Gly Gly Leu Glu Ala Ile Ala Gln Leu Glu
                325                 330                 335

Asp Asn Ile Phe Val Val Gly Val Glu Glu Thr Gly Asp Val Ile Val
            340                 345                 350

Val Asp Leu Ser Ala Asp Gln Pro Val Leu Val Gln Arg Tyr Glu Ser
        355                 360                 365

Ser Phe Asp Gly Val Met Ser Leu Asp Tyr Asn Ala Ala Thr Lys Gln
    370                 375                 380

Leu Ser Val Val Cys Asp Glu Ala Cys Asp Gly Leu Ser Glu Ile Leu
385                 390                 395                 400

Glu Trp Asp Gly Glu Lys Leu Tyr Lys Ser Asp Asp Lys Ile Tyr Glu
                405                 410                 415

Arg Pro Ala Asn Leu Gly Asn Trp Ala Asn Glu Gly Phe Gly Thr Tyr
            420                 425                 430

Thr Ser Glu Leu Lys Cys Glu Asn Gly Asn Thr Val Ser Val Thr Ser
        435                 440                 445

Tyr Leu Trp Ala Asp Asp Ala Ala Thr Asn Glu Gly Thr Ser Leu Asn
    450                 455                 460

Ser Ala Gln Val Ile Asn Gly Asp Cys Gly Asp Val Asn Ile Pro Gly
465                 470                 475                 480

Glu Ser Ser Ser Asp Asn Ser Ser Ser Asp Phe Ala Thr Gly Ser Ile
                485                 490                 495

Ala Gly Ala Phe Ala Thr Ala Val Leu Ala Val Val Gly Ile Ala Gly
            500                 505                 510

Ala Leu Gly Gly Phe Phe Gln Gln Ile Leu Ala Ala Phe Pro Ala Leu
        515                 520                 525

Gln Gln Val Ile Arg Phe
    530
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<210> 1143
<211> 1630
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1630)
<223> FRXA02398

<400> 1143
gtgtccaatg aatgcgttca ataaatgccc tctttaagca tattctctga gtgcattcat 60

tacaggcgtt aattaaatgc gttcatagaa gaacttgaaa gtg gtt gaa gtg aag 115
Val Val Glu Val Lys
1 5

aag cgt aat ctc ctc gta gct ccc ctc act gct tcc ctg gtg ttc tgt 163
Lys Arg Asn Leu Leu Val Ala Pro Leu Thr Ala Ser Leu Val Phe Cys
10 15 20

aac ttg gct gtt gca gca aac gcc gtt gaa gtt gag gcc gaa tca cca 211
Asn Leu Ala Val Ala Ala Asn Ala Val Glu Val Glu Ala Glu Ser Pro
25 30 35

gtt gtc atc aat gaa gtt gaa tcc aac agc gac cca gtt ggt gac tgg 259
Val Val Ile Asn Glu Val Glu Ser Asn Ser Asp Pro Val Gly Asp Trp
40 45 50

gtg gag ttg gct aac acc gac aac aac aac tcc atc gac att tcc ggt 307
Val Glu Leu Ala Asn Thr Asp Asn Asn Asn Ser Ile Asp Ile Ser Gly
55 60 65

tgg tcc tta gtc gat gac aag gaa gac ctg gaa aat gcc ctc gtc ctt 355
Trp Ser Leu Val Asp Asp Lys Glu Asp Leu Glu Asn Ala Leu Val Leu
70 75 80 85

cct gaa ggc act gag att gag tcc ggt gga tac ttt gtt atc tac acc 403
Pro Glu Gly Thr Glu Ile Glu Ser Gly Gly Tyr Phe Val Ile Tyr Thr
90 95 100

gac tct gct gat tac gtg cct acc aac aac acc ttt ggt ggc cag gaa 451
Asp Ser Ala Asp Tyr Val Pro Thr Asn Asn Thr Phe Gly Gly Gln Glu
105 110 115

tac ttc ggc ctc ggc aaa gat gac act gtt act ctg cgc aac gct gaa 499
Tyr Phe Gly Leu Gly Lys Asp Asp Thr Val Thr Leu Arg Asn Ala Glu
120 125 130

ggc gaa gta gtt gct acc tat tcc tgg aag gat ctg ggc gag cac gca 547
Gly Glu Val Val Ala Thr Tyr Ser Trp Lys Asp Leu Gly Glu His Ala
135 140 145

gaa aac acc tat ggt cgc atc cca gat atg act ggt gat ttc gca aac 595
Glu Asn Thr Tyr Gly Arg Ile Pro Asp Met Thr Gly Asp Phe Ala Asn
150 155 160 165

acc ggc gtt cca acc cca ggt gca aag aat gtt gct gct gaa ggc tcc 643
Thr Gly Val Pro Thr Pro Gly Ala Lys Asn Val Ala Ala Glu Gly Ser
170 175 180

```
ggc gaa gaa gaa ggc gtt gtt gca aac gcc cag ctt cca ttc cac aac   691
Gly Glu Glu Glu Gly Val Val Ala Asn Ala Gln Leu Pro Phe His Asn
            185                 190                 195

gtt gaa atc acc cca att cac ctc ggt gga gat ttc acc ggt gaa gat   739
Val Glu Ile Thr Pro Ile His Leu Gly Gly Asp Phe Thr Gly Glu Asp
        200                 205                 210

atg tcc ggc gtt gat ttc gat gca aac agc acc gca tgg atc gcc aac   787
Met Ser Gly Val Asp Phe Asp Ala Asn Ser Thr Ala Trp Ile Ala Asn
    215                 220                 225

aat gac att gga aag atc tac tcc ctc gcc cac gac ata gct aac aac   835
Asn Asp Ile Gly Lys Ile Tyr Ser Leu Ala His Asp Ile Ala Asn Asn
230                 235                 240                 245

acc tac aag ctg act ggc gaa tgg gaa acc ggc tac cca gaa ggc ggc   883
Thr Tyr Lys Leu Thr Gly Glu Trp Glu Thr Gly Tyr Pro Glu Gly Gly
                250                 255                 260

gga gag cca gac gct gaa ggc atc gtc gca gct acc aac ggt gac atc   931
Gly Glu Pro Asp Ala Glu Gly Ile Val Ala Ala Thr Asn Gly Asp Ile
            265                 270                 275

tac ctg tcc acc gag cgc aac aac gct gac aag aac gtc tct cgc cca   979
Tyr Leu Ser Thr Glu Arg Asn Asn Ala Asp Lys Asn Val Ser Arg Pro
        280                 285                 290

tcc atc ctg cgt ttt gct acc cca act ggc aag act ggc gta caa aac   1027
Ser Ile Leu Arg Phe Ala Thr Pro Thr Gly Lys Thr Gly Val Gln Asn
    295                 300                 305

gca gtt cag gaa tgg gac ctg tct gag ttc gtc ggc gac att cag ccc   1075
Ala Val Gln Glu Trp Asp Leu Ser Glu Phe Val Gly Asp Ile Gln Pro
310                 315                 320                 325

aat ggt ggt ctt gag gca atc gcg cag ctc gag gac aac atc ttc gtt   1123
Asn Gly Gly Leu Glu Ala Ile Ala Gln Leu Glu Asp Asn Ile Phe Val
                330                 335                 340

gtc ggt gtc gaa gag aca ggt gat gtc atc gtt gtt gat ctt tcc gct   1171
Val Gly Val Glu Glu Thr Gly Asp Val Ile Val Val Asp Leu Ser Ala
            345                 350                 355

gac cag cca gtt ctg gtt caa agg tac gaa tct tcc ttc gac ggt gtc   1219
Asp Gln Pro Val Leu Val Gln Arg Tyr Glu Ser Ser Phe Asp Gly Val
        360                 365                 370

atg tcg ctt gat tac aac gca gca acc aag cag ctc agc gtt gtg tgc   1267
Met Ser Leu Asp Tyr Asn Ala Ala Thr Lys Gln Leu Ser Val Val Cys
    375                 380                 385

gac gaa gca tgt gac ggc ttg tct gaa atc ctc gaa tgg gat ggc gag   1315
Asp Glu Ala Cys Asp Gly Leu Ser Glu Ile Leu Glu Trp Asp Gly Glu
390                 395                 400                 405

aag ctg tac aag tcc gac gac aag atc tac gag cgt cca gca aac ctg   1363
Lys Leu Tyr Lys Ser Asp Asp Lys Ile Tyr Glu Arg Pro Ala Asn Leu
                410                 415                 420
```

```
ggc aac tgg gct aac gaa ggc ttc ggc acc tac acc tca gag ctt aaa   1411
Gly Asn Trp Ala Asn Glu Gly Phe Gly Thr Tyr Thr Ser Glu Leu Lys
            425                 430                 435

tgc gag aac ggc aac acc gtt tct gtc acc agc tac ctc tgg gct gac   1459
Cys Glu Asn Gly Asn Thr Val Ser Val Thr Ser Tyr Leu Trp Ala Asp
        440                 445                 450

gat gca gca acc aac gaa ggc acc tcc ctc aac tcc gca cag gtc atc   1507
Asp Ala Ala Thr Asn Glu Gly Thr Ser Leu Asn Ser Ala Gln Val Ile
    455                 460                 465

aac gga gat tgc ggc gac gtc aac atc cct gga gag tcc tct tcc gac   1555
Asn Gly Asp Cys Gly Asp Val Asn Ile Pro Gly Glu Ser Ser Ser Asp
470                 475                 480                 485

aat tcc tct tct gac ttt gca acc ggc agc atc gca ggc gcc ttt gca   1603
Asn Ser Ser Ser Asp Phe Ala Thr Gly Ser Ile Ala Gly Ala Phe Ala
                490                 495                 500

acc gca gtg ctc gca gtc gta ggc att                              1630
Thr Ala Val Leu Ala Val Val Gly Ile
            505                 510
```

<210> 1144
<211> 510
<212> PRT
<213> Corynebacterium glutamicum

<400> 1144

```
Val Val Glu Val Lys Lys Arg Asn Leu Leu Val Ala Pro Leu Thr Ala
  1               5                  10                  15

Ser Leu Val Phe Cys Asn Leu Ala Val Ala Ala Asn Ala Val Glu Val
             20                  25                  30

Glu Ala Glu Ser Pro Val Val Ile Asn Glu Val Glu Ser Asn Ser Asp
         35                  40                  45

Pro Val Gly Asp Trp Val Glu Leu Ala Asn Thr Asp Asn Asn Asn Ser
     50                  55                  60

Ile Asp Ile Ser Gly Trp Ser Leu Val Asp Asp Lys Glu Asp Leu Glu
 65                  70                  75                  80

Asn Ala Leu Val Leu Pro Glu Gly Thr Glu Ile Glu Ser Gly Gly Tyr
                 85                  90                  95

Phe Val Ile Tyr Thr Asp Ser Ala Asp Tyr Val Pro Thr Asn Asn Thr
            100                 105                 110

Phe Gly Gly Gln Glu Tyr Phe Gly Leu Gly Lys Asp Asp Thr Val Thr
        115                 120                 125

Leu Arg Asn Ala Glu Gly Glu Val Val Ala Thr Tyr Ser Trp Lys Asp
    130                 135                 140

Leu Gly Glu His Ala Glu Asn Thr Tyr Gly Arg Ile Pro Asp Met Thr
145                 150                 155                 160
```

```
Gly Asp Phe Ala Asn Thr Gly Val Pro Thr Pro Gly Ala Lys Asn Val
                165                 170                 175

Ala Ala Glu Gly Ser Gly Glu Glu Glu Gly Val Val Ala Asn Ala Gln
            180                 185                 190

Leu Pro Phe His Asn Val Glu Ile Thr Pro Ile His Leu Gly Gly Asp
        195                 200                 205

Phe Thr Gly Glu Asp Met Ser Gly Val Asp Phe Asp Ala Asn Ser Thr
    210                 215                 220

Ala Trp Ile Ala Asn Asn Asp Ile Gly Lys Ile Tyr Ser Leu Ala His
225                 230                 235                 240

Asp Ile Ala Asn Asn Thr Tyr Lys Leu Thr Gly Glu Trp Glu Thr Gly
                245                 250                 255

Tyr Pro Glu Gly Gly Gly Glu Pro Asp Ala Glu Gly Ile Val Ala Ala
            260                 265                 270

Thr Asn Gly Asp Ile Tyr Leu Ser Thr Glu Arg Asn Asn Ala Asp Lys
        275                 280                 285

Asn Val Ser Arg Pro Ser Ile Leu Arg Phe Ala Thr Pro Thr Gly Lys
    290                 295                 300

Thr Gly Val Gln Asn Ala Val Gln Glu Trp Asp Leu Ser Glu Phe Val
305                 310                 315                 320

Gly Asp Ile Gln Pro Asn Gly Gly Leu Glu Ala Ile Ala Gln Leu Glu
                325                 330                 335

Asp Asn Ile Phe Val Val Gly Val Glu Glu Thr Gly Asp Val Ile Val
            340                 345                 350

Val Asp Leu Ser Ala Asp Gln Pro Val Leu Val Gln Arg Tyr Glu Ser
        355                 360                 365

Ser Phe Asp Gly Val Met Ser Leu Asp Tyr Asn Ala Ala Thr Lys Gln
    370                 375                 380

Leu Ser Val Val Cys Asp Glu Ala Cys Asp Gly Leu Ser Glu Ile Leu
385                 390                 395                 400

Glu Trp Asp Gly Glu Lys Leu Tyr Lys Ser Asp Asp Lys Ile Tyr Glu
                405                 410                 415

Arg Pro Ala Asn Leu Gly Asn Trp Ala Asn Glu Gly Phe Gly Thr Tyr
            420                 425                 430

Thr Ser Glu Leu Lys Cys Glu Asn Gly Asn Thr Val Ser Val Thr Ser
        435                 440                 445

Tyr Leu Trp Ala Asp Asp Ala Ala Thr Asn Glu Gly Thr Ser Leu Asn
    450                 455                 460

Ser Ala Gln Val Ile Asn Gly Asp Cys Gly Asp Val Asn Ile Pro Gly
465                 470                 475                 480

Glu Ser Ser Ser Asp Asn Ser Ser Ser Asp Phe Ala Thr Gly Ser Ile
```

```
                485                 490                 495

Ala Gly Ala Phe Ala Thr Ala Val Leu Ala Val Val Gly Ile
            500                 505                 510


<210> 1145
<211> 672
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(649)
<223> RXN02406

<400> 1145
cactctgata gccttttctc tgaaattgta ccgagcattt gattttgttc ccctatcaat 60

gctggttttg gtgacaaaaa ctcggcggaa ggaccaccga atg gaa acc ctt gca   115
                                              Met Glu Thr Leu Ala
                                                1               5

gca caa gcg cgc acc ctg cta gaa aaa tgg ggc gtc gcg ccg acg cac   163
Ala Gln Ala Arg Thr Leu Leu Glu Lys Trp Gly Val Ala Pro Thr His
                10                  15                  20

gca tct ttc gtc gaa tcc att gca aag gcc atc ccg att ctg tcg atc   211
Ala Ser Phe Val Glu Ser Ile Ala Lys Ala Ile Pro Ile Leu Ser Ile
            25                  30                  35

ctg ctg acg ctg att gtc acc gtg aat gga att tca agc gga aat ccg   259
Leu Leu Thr Leu Ile Val Thr Val Asn Gly Ile Ser Ser Gly Asn Pro
        40                  45                  50

gtc cag cca cca gca ctg gaa cag gta cgg acc gat gta gtg aac aag   307
Val Gln Pro Pro Ala Leu Glu Gln Val Arg Thr Asp Val Val Asn Lys
    55                  60                  65

atc aac tac gaa cgc aac cta aag ggc ctc gtc tcg atc agc ccg gag   355
Ile Asn Tyr Glu Arg Asn Leu Lys Gly Leu Val Ser Ile Ser Pro Glu
70                  75                  80                  85

ctt gaa tta cac acg gca gcc caa aca att gcg cag cga aat gca gac   403
Leu Glu Leu His Thr Ala Ala Gln Thr Ile Ala Gln Arg Asn Ala Asp
                90                  95                 100

tca gat tcc gaa gaa aaa gta ccg gat cca gag ggc aac ctg gtg gtt   451
Ser Asp Ser Glu Glu Lys Val Pro Asp Pro Glu Gly Asn Leu Val Val
            105                 110                 115

ctg caa cag aat ctg ccc tat gca aat gcc aac gcc gat acc atc gtt   499
Leu Gln Gln Asn Leu Pro Tyr Ala Asn Ala Asn Ala Asp Thr Ile Val
        120                 125                 130

gat cgg ttc tta aac tct cct gat cat gtc aaa cta ctg ctt gca aac   547
Asp Arg Phe Leu Asn Ser Pro Asp His Val Lys Leu Leu Leu Ala Asn
    135                 140                 145

gat tat gaa gcc atc gga gtt ggt gtg gcc tac aag ggt gat cat gcg   595
Asp Tyr Glu Ala Ile Gly Val Gly Val Ala Tyr Lys Gly Asp His Ala
```

```
150                 155                 160                 165

tgg ata gtg gtg gag ttc act gta gct ccc gct gat tcc gta gaa tca   643
Trp Ile Val Val Glu Phe Thr Val Ala Pro Ala Asp Ser Val Glu Ser
                170                 175                 180

aca gag tgaataccaa tccgtctgaa ttc                                 672
Thr Glu
```

<210> 1146
<211> 183
<212> PRT
<213> Corynebacterium glutamicum

<400> 1146

```
Met Glu Thr Leu Ala Ala Gln Ala Arg Thr Leu Leu Glu Lys Trp Gly
  1               5                  10                  15

Val Ala Pro Thr His Ala Ser Phe Val Glu Ser Ile Ala Lys Ala Ile
             20                  25                  30

Pro Ile Leu Ser Ile Leu Leu Thr Leu Ile Val Thr Val Asn Gly Ile
         35                  40                  45

Ser Ser Gly Asn Pro Val Gln Pro Pro Ala Leu Glu Gln Val Arg Thr
     50                  55                  60

Asp Val Val Asn Lys Ile Asn Tyr Glu Arg Asn Leu Lys Gly Leu Val
 65                  70                  75                  80

Ser Ile Ser Pro Glu Leu Glu Leu His Thr Ala Ala Gln Thr Ile Ala
                 85                  90                  95

Gln Arg Asn Ala Asp Ser Asp Ser Glu Glu Lys Val Pro Asp Pro Glu
            100                 105                 110

Gly Asn Leu Val Val Leu Gln Gln Asn Leu Pro Tyr Ala Asn Ala Asn
        115                 120                 125

Ala Asp Thr Ile Val Asp Arg Phe Leu Asn Ser Pro Asp His Val Lys
    130                 135                 140

Leu Leu Leu Ala Asn Asp Tyr Glu Ala Ile Gly Val Gly Val Ala Tyr
145                 150                 155                 160

Lys Gly Asp His Ala Trp Ile Val Val Glu Phe Thr Val Ala Pro Ala
                165                 170                 175

Asp Ser Val Glu Ser Thr Glu
            180
```

<210> 1147
<211> 672
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(649)
<223> FRXA02406

<400> 1147
cactctgata gccttttctc tgaaattgta ccgagcattt gattttgttc ccctatcaat 60

gctggttttg gtgacaaaaa ctcggcggaa ggaccaccga atg gaa acc ctt gca 115
Met Glu Thr Leu Ala
1 5

gca caa gcg cgc acc ctg cta gaa aaa tgg ggc gtc gcg ccg acg cac 163
Ala Gln Ala Arg Thr Leu Leu Glu Lys Trp Gly Val Ala Pro Thr His
10 15 20

gca tct ttc gtc gaa tcc att gca aag gcc atc ccg att ctg tcg atc 211
Ala Ser Phe Val Glu Ser Ile Ala Lys Ala Ile Pro Ile Leu Ser Ile
25 30 35

ctg ctg acg ctg att gtc acc gtg aat gga att tca agc gga aat ccg 259
Leu Leu Thr Leu Ile Val Thr Val Asn Gly Ile Ser Ser Gly Asn Pro
40 45 50

gtc cag cca cca gca ctg gaa cag gta cgg acc gat gta gtg aac aag 307
Val Gln Pro Pro Ala Leu Glu Gln Val Arg Thr Asp Val Val Asn Lys
55 60 65

atc aac tac gaa cgc aac cta aag ggc ctc gtc tcg atc agc ccg gag 355
Ile Asn Tyr Glu Arg Asn Leu Lys Gly Leu Val Ser Ile Ser Pro Glu
70 75 80 85

ctt gaa tta cac acg gca gcc caa aca att gcg cag cga aat gca gac 403
Leu Glu Leu His Thr Ala Ala Gln Thr Ile Ala Gln Arg Asn Ala Asp
90 95 100

tca gat tcc gaa gaa aaa gta ccg gat cca gag gga acc ttg gtg gtt 451
Ser Asp Ser Glu Glu Lys Val Pro Asp Pro Glu Gly Thr Leu Val Val
105 110 115

ctg caa cag aat ctg ccc tat gca aat gcc aac gcc gat acc atc gtt 499
Leu Gln Gln Asn Leu Pro Tyr Ala Asn Ala Asn Ala Asp Thr Ile Val
120 125 130

gat cgg ttc tta aac tct cct gat cat gtc aaa cta ctg ctt gca aac 547
Asp Arg Phe Leu Asn Ser Pro Asp His Val Lys Leu Leu Leu Ala Asn
135 140 145

gat tat gaa gcc atc gga gtt ggt gtg gcc tac aag ggt gat cat gcg 595
Asp Tyr Glu Ala Ile Gly Val Gly Val Ala Tyr Lys Gly Asp His Ala
150 155 160 165

tgg ata gtg gtg gag ttc act gta gct ccc gct gat tcc gta gaa tca 643
Trp Ile Val Val Glu Phe Thr Val Ala Pro Ala Asp Ser Val Glu Ser
170 175 180

aca gag tgaataccaa tccgtctgaa ttc 672
Thr Glu

<210> 1148
<211> 183

<212> PRT
<213> Corynebacterium glutamicum

<400> 1148

```
Met Glu Thr Leu Ala Ala Gln Ala Arg Thr Leu Leu Glu Lys Trp Gly
  1               5                  10                  15

Val Ala Pro Thr His Ala Ser Phe Val Glu Ser Ile Ala Lys Ala Ile
             20                  25                  30

Pro Ile Leu Ser Ile Leu Leu Thr Leu Ile Val Thr Val Asn Gly Ile
         35                  40                  45

Ser Ser Gly Asn Pro Val Gln Pro Pro Ala Leu Glu Gln Val Arg Thr
     50                  55                  60

Asp Val Val Asn Lys Ile Asn Tyr Glu Arg Asn Leu Lys Gly Leu Val
 65                  70                  75                  80

Ser Ile Ser Pro Glu Leu Glu Leu His Thr Ala Ala Gln Thr Ile Ala
                 85                  90                  95

Gln Arg Asn Ala Asp Ser Asp Ser Glu Glu Lys Val Pro Asp Pro Glu
            100                 105                 110

Gly Thr Leu Val Val Leu Gln Gln Asn Leu Pro Tyr Ala Asn Ala Asn
        115                 120                 125

Ala Asp Thr Ile Val Asp Arg Phe Leu Asn Ser Pro Asp His Val Lys
    130                 135                 140

Leu Leu Leu Ala Asn Asp Tyr Glu Ala Ile Gly Val Gly Val Ala Tyr
145                 150                 155                 160

Lys Gly Asp His Ala Trp Ile Val Val Glu Phe Thr Val Ala Pro Ala
                165                 170                 175

Asp Ser Val Glu Ser Thr Glu
            180
```

<210> 1149
<211> 495
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(472)
<223> RXN02407

<400> 1149

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ggataaaaat ttggatgaca tatcacctaa gcttgcaatt tctactggaa tagcgcgact 60

actctgcacc aacgcatagt tgttgactag gctatttgtc atg aat agg caa aac   115
                                               Met Asn Arg Gln Asn
                                                 1               5

caa ctt cac tac ccg cag gaa gtg aag gca gtg gaa agt gtg gaa tca   163
Gln Leu His Tyr Pro Gln Glu Val Lys Ala Val Glu Ser Val Glu Ser
                10                  15                  20
```

```
agc ttg aac atg tcg tca cct tct gca ccg ctt gcc acg cca gat gtt   211
Ser Leu Asn Met Ser Ser Pro Ser Ala Pro Leu Ala Thr Pro Asp Val
            25                  30                  35

gag ctt gat gtg cac acg ttg tcg agc gaa aac ctg cct tgg ttg tgc   259
Glu Leu Asp Val His Thr Leu Ser Ser Glu Asn Leu Pro Trp Leu Cys
        40                  45                  50

atc gtg tgg gat gat ccg gtc aat ttg atg agc tat gtc acc tac gtt   307
Ile Val Trp Asp Asp Pro Val Asn Leu Met Ser Tyr Val Thr Tyr Val
    55                  60                  65

ttt cag act gtg ttg ggc ttc agt aag aag agg gcc act gag ctg atg   355
Phe Gln Thr Val Leu Gly Phe Ser Lys Lys Arg Ala Thr Glu Leu Met
70                  75                  80                  85

atg cag gtg cac acc gaa ggt aaa gcc gtg gtg agt tct ggc gag aag   403
Met Gln Val His Thr Glu Gly Lys Ala Val Val Ser Ser Gly Glu Lys
                90                  95                  100

gac aaa gtg gag ggt gat gtg aag aaa ctc cac acc gca ggg ctg tgg   451
Asp Lys Val Glu Gly Asp Val Lys Lys Leu His Thr Ala Gly Leu Trp
            105                 110                 115

gcg aca atg cag cag gca ggg taggggagaa ttttcatgca gca            495
Ala Thr Met Gln Gln Ala Gly
        120
```

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<210> 1150
<211> 124
<212> PRT
<213> Corynebacterium glutamicum

<400> 1150

```
Met Asn Arg Gln Asn Gln Leu His Tyr Pro Gln Glu Val Lys Ala Val
  1               5                  10                  15

Glu Ser Val Glu Ser Ser Leu Asn Met Ser Ser Pro Ser Ala Pro Leu
            20                  25                  30

Ala Thr Pro Asp Val Glu Leu Asp Val His Thr Leu Ser Ser Glu Asn
        35                  40                  45

Leu Pro Trp Leu Cys Ile Val Trp Asp Asp Pro Val Asn Leu Met Ser
    50                  55                  60

Tyr Val Thr Tyr Val Phe Gln Thr Val Leu Gly Phe Ser Lys Lys Arg
65                  70                  75                  80

Ala Thr Glu Leu Met Met Gln Val His Thr Glu Gly Lys Ala Val Val
                85                  90                  95

Ser Ser Gly Glu Lys Asp Lys Val Glu Gly Asp Val Lys Lys Leu His
            100                 105                 110

Thr Ala Gly Leu Trp Ala Thr Met Gln Gln Ala Gly
        115                 120
```

<210> 1151
<211> 406
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(406)
<223> FRXA02407

<400> 1151
ggataaaaat ttggatgaca tatcacctaa gcttgcaatt tctactggaa tagcgcgact 60

actctgcacc aacgcatagt tgttgactag gctatttgtc atg aat agg caa aac 115
Met Asn Arg Gln Asn
1 5

caa ctt cac tac ccg cag gaa gtg aag gca gtg gaa agt gtg gaa tca 163
Gln Leu His Tyr Pro Gln Glu Val Lys Ala Val Glu Ser Val Glu Ser
10 15 20

agc ttg aac atg tcg tca cct tct gca ccg ctt gcc acg cca gat gtt 211
Ser Leu Asn Met Ser Ser Pro Ser Ala Pro Leu Ala Thr Pro Asp Val
25 30 35

gag ctt gat gtg cac acg ttg tcg agc gaa aac ctg cct tgg ttg tgc 259
Glu Leu Asp Val His Thr Leu Ser Ser Glu Asn Leu Pro Trp Leu Cys
40 45 50

atc gtg tgg gat gat ccg gtc aat ttg atg agc tat gtc acc tac gtt 307
Ile Val Trp Asp Asp Pro Val Asn Leu Met Ser Tyr Val Thr Tyr Val
55 60 65

ttt cag act gtg ttg ggc ttc agt aag aag agg gcc act gag ctg atg 355
Phe Gln Thr Val Leu Gly Phe Ser Lys Lys Arg Ala Thr Glu Leu Met
70 75 80 85

atg cag gtg cac acc gaa ggt aaa gcc gtg gtg agt tct ggc gag aag 403
Met Gln Val His Thr Glu Gly Lys Ala Val Val Ser Ser Gly Glu Lys
90 95 100

gac 406
Asp

<210> 1152
<211> 102
<212> PRT
<213> Corynebacterium glutamicum

<400> 1152
Met Asn Arg Gln Asn Gln Leu His Tyr Pro Gln Glu Val Lys Ala Val
1 5 10 15

Glu Ser Val Glu Ser Ser Leu Asn Met Ser Ser Pro Ser Ala Pro Leu
20 25 30

Ala Thr Pro Asp Val Glu Leu Asp Val His Thr Leu Ser Ser Glu Asn
35 40 45

```
Leu Pro Trp Leu Cys Ile Val Trp Asp Asp Pro Val Asn Leu Met Ser
     50                  55                  60

Tyr Val Thr Tyr Val Phe Gln Thr Val Leu Gly Phe Ser Lys Lys Arg
 65                  70                  75                  80

Ala Thr Glu Leu Met Met Gln Val His Thr Glu Gly Lys Ala Val Val
                 85                  90                  95

Ser Ser Gly Glu Lys Asp
            100


<210> 1153
<211> 1035
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1012)
<223> RXN02408

<400> 1153
gtgatgtacg cggcggggaa gccgccgagg aagaccgcga aaacctcgtg cagtggcttg 60

cctacaatca agagtccttg ctggaagcga tgatgaatta atg ctt atc gac gtc   115
                                        Met Leu Ile Asp Val
                                          1               5

gcg ggc ttc ctt tta ggc cac gtc acg aag ggg gat acg ggt tgc tca   163
Ala Gly Phe Leu Leu Gly His Val Thr Lys Gly Asp Thr Gly Cys Ser
                 10                  15                  20

gtg gtc att gca cct aac ggt gca ttt gcg ggc gtc gat gtc cgt ggg   211
Val Val Ile Ala Pro Asn Gly Ala Phe Ala Gly Val Asp Val Arg Gly
             25                  30                  35

gga ggc cca ggc acc agg gaa acc gac ctt cta gaa cca cac aat tct   259
Gly Gly Pro Gly Thr Arg Glu Thr Asp Leu Leu Glu Pro His Asn Ser
         40                  45                  50

gtg cag caa gca cat gcc gtg gtg ttg tgt ggc ggt tcg gcg ttc ggg   307
Val Gln Gln Ala His Ala Val Val Leu Cys Gly Gly Ser Ala Phe Gly
     55                  60                  65

ttg gct gct gcc gat gga gtg atg aca gcc cta gaa aac cgc ggt att   355
Leu Ala Ala Ala Asp Gly Val Met Thr Ala Leu Glu Asn Arg Gly Ile
 70                  75                  80                  85

ggt ttc cct gtc cgt ccc gaa ggg cct atc gtg cca atc gtt cca ggc   403
Gly Phe Pro Val Arg Pro Glu Gly Pro Ile Val Pro Ile Val Pro Gly
                 90                  95                 100

gct gtg att ttt gat ttg ttg gtg ggc gat ccc aaa aac agg ccc acg   451
Ala Val Ile Phe Asp Leu Leu Val Gly Asp Pro Lys Asn Arg Pro Thr
            105                 110                 115

gca gct gat ggg gaa caa gca gtt gaa aac gct ttc gct ggt aca cac   499
Ala Ala Asp Gly Glu Gln Ala Val Glu Asn Ala Phe Ala Gly Thr His
        120                 125                 130
```

```
aac ggt tcg ggc agc gtc ggt gca gga acg ggt gct aca gca ggt cgg   547
Asn Gly Ser Gly Ser Val Gly Ala Gly Thr Gly Ala Thr Ala Gly Arg
    135                 140                 145

ctg cgt ggc ggt ttt ggc caa agc tcg cgc cgg gtc gga aag tac acc   595
Leu Arg Gly Gly Phe Gly Gln Ser Ser Arg Arg Val Gly Lys Tyr Thr
150                 155                 160                 165

atc gcg gca ggg gtc gtg gcg aat cct gtt ggg gaa gtc gtg gac cta   643
Ile Ala Ala Gly Val Val Ala Asn Pro Val Gly Glu Val Val Asp Leu
                170                 175                 180

aca act gga gct ttg ttt ggt agg ccc gaa gtg atg ggg gtg ggc gtc   691
Thr Thr Gly Ala Leu Phe Gly Arg Pro Glu Val Met Gly Val Gly Val
            185                 190                 195

gat aag cta aaa agc gcg gca gag acg ctg aac acg acc atc ggc gtc   739
Asp Lys Leu Lys Ser Ala Ala Glu Thr Leu Asn Thr Thr Ile Gly Val
        200                 205                 210

gtg gca act gac gcg ccg gtg aca aaa gcc caa gcg aag cgc ttg gcg   787
Val Ala Thr Asp Ala Pro Val Thr Lys Ala Gln Ala Lys Arg Leu Ala
    215                 220                 225

ctg gtg gcc cat gat ggt ttg gcg agg gca gtg cgg ccg tcg cat tca   835
Leu Val Ala His Asp Gly Leu Ala Arg Ala Val Arg Pro Ser His Ser
230                 235                 240                 245

ccg atg gac ggt gac aca ttt ttc gcc atg tca tcg ggt gat ggt agt   883
Pro Met Asp Gly Asp Thr Phe Phe Ala Met Ser Ser Gly Asp Gly Ser
                250                 255                 260

ggc gtt acc ccg gtt gag ctg gcg gaa ttg tcg gct cat gct gca gat   931
Gly Val Thr Pro Val Glu Leu Ala Glu Leu Ser Ala His Ala Ala Asp
            265                 270                 275

tgc gta cag gac gct atc atc gac gcc ata ctt acc gcg agt ccg gga   979
Cys Val Gln Asp Ala Ile Ile Asp Ala Ile Leu Thr Ala Ser Pro Gly
        280                 285                 290

ctc ggg ctc aaa agc ttc agg gaa ctt tta cca tgagttacaa cagcccgtat 1032
Leu Gly Leu Lys Ser Phe Arg Glu Leu Leu Pro
    295                 300

aac                                                               1035
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<210> 1154
<211> 304
<212> PRT
<213> Corynebacterium glutamicum

<400> 1154

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Met Leu Ile Asp Val Ala Gly Phe Leu Leu Gly His Val Thr Lys Gly
  1               5                  10                  15

Asp Thr Gly Cys Ser Val Val Ile Ala Pro Asn Gly Ala Phe Ala Gly
             20                  25                  30

Val Asp Val Arg Gly Gly Gly Pro Gly Thr Arg Glu Thr Asp Leu Leu
```

```
         35                  40                  45

Glu Pro His Asn Ser Val Gln Gln Ala His Ala Val Val Leu Cys Gly
     50                  55                  60

Gly Ser Ala Phe Gly Leu Ala Ala Ala Asp Gly Val Met Thr Ala Leu
 65                  70                  75                  80

Glu Asn Arg Gly Ile Gly Phe Pro Val Arg Pro Glu Gly Pro Ile Val
                 85                  90                  95

Pro Ile Val Pro Gly Ala Val Ile Phe Asp Leu Leu Val Gly Asp Pro
            100                 105                 110

Lys Asn Arg Pro Thr Ala Ala Asp Gly Glu Gln Ala Val Glu Asn Ala
        115                 120                 125

Phe Ala Gly Thr His Asn Gly Ser Gly Ser Val Gly Ala Gly Thr Gly
    130                 135                 140

Ala Thr Ala Gly Arg Leu Arg Gly Gly Phe Gly Gln Ser Ser Arg Arg
145                 150                 155                 160

Val Gly Lys Tyr Thr Ile Ala Ala Gly Val Val Ala Asn Pro Val Gly
                165                 170                 175

Glu Val Val Asp Leu Thr Thr Gly Ala Leu Phe Gly Arg Pro Glu Val
            180                 185                 190

Met Gly Val Gly Val Asp Lys Leu Lys Ser Ala Ala Glu Thr Leu Asn
        195                 200                 205

Thr Thr Ile Gly Val Val Ala Thr Asp Ala Pro Val Thr Lys Ala Gln
    210                 215                 220

Ala Lys Arg Leu Ala Leu Val Ala His Asp Gly Leu Ala Arg Ala Val
225                 230                 235                 240

Arg Pro Ser His Ser Pro Met Asp Gly Asp Thr Phe Phe Ala Met Ser
                245                 250                 255

Ser Gly Asp Gly Ser Gly Val Thr Pro Val Glu Leu Ala Glu Leu Ser
            260                 265                 270

Ala His Ala Ala Asp Cys Val Gln Asp Ala Ile Ile Asp Ala Ile Leu
        275                 280                 285

Thr Ala Ser Pro Gly Leu Gly Leu Lys Ser Phe Arg Glu Leu Leu Pro
    290                 295                 300
```

<210> 1155
<211> 928
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(928)
<223> FRXA02408

<400> 1155
gtgatgtacg cggcggggaa gccgccgagg aagaccgcga aaacctcgtg cagtggcttg 60

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cctacaatca agagtccttg ctggaagcga tgatgaatta atg ctt atc gac gtc   115
                                          Met Leu Ile Asp Val
                                            1               5

gcg ggc ttc ctt tta ggc cac gtc acg aag ggg gat acg ggt tgc tca   163
Ala Gly Phe Leu Leu Gly His Val Thr Lys Gly Asp Thr Gly Cys Ser
                10                  15                  20

gtg gtc att gca cct aac ggt gca ttt gcg ggc gtc gat gtc cgt ggg   211
Val Val Ile Ala Pro Asn Gly Ala Phe Ala Gly Val Asp Val Arg Gly
            25                  30                  35

gga ggc cca ggc acc agg gaa acc gac ctt cta gaa cca cac aat tct   259
Gly Gly Pro Gly Thr Arg Glu Thr Asp Leu Leu Glu Pro His Asn Ser
        40                  45                  50

gtg cag caa gca cat gcc gtg gtg ttg tgt ggc ggt tcg gcg ttc ggg   307
Val Gln Gln Ala His Ala Val Val Leu Cys Gly Gly Ser Ala Phe Gly
    55                  60                  65

ttg gct gct gcc gat gga gtg atg aca gcc cta gaa aac cgc ggt att   355
Leu Ala Ala Ala Asp Gly Val Met Thr Ala Leu Glu Asn Arg Gly Ile
70                  75                  80                  85

ggt ttc cct gtc cgt ccc gaa ggg cct atc gtg cca atc gtt cca ggc   403
Gly Phe Pro Val Arg Pro Glu Gly Pro Ile Val Pro Ile Val Pro Gly
                90                  95                 100

gct gtg att ttt gat ttg ttg gtg ggc gat ccc aaa aac agg ccc acg   451
Ala Val Ile Phe Asp Leu Leu Val Gly Asp Pro Lys Asn Arg Pro Thr
            105                 110                 115

gca gct gat ggg gaa caa gca gtt gaa aac gct ttc gct ggt aca cac   499
Ala Ala Asp Gly Glu Gln Ala Val Glu Asn Ala Phe Ala Gly Thr His
        120                 125                 130

aac ggt tcg ggc agc gtc ggt gca gga acg ggt gct aca gca ggt cgg   547
Asn Gly Ser Gly Ser Val Gly Ala Gly Thr Gly Ala Thr Ala Gly Arg
    135                 140                 145

ctg cgt ggc ggt ttt ggc caa agc tcg cgc cgg gtc gga aag tac acc   595
Leu Arg Gly Gly Phe Gly Gln Ser Ser Arg Arg Val Gly Lys Tyr Thr
150                 155                 160                 165

atc gcg gca ggg gtc gtg gcg aat cct gtt ggg gaa gtc gtg gac cta   643
Ile Ala Ala Gly Val Val Ala Asn Pro Val Gly Glu Val Val Asp Leu
                170                 175                 180

aca act gga gct ttg ttt ggt agg ccc gaa gtg atg ggg gtg ggc gtc   691
Thr Thr Gly Ala Leu Phe Gly Arg Pro Glu Val Met Gly Val Gly Val
            185                 190                 195

gat aag cta aaa agc gcg gca gag acg ctg aac acg acc atc ggc gtc   739
Asp Lys Leu Lys Ser Ala Ala Glu Thr Leu Asn Thr Thr Ile Gly Val
        200                 205                 210
```

```
gtg gca act gac gcg ccg gtg aca aaa gcc caa gcg aag cgc ttg gcg   787
Val Ala Thr Asp Ala Pro Val Thr Lys Ala Gln Ala Lys Arg Leu Ala
    215                 220                 225

ctg gtg gcc cat gat ggt ttg gcg agg gca gtg cgg ccg tcg cat tca   835
Leu Val Ala His Asp Gly Leu Ala Arg Ala Val Arg Pro Ser His Ser
230                 235                 240                 245

ccg atg gac ggt gac aca ttt ttc gcc atg tca tcg ggt gat ggt agt   883
Pro Met Asp Gly Asp Thr Phe Phe Ala Met Ser Ser Gly Asp Gly Ser
                250                 255                 260

ggc gtt acc ccg gtt gag ctg ggg gaa ttg tcg gct cat gct gca       928
Gly Val Thr Pro Val Glu Leu Gly Glu Leu Ser Ala His Ala Ala
            265                 270                 275
```

<210> 1156
<211> 276
<212> PRT
<213> Corynebacterium glutamicum

<400> 1156

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Met Leu Ile Asp Val Ala Gly Phe Leu Leu Gly His Val Thr Lys Gly
  1               5                  10                  15

Asp Thr Gly Cys Ser Val Val Ile Ala Pro Asn Gly Ala Phe Ala Gly
             20                  25                  30

Val Asp Val Arg Gly Gly Gly Pro Gly Thr Arg Glu Thr Asp Leu Leu
         35                  40                  45

Glu Pro His Asn Ser Val Gln Gln Ala His Ala Val Val Leu Cys Gly
     50                  55                  60

Gly Ser Ala Phe Gly Leu Ala Ala Ala Asp Gly Val Met Thr Ala Leu
 65                  70                  75                  80

Glu Asn Arg Gly Ile Gly Phe Pro Val Arg Pro Glu Gly Pro Ile Val
                 85                  90                  95

Pro Ile Val Pro Gly Ala Val Ile Phe Asp Leu Leu Val Gly Asp Pro
            100                 105                 110

Lys Asn Arg Pro Thr Ala Ala Asp Gly Glu Gln Ala Val Glu Asn Ala
        115                 120                 125

Phe Ala Gly Thr His Asn Gly Ser Gly Ser Val Gly Ala Gly Thr Gly
    130                 135                 140

Ala Thr Ala Gly Arg Leu Arg Gly Gly Phe Gly Gln Ser Ser Arg Arg
145                 150                 155                 160

Val Gly Lys Tyr Thr Ile Ala Ala Gly Val Val Ala Asn Pro Val Gly
                165                 170                 175

Glu Val Val Asp Leu Thr Thr Gly Ala Leu Phe Gly Arg Pro Glu Val
            180                 185                 190

Met Gly Val Gly Val Asp Lys Leu Lys Ser Ala Ala Glu Thr Leu Asn
```

```
        195                 200                 205

Thr Thr Ile Gly Val Val Ala Thr Asp Ala Pro Val Thr Lys Ala Gln
    210                 215                 220

Ala Lys Arg Leu Ala Leu Val Ala His Asp Gly Leu Ala Arg Ala Val
225                 230                 235                 240

Arg Pro Ser His Ser Pro Met Asp Gly Asp Thr Phe Phe Ala Met Ser
                245                 250                 255

Ser Gly Asp Gly Ser Gly Val Thr Pro Val Glu Leu Gly Glu Leu Ser
            260                 265                 270

Ala His Ala Ala
        275


<210> 1157
<211> 660
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(637)
<223> RXN02409

<400> 1157
gagttctggc gagaaggaca aagtggaggg tgatgtgaag aaactccaca ccgcagggct 60

gtgggcgaca atgcagcagg cagggtaggg gagaattttc atg cag cag tgg aag   115
                                            Met Gln Gln Trp Lys
                                              1               5

aag aaa aaa ggg ctg atg cgc cag gct cgt tac gcg gtg gtt ttt gag   163
Lys Lys Lys Gly Leu Met Arg Gln Ala Arg Tyr Ala Val Val Phe Glu
                10                  15                  20

ccg atg gag cgg gaa gtg ttg ggt gat ttg tca gct gcg gtc agt gag   211
Pro Met Glu Arg Glu Val Leu Gly Asp Leu Ser Ala Ala Val Ser Glu
            25                  30                  35

gcg ttg att cag cgt gca cag tct gtg ccg aag gat cct ctg gca gag   259
Ala Leu Ile Gln Arg Ala Gln Ser Val Pro Lys Asp Pro Leu Ala Glu
        40                  45                  50

atg acc ggc atg aca agt gga cac aaa gaa gca cca acc gat ccg gcg   307
Met Thr Gly Met Thr Ser Gly His Lys Glu Ala Pro Thr Asp Pro Ala
    55                  60                  65

ctt gcg cgt ttg ctc cct gat ttt cag cac gag ggc gat gag gaa tac   355
Leu Ala Arg Leu Leu Pro Asp Phe Gln His Glu Gly Asp Glu Glu Tyr
70                  75                  80                  85

gac ggc gat aat tct ttc ctc cgt tca ctc cat gaa ggc gac atc acc   403
Asp Gly Asp Asn Ser Phe Leu Arg Ser Leu His Glu Gly Asp Ile Thr
                90                  95                 100

cga gca aaa ctg gaa aat ctg cgc gtg att aac gat gcg ctg gga ccc   451
Arg Ala Lys Leu Glu Asn Leu Arg Val Ile Asn Asp Ala Leu Gly Pro
```

```
            105                 110                 115

gac gga aat gtt gcg gtc acc gcc tct gag gag gaa gcg cac gct tgg   499
Asp Gly Asn Val Ala Val Thr Ala Ser Glu Glu Glu Ala His Ala Trp
        120                 125                 130

ttg gct gcg ctc aat gac atc cgc ctg tac gtt gcc tcc ggt gat gta   547
Leu Ala Ala Leu Asn Asp Ile Arg Leu Tyr Val Ala Ser Gly Asp Val
    135                 140                 145

cgc ggc ggg gaa gcc gcc gag gaa gac cgc gaa aac ctc gtg cag tgg   595
Arg Gly Gly Glu Ala Ala Glu Glu Asp Arg Glu Asn Leu Val Gln Trp
150                 155                 160                 165

ctt gcc tac aat caa gag tcc ttg ctg gaa gcg atg atg aat           637
Leu Ala Tyr Asn Gln Glu Ser Leu Leu Glu Ala Met Met Asn
                170                 175

taatgcttat cgacgtcgcg ggc                                        660


<210> 1158
<211> 179
<212> PRT
<213> Corynebacterium glutamicum

<400> 1158
Met Gln Gln Trp Lys Lys Lys Lys Gly Leu Met Arg Gln Ala Arg Tyr
  1               5                  10                  15

Ala Val Val Phe Glu Pro Met Glu Arg Glu Val Leu Gly Asp Leu Ser
             20                  25                  30

Ala Ala Val Ser Glu Ala Leu Ile Gln Arg Ala Gln Ser Val Pro Lys
         35                  40                  45

Asp Pro Leu Ala Glu Met Thr Gly Met Thr Ser Gly His Lys Glu Ala
     50                  55                  60

Pro Thr Asp Pro Ala Leu Ala Arg Leu Leu Pro Asp Phe Gln His Glu
 65                  70                  75                  80

Gly Asp Glu Glu Tyr Asp Gly Asp Asn Ser Phe Leu Arg Ser Leu His
                 85                  90                  95

Glu Gly Asp Ile Thr Arg Ala Lys Leu Glu Asn Leu Arg Val Ile Asn
            100                 105                 110

Asp Ala Leu Gly Pro Asp Gly Asn Val Ala Val Thr Ala Ser Glu Glu
        115                 120                 125

Glu Ala His Ala Trp Leu Ala Ala Leu Asn Asp Ile Arg Leu Tyr Val
    130                 135                 140

Ala Ser Gly Asp Val Arg Gly Gly Glu Ala Ala Glu Glu Asp Arg Glu
145                 150                 155                 160

Asn Leu Val Gln Trp Leu Ala Tyr Asn Gln Glu Ser Leu Leu Glu Ala
                165                 170                 175

Met Met Asn
```

<210> 1159
<211> 437
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(414)
<223> FRXA02409

<400> 1159
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cgt gca cag tct gtg ccg aag gat cct ctg gca gag atg acc ggc atg   48
Arg Ala Gln Ser Val Pro Lys Asp Pro Leu Ala Glu Met Thr Gly Met
  1               5                  10                  15

aca agt gga cac aaa gaa gca cca acc gat ccg gcg ctt gcg cgt ttg   96
Thr Ser Gly His Lys Glu Ala Pro Thr Asp Pro Ala Leu Ala Arg Leu
             20                  25                  30

ctc cct gat ttt cag cac gag ggc gat gag gaa tac gac ggc gat aat  144
Leu Pro Asp Phe Gln His Glu Gly Asp Glu Glu Tyr Asp Gly Asp Asn
         35                  40                  45

tct ttc ctc cgt tca ctc cat gaa ggc gac atc acc cga gca aaa ctg  192
Ser Phe Leu Arg Ser Leu His Glu Gly Asp Ile Thr Arg Ala Lys Leu
     50                  55                  60

gaa aat ctg cgc gtg att aac gat gcg ctg gga ccc gac gga aat gtt  240
Glu Asn Leu Arg Val Ile Asn Asp Ala Leu Gly Pro Asp Gly Asn Val
 65                  70                  75                  80

gcg gtc acc gcc tct gag gag gaa gcg cac gct tgg ttg gct gcg ctc  288
Ala Val Thr Ala Ser Glu Glu Glu Ala His Ala Trp Leu Ala Ala Leu
                 85                  90                  95

aat gac atc cgc ctg tac gtt gcc tcc ggt gat gta cgc ggc ggg gaa  336
Asn Asp Ile Arg Leu Tyr Val Ala Ser Gly Asp Val Arg Gly Gly Glu
            100                 105                 110

gcc gcc gag gaa gac cgc gaa aac ctc gtg cag tgg ctt gcc tac aat  384
Ala Ala Glu Glu Asp Arg Glu Asn Leu Val Gln Trp Leu Ala Tyr Asn
        115                 120                 125

caa gag tcc ttg ctg gaa gcg atg atg aat taatgcttat cgacgtcgcg    434
Gln Glu Ser Leu Leu Glu Ala Met Met Asn
    130                 135

ggc                                                             437
```

<210> 1160
<211> 138
<212> PRT
<213> Corynebacterium glutamicum

<400> 1160
```
Arg Ala Gln Ser Val Pro Lys Asp Pro Leu Ala Glu Met Thr Gly Met
  1               5                  10                  15
```

```
Thr Ser Gly His Lys Glu Ala Pro Thr Asp Pro Ala Leu Ala Arg Leu
            20                  25                  30

Leu Pro Asp Phe Gln His Glu Gly Asp Glu Glu Tyr Asp Gly Asp Asn
        35                  40                  45

Ser Phe Leu Arg Ser Leu His Glu Gly Asp Ile Thr Arg Ala Lys Leu
    50                  55                  60

Glu Asn Leu Arg Val Ile Asn Asp Ala Leu Gly Pro Asp Gly Asn Val
65                  70                  75                  80

Ala Val Thr Ala Ser Glu Glu Glu Ala His Ala Trp Leu Ala Ala Leu
                85                  90                  95

Asn Asp Ile Arg Leu Tyr Val Ala Ser Gly Asp Val Arg Gly Gly Glu
            100                 105                 110

Ala Ala Glu Glu Asp Arg Glu Asn Leu Val Gln Trp Leu Ala Tyr Asn
        115                 120                 125

Gln Glu Ser Leu Leu Glu Ala Met Met Asn
    130                 135


<210> 1161
<211> 1257
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1234)
<223> RXN02428

<400> 1161
cgaaagatat gcataaagtg atgatgaaat agctttgtcg aaaggtttgc tcccggtgca 60

ttcagttagc gtgaaggtgc catcatcaca agggttgatg atg gcc gcg acg tta   115
                                            Met Ala Ala Thr Leu
                                              1               5

gat ctt cca gat aca gat ccc att gcc tat gca atg ttt gcc cac tgt   163
Asp Leu Pro Asp Thr Asp Pro Ile Ala Tyr Ala Met Phe Ala His Cys
                10                  15                  20

ttc acc ggc tca cgg ttc acg cca gcc gcc gcg cga gtc agt aaa aca   211
Phe Thr Gly Ser Arg Phe Thr Pro Ala Ala Ala Arg Val Ser Lys Thr
            25                  30                  35

ctc gca gaa tcc ggc gtc gcc tgc ctg cgt ttc gat ttc cca gga ctg   259
Leu Ala Glu Ser Gly Val Ala Cys Leu Arg Phe Asp Phe Pro Gly Leu
        40                  45                  50

agc caa tca gaa ggt gac ttc tcc aaa acc acc ttc aac tcc aat gtg   307
Ser Gln Ser Glu Gly Asp Phe Ser Lys Thr Thr Phe Asn Ser Asn Val
    55                  60                  65

gac gat atc gtg gcg gcc tcg cag tgg ttg acg gaa cac tac tcc gct   355
Asp Asp Ile Val Ala Ala Ser Gln Trp Leu Thr Glu His Tyr Ser Ala
```

```
 70                  75                  80                  85

cca cag ttg ctc att gga cac tcc ttg ggt ggt gca gca tca ctg aaa   403
Pro Gln Leu Leu Ile Gly His Ser Leu Gly Gly Ala Ala Ser Leu Lys
                90                  95                 100

gct gcc acc aaa atc tcc tgc ctc aaa gca gta gca acg ata ggt gca   451
Ala Ala Thr Lys Ile Ser Cys Leu Lys Ala Val Ala Thr Ile Gly Ala
            105                 110                 115

cct ttt gat cct gcg cac gca gtc ctg cac ttt gct gat cgc ata tgt   499
Pro Phe Asp Pro Ala His Ala Val Leu His Phe Ala Asp Arg Ile Cys
        120                 125                 130

gat gta gat gat caa ggt gct gtc act ctg cag ctc gga ggc cgg gat   547
Asp Val Asp Asp Gln Gly Ala Val Thr Leu Gln Leu Gly Gly Arg Asp
    135                 140                 145

gtc acc att tcc cgc gaa ttc ctc gaa gac ctt gca gag gtc aac ccc   595
Val Thr Ile Ser Arg Glu Phe Leu Glu Asp Leu Ala Glu Val Asn Pro
150                 155                 160                 165

gaa gat cac ctc cgc agg ctc cgc aaa cca ctg ctt tta ctg cat tcc   643
Glu Asp His Leu Arg Arg Leu Arg Lys Pro Leu Leu Leu Leu His Ser
                170                 175                 180

ccc acc gac caa acc gtc ggc gtg gac aac gcg cag ctc atc ttc aga   691
Pro Thr Asp Gln Thr Val Gly Val Asp Asn Ala Gln Leu Ile Phe Arg
            185                 190                 195

gtc act cgc tac cct aaa tcc ttg atg act ttg gac aag gca gat cac   739
Val Thr Arg Tyr Pro Lys Ser Leu Met Thr Leu Asp Lys Ala Asp His
        200                 205                 210

ctg ctc acc aaa gat ggc acc gca cag cgt gca gcc cgg atc atc gcg   787
Leu Leu Thr Lys Asp Gly Thr Ala Gln Arg Ala Ala Arg Ile Ile Ala
    215                 220                 225

aac tgg gtc gag ccc tac ctg gtt cca gaa aac gtc tgt gag gat ctt   835
Asn Trp Val Glu Pro Tyr Leu Val Pro Glu Asn Val Cys Glu Asp Leu
230                 235                 240                 245

ccg gag ttt gtc gcc gaa gcc tca acc atc aaa gcc agc aaa tac ggc   883
Pro Glu Phe Val Ala Glu Ala Ser Thr Ile Lys Ala Ser Lys Tyr Gly
                250                 255                 260

gca gcc atc cgc acc ggt ggt cac aat ttc atc acc gac cgc gac aaa   931
Ala Ala Ile Arg Thr Gly Gly His Asn Phe Ile Thr Asp Arg Asp Lys
            265                 270                 275

tcc cag ggt ggc aaa aac ctc ggc ttc acc cct act tcc ctg ctg gtt   979
Ser Gln Gly Gly Lys Asn Leu Gly Phe Thr Pro Thr Ser Leu Leu Val
        280                 285                 290

tcc gcg ctt gct gct gca aac tct caa acg atc aaa caa gca gcc atc   1027
Ser Ala Leu Ala Ala Ala Asn Ser Gln Thr Ile Lys Gln Ala Ala Ile
    295                 300                 305

gac aac cgc atc aaa ggc ctt gac gat gtc aaa gtg acg atc tcc cag   1075
Asp Asn Arg Ile Lys Gly Leu Asp Asp Val Lys Val Thr Ile Ser Gln
310                 315                 320                 325
```

```
gaa caa tca gcc gac cac ggc cag atc aaa ctc cgc cga aag atc tct   1123
Glu Gln Ser Ala Asp His Gly Gln Ile Lys Leu Arg Arg Lys Ile Ser
                330                 335                 340

ttg atc ggc aac ctc agc gat gct gac agt gct tca ctt cgg gcc gca   1171
Leu Ile Gly Asn Leu Ser Asp Ala Asp Ser Ala Ser Leu Arg Ala Ala
            345                 350                 355

tct aat tcc tgc tcg att acc caa ctg ctc gcg cag gga atc gtc atc   1219
Ser Asn Ser Cys Ser Ile Thr Gln Leu Leu Ala Gln Gly Ile Val Ile
        360                 365                 370

gac gac gag gtg aac tagcgtggat tttgagttgg gta                    1257
Asp Asp Glu Val Asn
    375
```

<210> 1162
<211> 378
<212> PRT
<213> Corynebacterium glutamicum

<400> 1162

```
Met Ala Ala Thr Leu Asp Leu Pro Asp Thr Asp Pro Ile Ala Tyr Ala
  1               5                  10                  15

Met Phe Ala His Cys Phe Thr Gly Ser Arg Phe Thr Pro Ala Ala Ala
             20                  25                  30

Arg Val Ser Lys Thr Leu Ala Glu Ser Gly Val Ala Cys Leu Arg Phe
         35                  40                  45

Asp Phe Pro Gly Leu Ser Gln Ser Glu Gly Asp Phe Ser Lys Thr Thr
     50                  55                  60

Phe Asn Ser Asn Val Asp Asp Ile Val Ala Ala Ser Gln Trp Leu Thr
 65                  70                  75                  80

Glu His Tyr Ser Ala Pro Gln Leu Leu Ile Gly His Ser Leu Gly Gly
                 85                  90                  95

Ala Ala Ser Leu Lys Ala Ala Thr Lys Ile Ser Cys Leu Lys Ala Val
            100                 105                 110

Ala Thr Ile Gly Ala Pro Phe Asp Pro Ala His Ala Val Leu His Phe
        115                 120                 125

Ala Asp Arg Ile Cys Asp Val Asp Asp Gln Gly Ala Val Thr Leu Gln
    130                 135                 140

Leu Gly Gly Arg Asp Val Thr Ile Ser Arg Glu Phe Leu Glu Asp Leu
145                 150                 155                 160

Ala Glu Val Asn Pro Glu Asp His Leu Arg Arg Leu Arg Lys Pro Leu
                165                 170                 175

Leu Leu Leu His Ser Pro Thr Asp Gln Thr Val Gly Val Asp Asn Ala
            180                 185                 190

Gln Leu Ile Phe Arg Val Thr Arg Tyr Pro Lys Ser Leu Met Thr Leu
```

```
        195                 200                 205

Asp Lys Ala Asp His Leu Leu Thr Lys Asp Gly Thr Ala Gln Arg Ala
    210                 215                 220

Ala Arg Ile Ile Ala Asn Trp Val Glu Pro Tyr Leu Val Pro Glu Asn
225                 230                 235                 240

Val Cys Glu Asp Leu Pro Glu Phe Val Ala Glu Ala Ser Thr Ile Lys
                245                 250                 255

Ala Ser Lys Tyr Gly Ala Ala Ile Arg Thr Gly Gly His Asn Phe Ile
            260                 265                 270

Thr Asp Arg Asp Lys Ser Gln Gly Gly Lys Asn Leu Gly Phe Thr Pro
        275                 280                 285

Thr Ser Leu Leu Val Ser Ala Leu Ala Ala Ala Asn Ser Gln Thr Ile
    290                 295                 300

Lys Gln Ala Ala Ile Asp Asn Arg Ile Lys Gly Leu Asp Asp Val Lys
305                 310                 315                 320

Val Thr Ile Ser Gln Glu Gln Ser Ala Asp His Gly Gln Ile Lys Leu
                325                 330                 335

Arg Arg Lys Ile Ser Leu Ile Gly Asn Leu Ser Asp Ala Asp Ser Ala
            340                 345                 350

Ser Leu Arg Ala Ala Ser Asn Ser Cys Ser Ile Thr Gln Leu Leu Ala
        355                 360                 365

Gln Gly Ile Val Ile Asp Asp Glu Val Asn
    370                 375


<210> 1163
<211> 1257
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1234)
<223> FRXA02428

<400> 1163
cgaaagatat gcataaagtg atgatgaaat agctttgtcg aaaggtttgc tcccggtgca 60

ttcagttagc gtgaaggtgc catcatcaca agggttgatg atg gcc gcg acg tta   115
                                              Met Ala Ala Thr Leu
                                                1               5

gat ctt cca gat aca gat ccc att gcc tat gca atg ttt gcc cac tgt   163
Asp Leu Pro Asp Thr Asp Pro Ile Ala Tyr Ala Met Phe Ala His Cys
                10                  15                  20

ttc acc ggc tca cgg ttc acg cca gcc gcc gcg cga gtc agt aaa aca   211
Phe Thr Gly Ser Arg Phe Thr Pro Ala Ala Ala Arg Val Ser Lys Thr
            25                  30                  35
```

```
ctc gca gaa tcc ggc gtc gcc tgc ctg cgt ttc gat ttc cca gga ctg   259
Leu Ala Glu Ser Gly Val Ala Cys Leu Arg Phe Asp Phe Pro Gly Leu
         40                  45                  50

agc caa tca gaa ggt gac ttc tcc aaa acc acc ttc aac tcc aat gtg   307
Ser Gln Ser Glu Gly Asp Phe Ser Lys Thr Thr Phe Asn Ser Asn Val
     55                  60                  65

gac gat atc gtg gcg gcc tcg cag tgg ttg acg gaa cac tac tcc gct   355
Asp Asp Ile Val Ala Ala Ser Gln Trp Leu Thr Glu His Tyr Ser Ala
 70                  75                  80                  85

cca cag ttg ctc att gga cac tcc ttg ggt ggt gca gca tca ctg aaa   403
Pro Gln Leu Leu Ile Gly His Ser Leu Gly Gly Ala Ala Ser Leu Lys
                90                  95                 100

gct gcc acc aaa atc tcc tgc ctc aaa gca gta gca acg ata ggt gca   451
Ala Ala Thr Lys Ile Ser Cys Leu Lys Ala Val Ala Thr Ile Gly Ala
            105                 110                 115

cct ttt gat cct gcg cac gca gtc ctg cac ttt gct gat cgc ata tgt   499
Pro Phe Asp Pro Ala His Ala Val Leu His Phe Ala Asp Arg Ile Cys
        120                 125                 130

gat gta gat gat caa ggt gct gtc act ctg cag ctc gga ggc cgg gat   547
Asp Val Asp Asp Gln Gly Ala Val Thr Leu Gln Leu Gly Gly Arg Asp
    135                 140                 145

gtc acc att tcc cgc gaa ttc ctc gaa gac ctt gca gag gtc aac ccc   595
Val Thr Ile Ser Arg Glu Phe Leu Glu Asp Leu Ala Glu Val Asn Pro
150                 155                 160                 165

gaa gat cac ctc cgc agg ctc cgc aaa cca ctg ctt tta ctg cat tcc   643
Glu Asp His Leu Arg Arg Leu Arg Lys Pro Leu Leu Leu Leu His Ser
                170                 175                 180

ccc acc gac caa acc gtc ggc gtg gac aac gcg cag ctc atc ttc aga   691
Pro Thr Asp Gln Thr Val Gly Val Asp Asn Ala Gln Leu Ile Phe Arg
            185                 190                 195

gtc act cgc tac cct aaa tcc ttg atg act ttg gac aag gca gat cac   739
Val Thr Arg Tyr Pro Lys Ser Leu Met Thr Leu Asp Lys Ala Asp His
        200                 205                 210

ctg ctc acc aaa gat ggc acc gca cag cgt gca gcc cgg atc atc gcg   787
Leu Leu Thr Lys Asp Gly Thr Ala Gln Arg Ala Ala Arg Ile Ile Ala
    215                 220                 225

aac tgg gtc gag ccc tac ctg gtt cca gaa aac gtc tgt gag gat ctt   835
Asn Trp Val Glu Pro Tyr Leu Val Pro Glu Asn Val Cys Glu Asp Leu
230                 235                 240                 245

ccg gag ttt gtc gcc gaa gcc tca acc atc aaa gcc agc aaa tac ggc   883
Pro Glu Phe Val Ala Glu Ala Ser Thr Ile Lys Ala Ser Lys Tyr Gly
                250                 255                 260

gca gcc atc cgc acc ggt ggt cac aat ttc atc acc gac cgc gac aaa   931
Ala Ala Ile Arg Thr Gly Gly His Asn Phe Ile Thr Asp Arg Asp Lys
            265                 270                 275

tcc cag ggt ggc aaa aac ctc ggc ttc acc cct act tcc ctg ctg gtt   979
```

```
Ser Gln Gly Gly Lys Asn Leu Gly Phe Thr Pro Thr Ser Leu Leu Val
        280                 285                 290

tcc gcg ctt gct gct gca aac tct caa acg atc aaa caa gca gcc atc   1027
Ser Ala Leu Ala Ala Ala Asn Ser Gln Thr Ile Lys Gln Ala Ala Ile
    295                 300                 305

gac aac cgc atc aaa ggc ctt gac gat gtc aaa gtg acg atc tcc cag   1075
Asp Asn Arg Ile Lys Gly Leu Asp Asp Val Lys Val Thr Ile Ser Gln
310                 315                 320                 325

gaa caa tca gcc gac cac ggc cag atc aaa ctc cgc cga aag atc tct   1123
Glu Gln Ser Ala Asp His Gly Gln Ile Lys Leu Arg Arg Lys Ile Ser
                330                 335                 340

ttg atc ggc aac ctc agc gat gct gac agt gct tca ctt cgg gcc gca   1171
Leu Ile Gly Asn Leu Ser Asp Ala Asp Ser Ala Ser Leu Arg Ala Ala
            345                 350                 355

tct aat tcc tgc tcg att acc caa ctg ctc gcg cag gga atc gtc atc   1219
Ser Asn Ser Cys Ser Ile Thr Gln Leu Leu Ala Gln Gly Ile Val Ile
        360                 365                 370

gac gac gag gtg aac tagcgtggat tttgagttgg gta                    1257
Asp Asp Glu Val Asn
    375


<210> 1164
<211> 378
<212> PRT
<213> Corynebacterium glutamicum

<400> 1164
Met Ala Ala Thr Leu Asp Leu Pro Asp Thr Asp Pro Ile Ala Tyr Ala
  1               5                  10                  15

Met Phe Ala His Cys Phe Thr Gly Ser Arg Phe Thr Pro Ala Ala Ala
             20                  25                  30

Arg Val Ser Lys Thr Leu Ala Glu Ser Gly Val Ala Cys Leu Arg Phe
         35                  40                  45

Asp Phe Pro Gly Leu Ser Gln Ser Glu Gly Asp Phe Ser Lys Thr Thr
     50                  55                  60

Phe Asn Ser Asn Val Asp Asp Ile Val Ala Ala Ser Gln Trp Leu Thr
 65                  70                  75                  80

Glu His Tyr Ser Ala Pro Gln Leu Leu Ile Gly His Ser Leu Gly Gly
                 85                  90                  95

Ala Ala Ser Leu Lys Ala Ala Thr Lys Ile Ser Cys Leu Lys Ala Val
            100                 105                 110

Ala Thr Ile Gly Ala Pro Phe Asp Pro Ala His Ala Val Leu His Phe
        115                 120                 125

Ala Asp Arg Ile Cys Asp Val Asp Asp Gln Gly Ala Val Thr Leu Gln
    130                 135                 140
```

```
Leu Gly Gly Arg Asp Val Thr Ile Ser Arg Glu Phe Leu Glu Asp Leu
145                 150                 155                 160

Ala Glu Val Asn Pro Glu Asp His Leu Arg Arg Leu Arg Lys Pro Leu
                165                 170                 175

Leu Leu Leu His Ser Pro Thr Asp Gln Thr Val Gly Val Asp Asn Ala
            180                 185                 190

Gln Leu Ile Phe Arg Val Thr Arg Tyr Pro Lys Ser Leu Met Thr Leu
        195                 200                 205

Asp Lys Ala Asp His Leu Leu Thr Lys Asp Gly Thr Ala Gln Arg Ala
    210                 215                 220

Ala Arg Ile Ile Ala Asn Trp Val Glu Pro Tyr Leu Val Pro Glu Asn
225                 230                 235                 240

Val Cys Glu Asp Leu Pro Glu Phe Val Ala Glu Ala Ser Thr Ile Lys
                245                 250                 255

Ala Ser Lys Tyr Gly Ala Ala Ile Arg Thr Gly Gly His Asn Phe Ile
            260                 265                 270

Thr Asp Arg Asp Lys Ser Gln Gly Gly Lys Asn Leu Gly Phe Thr Pro
        275                 280                 285

Thr Ser Leu Leu Val Ser Ala Leu Ala Ala Ala Asn Ser Gln Thr Ile
    290                 295                 300

Lys Gln Ala Ala Ile Asp Asn Arg Ile Lys Gly Leu Asp Asp Val Lys
305                 310                 315                 320

Val Thr Ile Ser Gln Glu Gln Ser Ala Asp His Gly Gln Ile Lys Leu
                325                 330                 335

Arg Arg Lys Ile Ser Leu Ile Gly Asn Leu Ser Asp Ala Asp Ser Ala
            340                 345                 350

Ser Leu Arg Ala Ala Ser Asn Ser Cys Ser Ile Thr Gln Leu Leu Ala
        355                 360                 365

Gln Gly Ile Val Ile Asp Asp Glu Val Asn
    370                 375


<210> 1165
<211> 1365
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1342)
<223> RXN02454

<400> 1165
ggcaagcgcc tcccttaagc ccgcgtaccg gctaccccga ggcacgtaat gagtagggca 60

gttctagcca taatcagcag aaaaggtgga gtgattcgcc atg aaa gag tcc atg   115
                                              Met Lys Glu Ser Met
```

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                                                    1               5

agc atc acc tcg tcg acg tac gcg tcg gca ctg ctg aca ctg ccc tgg   163
Ser Ile Thr Ser Ser Thr Tyr Ala Ser Ala Leu Leu Thr Leu Pro Trp
                10                  15                  20

ggt aca ccc ctg gaa cag tgg ccc gat aat ctc atc gcc gcg ctg ccc   211
Gly Thr Pro Leu Glu Gln Trp Pro Asp Asn Leu Ile Ala Ala Leu Pro
            25                  30                  35

agg ggt att tcc cgg cac atc gtg cgt ttc gtg ggg atc aac cgt ggc   259
Arg Gly Ile Ser Arg His Ile Val Arg Phe Val Gly Ile Asn Arg Gly
        40                  45                  50

atc gtc gcg gtc aaa gaa att ggt gcg cgt acc gcc cac cac gag tac   307
Ile Val Ala Val Lys Glu Ile Gly Ala Arg Thr Ala His His Glu Tyr
    55                  60                  65

aag atg ctg cgt gaa ctg cag cgc ctt ggt gcc ccc agt gtg cgc ccc   355
Lys Met Leu Arg Glu Leu Gln Arg Leu Gly Ala Pro Ser Val Arg Pro
70                  75                  80                  85

gta gcc gtg atc acc gga cgc cat ccg gca gag gaa gac tac ggg gag   403
Val Ala Val Ile Thr Gly Arg His Pro Ala Glu Glu Asp Tyr Gly Glu
                90                  95                  100

ctc acc gca gct ttg gtg acc gag cac ttg gag ttt tcc ctg ccc tat   451
Leu Thr Ala Ala Leu Val Thr Glu His Leu Glu Phe Ser Leu Pro Tyr
            105                 110                 115

cgc gag atc ttt tct cgg cac ctc acg gtc gtg gaa tcg gag aag ctc   499
Arg Glu Ile Phe Ser Arg His Leu Thr Val Val Glu Ser Glu Lys Leu
        120                 125                 130

atc cgc gcc ctg tcc gtg ctg ttg gtg cgg atg cat ctg ctc aac ttc   547
Ile Arg Ala Leu Ser Val Leu Leu Val Arg Met His Leu Leu Asn Phe
    135                 140                 145

tac tgg gga gat gtg tca ctg tct aat act ctc ttt cgt cgc gat gct   595
Tyr Trp Gly Asp Val Ser Leu Ser Asn Thr Leu Phe Arg Arg Asp Ala
150                 155                 160                 165

gaa acc tat tcc gcc tat ctc gtc gat gcc gaa acc ggg gag ttc cag   643
Glu Thr Tyr Ser Ala Tyr Leu Val Asp Ala Glu Thr Gly Glu Phe Gln
                170                 175                 180

ccc aac ctc tct gaa tca cgc agg ctt tac gac gtc gac atc gcc cgc   691
Pro Asn Leu Ser Glu Ser Arg Arg Leu Tyr Asp Val Asp Ile Ala Arg
            185                 190                 195

gtc aac atc att ggc gaa ctc atg gac cta cag gcg ggt gaa tgc cta   739
Val Asn Ile Ile Gly Glu Leu Met Asp Leu Gln Ala Gly Glu Cys Leu
        200                 205                 210

gat aag tcc atc gat gtc atc gcc cta gga ggc ctt gtc gaa agc tct   787
Asp Lys Ser Ile Asp Val Ile Ala Leu Gly Gly Leu Val Glu Ser Ser
    215                 220                 225

tat ctt gaa ttg tgg acg gag ctc acc gcg gag gaa tcc gtc gat gcc   835
Tyr Leu Glu Leu Trp Thr Glu Leu Thr Ala Glu Glu Ser Val Asp Ala
230                 235                 240                 245
```

```
agt gaa tat tgg cgc ctc tct gag aga att gac cgg ctc aat caa ctg   883
Ser Glu Tyr Trp Arg Leu Ser Glu Arg Ile Asp Arg Leu Asn Gln Leu
                250                 255                 260

ggc ttt gac gta ggg gag ctc aag gtc acg aag gac gat tcg cgg cag   931
Gly Phe Asp Val Gly Glu Leu Lys Val Thr Lys Asp Asp Ser Arg Gln
            265                 270                 275

gtt gtg cgc att cgc cct gta gtg gtg gat ccg ggc cac tat cgt gca   979
Val Val Arg Ile Arg Pro Val Val Val Asp Pro Gly His Tyr Arg Ala
        280                 285                 290

gag cta ttg agc tta acc ggg ctg agc gtc gag gaa cac cag gcc caa   1027
Glu Leu Leu Ser Leu Thr Gly Leu Ser Val Glu Glu His Gln Ala Gln
    295                 300                 305

cgc cta ttg ggc tcg atc cag gcc tat cag gcc gtc gaa tgc gga ccg   1075
Arg Leu Leu Gly Ser Ile Gln Ala Tyr Gln Ala Val Glu Cys Gly Pro
310                 315                 320                 325

cat gta ggt ctt acc caa gcc gcg cat ctc tgg atg acg aat gaa tac   1123
His Val Gly Leu Thr Gln Ala Ala His Leu Trp Met Thr Asn Glu Tyr
                330                 335                 340

gaa ccg act atc gcc gcc gtc ccc gtg gag atg tta gac aag ctg gag   1171
Glu Pro Thr Ile Ala Ala Val Pro Val Glu Met Leu Asp Lys Leu Glu
            345                 350                 355

cca gca caa atc ttc cac gaa atc gtc gac cac cgc tgg ttc ctc gcc   1219
Pro Ala Gln Ile Phe His Glu Ile Val Asp His Arg Trp Phe Leu Ala
        360                 365                 370

caa gaa agg gga ggg gct gtc acc ctc cca gag gcc acg gca tcc tat   1267
Gln Glu Arg Gly Gly Ala Val Thr Leu Pro Glu Ala Thr Ala Ser Tyr
    375                 380                 385

ctt gaa tcc gtg ctt ccg gcc cgc cgc gac gag gct cgc ctc ctc agc   1315
Leu Glu Ser Val Leu Pro Ala Arg Arg Asp Glu Ala Arg Leu Leu Ser
390                 395                 400                 405

aca aac cct tca gac gaa gac ttg tca taacctctcg cgtgccccaa         1362
Thr Asn Pro Ser Asp Glu Asp Leu Ser
                410

cgg                                                              1365
```

<210> 1166
<211> 414
<212> PRT
<213> Corynebacterium glutamicum

<400> 1166

```
Met Lys Glu Ser Met Ser Ile Thr Ser Ser Thr Tyr Ala Ser Ala Leu
  1               5                  10                  15

Leu Thr Leu Pro Trp Gly Thr Pro Leu Glu Gln Trp Pro Asp Asn Leu
             20                  25                  30

Ile Ala Ala Leu Pro Arg Gly Ile Ser Arg His Ile Val Arg Phe Val
```

```
         35                  40                  45

Gly Ile Asn Arg Gly Ile Val Ala Val Lys Glu Ile Gly Ala Arg Thr
     50                  55                  60

Ala His His Glu Tyr Lys Met Leu Arg Glu Leu Gln Arg Leu Gly Ala
 65                  70                  75                  80

Pro Ser Val Arg Pro Val Ala Val Ile Thr Gly Arg His Pro Ala Glu
                85                  90                  95

Glu Asp Tyr Gly Glu Leu Thr Ala Ala Leu Val Thr Glu His Leu Glu
            100                 105                 110

Phe Ser Leu Pro Tyr Arg Glu Ile Phe Ser Arg His Leu Thr Val Val
        115                 120                 125

Glu Ser Glu Lys Leu Ile Arg Ala Leu Ser Val Leu Leu Val Arg Met
    130                 135                 140

His Leu Leu Asn Phe Tyr Trp Gly Asp Val Ser Leu Ser Asn Thr Leu
145                 150                 155                 160

Phe Arg Arg Asp Ala Glu Thr Tyr Ser Ala Tyr Leu Val Asp Ala Glu
                165                 170                 175

Thr Gly Glu Phe Gln Pro Asn Leu Ser Glu Ser Arg Arg Leu Tyr Asp
            180                 185                 190

Val Asp Ile Ala Arg Val Asn Ile Ile Gly Glu Leu Met Asp Leu Gln
        195                 200                 205

Ala Gly Glu Cys Leu Asp Lys Ser Ile Asp Val Ile Ala Leu Gly Gly
    210                 215                 220

Leu Val Glu Ser Ser Tyr Leu Glu Leu Trp Thr Glu Leu Thr Ala Glu
225                 230                 235                 240

Glu Ser Val Asp Ala Ser Glu Tyr Trp Arg Leu Ser Glu Arg Ile Asp
                245                 250                 255

Arg Leu Asn Gln Leu Gly Phe Asp Val Gly Glu Leu Lys Val Thr Lys
            260                 265                 270

Asp Asp Ser Arg Gln Val Val Arg Ile Arg Pro Val Val Val Asp Pro
        275                 280                 285

Gly His Tyr Arg Ala Glu Leu Leu Ser Leu Thr Gly Leu Ser Val Glu
    290                 295                 300

Glu His Gln Ala Gln Arg Leu Leu Gly Ser Ile Gln Ala Tyr Gln Ala
305                 310                 315                 320

Val Glu Cys Gly Pro His Val Gly Leu Thr Gln Ala Ala His Leu Trp
                325                 330                 335

Met Thr Asn Glu Tyr Glu Pro Thr Ile Ala Ala Val Pro Val Glu Met
            340                 345                 350

Leu Asp Lys Leu Glu Pro Ala Gln Ile Phe His Glu Ile Val Asp His
        355                 360                 365
```

```
Arg Trp Phe Leu Ala Gln Glu Arg Gly Gly Ala Val Thr Leu Pro Glu
    370                 375                 380

Ala Thr Ala Ser Tyr Leu Glu Ser Val Leu Pro Ala Arg Arg Asp Glu
385                 390                 395                 400

Ala Arg Leu Leu Ser Thr Asn Pro Ser Asp Glu Asp Leu Ser
                405                 410


<210> 1167
<211> 836
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(813)
<223> FRXA02454

<400> 1167
atg cat ctg ctc aac ttc tac tgg gga gat gtg tca ctg tct aat act   48
Met His Leu Leu Asn Phe Tyr Trp Gly Asp Val Ser Leu Ser Asn Thr
  1               5                  10                  15

ctc ttt cgt cgc gat gct gaa acc tat tcc gcc tat ctc gtc gat gcc   96
Leu Phe Arg Arg Asp Ala Glu Thr Tyr Ser Ala Tyr Leu Val Asp Ala
             20                  25                  30

gaa acc ggg gag ttc cag ccc aac ctc tct gaa tca cgc agg ctt tac   144
Glu Thr Gly Glu Phe Gln Pro Asn Leu Ser Glu Ser Arg Arg Leu Tyr
         35                  40                  45

gac gtc gac atc gcc cgc gtc aac atc att ggc gaa ctc atg gac cta   192
Asp Val Asp Ile Ala Arg Val Asn Ile Ile Gly Glu Leu Met Asp Leu
     50                  55                  60

cag gcg ggt gaa tgc cta gat aag tcc atc gat gtc atc gcc cta gga   240
Gln Ala Gly Glu Cys Leu Asp Lys Ser Ile Asp Val Ile Ala Leu Gly
 65                  70                  75                  80

ggc ctt gtc gaa agc tct tat ctt gaa ttg tgg acg gag ctc acc gcg   288
Gly Leu Val Glu Ser Ser Tyr Leu Glu Leu Trp Thr Glu Leu Thr Ala
                 85                  90                  95

gag gaa tcc gtc gat gcc agt gaa tat tgg cgc ctc tct gag aga att   336
Glu Glu Ser Val Asp Ala Ser Glu Tyr Trp Arg Leu Ser Glu Arg Ile
            100                 105                 110

gac cgg ctc aat caa ctg ggc ttt gac gta ggg gag ctc aag gtc acg   384
Asp Arg Leu Asn Gln Leu Gly Phe Asp Val Gly Glu Leu Lys Val Thr
        115                 120                 125

aag gac gat tcg cgg cag gtt gtg cgc att cgc cct gta gtg gtg gat   432
Lys Asp Asp Ser Arg Gln Val Val Arg Ile Arg Pro Val Val Val Asp
    130                 135                 140

ccg ggc cac tat cgt gca gag cta ttg agc tta acc ggg ctg agc gtc   480
Pro Gly His Tyr Arg Ala Glu Leu Leu Ser Leu Thr Gly Leu Ser Val
145                 150                 155                 160
```

```
gag gaa cac cag gcc caa cgc cta ttg ggc tcg atc cag gcc tat cag   528
Glu Glu His Gln Ala Gln Arg Leu Leu Gly Ser Ile Gln Ala Tyr Gln
                165                 170                 175

gcc gtc gaa tgc gga ccg cat gta ggt ctt acc caa gcc gcg cat ctc   576
Ala Val Glu Cys Gly Pro His Val Gly Leu Thr Gln Ala Ala His Leu
            180                 185                 190

tgg atg acg aat gaa tac gaa ccg act atc gcc gcc gtc ccc gtg gag   624
Trp Met Thr Asn Glu Tyr Glu Pro Thr Ile Ala Ala Val Pro Val Glu
        195                 200                 205

atg tta gac aag ctg gag cca gca caa atc ttc cac gaa atc gtc gac   672
Met Leu Asp Lys Leu Glu Pro Ala Gln Ile Phe His Glu Ile Val Asp
    210                 215                 220

cac cgc tgg ttc ctc gcc caa gaa agg gga ggg gct gtc acc ctc cca   720
His Arg Trp Phe Leu Ala Gln Glu Arg Gly Gly Ala Val Thr Leu Pro
225                 230                 235                 240

gag gcc acg gca tcc tat ctt gaa tcc gtg ctt ccg gcc cgc cgc gac   768
Glu Ala Thr Ala Ser Tyr Leu Glu Ser Val Leu Pro Ala Arg Arg Asp
                245                 250                 255

gag gct cgc ctc ctc agc aca aac cct tca gac gaa gac ttg tca       813
Glu Ala Arg Leu Leu Ser Thr Asn Pro Ser Asp Glu Asp Leu Ser
            260                 265                 270

taacctctcg cgtgccccaa cgg                                        836


<210> 1168
<211> 271
<212> PRT
<213> Corynebacterium glutamicum

<400> 1168
Met His Leu Leu Asn Phe Tyr Trp Gly Asp Val Ser Leu Ser Asn Thr
  1               5                  10                  15

Leu Phe Arg Arg Asp Ala Glu Thr Tyr Ser Ala Tyr Leu Val Asp Ala
             20                  25                  30

Glu Thr Gly Glu Phe Gln Pro Asn Leu Ser Glu Ser Arg Arg Leu Tyr
         35                  40                  45

Asp Val Asp Ile Ala Arg Val Asn Ile Ile Gly Glu Leu Met Asp Leu
     50                  55                  60

Gln Ala Gly Glu Cys Leu Asp Lys Ser Ile Asp Val Ile Ala Leu Gly
 65                  70                  75                  80

Gly Leu Val Glu Ser Ser Tyr Leu Glu Leu Trp Thr Glu Leu Thr Ala
                 85                  90                  95

Glu Glu Ser Val Asp Ala Ser Glu Tyr Trp Arg Leu Ser Glu Arg Ile
            100                 105                 110

Asp Arg Leu Asn Gln Leu Gly Phe Asp Val Gly Glu Leu Lys Val Thr
        115                 120                 125
```

```
Lys Asp Asp Ser Arg Gln Val Val Arg Ile Arg Pro Val Val Val Asp
    130                 135                 140

Pro Gly His Tyr Arg Ala Glu Leu Leu Ser Leu Thr Gly Leu Ser Val
145                 150                 155                 160

Glu Glu His Gln Ala Gln Arg Leu Leu Gly Ser Ile Gln Ala Tyr Gln
                165                 170                 175

Ala Val Glu Cys Gly Pro His Val Gly Leu Thr Gln Ala Ala His Leu
            180                 185                 190

Trp Met Thr Asn Glu Tyr Glu Pro Thr Ile Ala Ala Val Pro Val Glu
        195                 200                 205

Met Leu Asp Lys Leu Glu Pro Ala Gln Ile Phe His Glu Ile Val Asp
    210                 215                 220

His Arg Trp Phe Leu Ala Gln Glu Arg Gly Gly Ala Val Thr Leu Pro
225                 230                 235                 240

Glu Ala Thr Ala Ser Tyr Leu Glu Ser Val Leu Pro Ala Arg Arg Asp
                245                 250                 255

Glu Ala Arg Leu Leu Ser Thr Asn Pro Ser Asp Glu Asp Leu Ser
            260                 265                 270
```

<210> 1169
<211> 1233
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1210)
<223> RXN02457

<400> 1169

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ctgtaaagcc acgtgagctg ttgcttagac tttactctac ccccgcgtgt ccaccacatc 60

agttagaaca tatgtaccac ttcaaatcta gggggaaaca atg ttc tac ttc acc   115
                                              Met Phe Tyr Phe Thr
                                                1               5

gtc aat aat ccg cag gat cct tta agc acc gaa att gtt gag act aat   163
Val Asn Asn Pro Gln Asp Pro Leu Ser Thr Glu Ile Val Glu Thr Asn
                10                  15                  20

cgc cgt gac ctc gca ttt tgg cat cga tta cgc ccc aaa gat gac gat   211
Arg Arg Asp Leu Ala Phe Trp His Arg Leu Arg Pro Lys Asp Asp Asp
            25                  30                  35

gat tta gcc aca gcc atc aac aaa ata tgc gtg cgc aca ggc tta tcc   259
Asp Leu Ala Thr Ala Ile Asn Lys Ile Cys Val Arg Thr Gly Leu Ser
        40                  45                  50

cgc aaa ctg atc gcc gct tgt tta ttt agc atc tgc ttc ctg ccg tac   307
Arg Lys Leu Ile Ala Ala Cys Leu Phe Ser Ile Cys Phe Leu Pro Tyr
    55                  60                  65
```

```
tta ccc aac ttc cac aaa ctc gtc gaa aag ctt ggt cat ctc gac atg   355
Leu Pro Asn Phe His Lys Leu Val Glu Lys Leu Gly His Leu Asp Met
 70                  75                  80                  85

gcg cgc atc aac gcg atc act aaa gct ggc gaa aaa gtg cca agc gag   403
Ala Arg Ile Asn Ala Ile Thr Lys Ala Gly Glu Lys Val Pro Ser Glu
                90                  95                 100

aag aga gag ctt ttc gac gcc tac ctc gtc gat tac ctg acg cct cga   451
Lys Arg Glu Leu Phe Asp Ala Tyr Leu Val Asp Tyr Leu Thr Pro Arg
            105                 110                 115

gcg gag gct cag tgc ttg ccc cag gca agc tca att tcc gca atg atg   499
Ala Glu Ala Gln Cys Leu Pro Gln Ala Ser Ser Ile Ser Ala Met Met
        120                 125                 130

cgg aaa ttt atc gca caa cac tgc ccc gac gac aag gcc tcc tca gcc   547
Arg Lys Phe Ile Ala Gln His Cys Pro Asp Asp Lys Ala Ser Ser Ala
    135                 140                 145

acc aat gat ggc tcc atc cgc tac cgc aga aac aac aaa ggc ggg atc   595
Thr Asn Asp Gly Ser Ile Arg Tyr Arg Arg Asn Asn Lys Gly Gly Ile
150                 155                 160                 165

agt atc acc gtc gat gcc acc gcc agc gaa gta aca gaa atc aaa gct   643
Ser Ile Thr Val Asp Ala Thr Ala Ser Glu Val Thr Glu Ile Lys Ala
                170                 175                 180

gcc ctg gaa caa atg tcc aaa gat aag gac tgc aca cca ggc act tcc   691
Ala Leu Glu Gln Met Ser Lys Asp Lys Asp Cys Thr Pro Gly Thr Ser
            185                 190                 195

cta ctc cac atc att cgt ggc ctg ccg aca aaa gtc gta ctc aac acc   739
Leu Leu His Ile Ile Arg Gly Leu Pro Thr Lys Val Val Leu Asn Thr
        200                 205                 210

tac ggc acc aaa gac agc cct gaa tac tta gaa gga gga acc tgg ctg   787
Tyr Gly Thr Lys Asp Ser Pro Glu Tyr Leu Glu Gly Gly Thr Trp Leu
    215                 220                 225

tca aag gaa cag tct gag ttc tgg aaa acc cga acc acg tcc agt cgg   835
Ser Lys Glu Gln Ser Glu Phe Trp Lys Thr Arg Thr Thr Ser Ser Arg
230                 235                 240                 245

gat atg gac gcc gcc cac ttc tct tac acc acc gcc tac gct cca acc   883
Asp Met Asp Ala Ala His Phe Ser Tyr Thr Thr Ala Tyr Ala Pro Thr
                250                 255                 260

cga gaa atg cgc gtc tac atc aaa ggt cta cgc acc acc tgt agc gtc   931
Arg Glu Met Arg Val Tyr Ile Lys Gly Leu Arg Thr Thr Cys Ser Val
            265                 270                 275

cct ggc tgc agt gta gcg gtc gaa aac tgc caa ctg gac cac atc atc   979
Pro Gly Cys Ser Val Ala Val Glu Asn Cys Gln Leu Asp His Ile Ile
        280                 285                 290

ccc tgg ggt gaa gga ggg ccg aca aca ccg tgg aat att cat ccc ctg   1027
Pro Trp Gly Glu Gly Gly Pro Thr Thr Pro Trp Asn Ile His Pro Leu
    295                 300                 305
```

```
tgt gtc ttc cac cac atc cag aag act gaa ggg agg ctc cag tgc tat   1075
Cys Val Phe His His Ile Gln Lys Thr Glu Gly Arg Leu Gln Cys Tyr
310                 315                 320                 325

cca cta ccg gac ggc acc gtc cta ttc cta gtg gat gga ata ccg gtg   1123
Pro Leu Pro Asp Gly Thr Val Leu Phe Leu Val Asp Gly Ile Pro Val
                330                 335                 340

ttc tcc atc ccc gac ggg cct tta tct aaa tcg aat aaa acc tgg ggg   1171
Phe Ser Ile Pro Asp Gly Pro Leu Ser Lys Ser Asn Lys Thr Trp Gly
            345                 350                 355

aca aag ttc ggc aaa tac atg gag cgt cga atc gcc gcc taatccagca    1220
Thr Lys Phe Gly Lys Tyr Met Glu Arg Arg Ile Ala Ala
        360                 365                 370

agccagcgtg atc                                                   1233
```

<210> 1170
<211> 370
<212> PRT
<213> Corynebacterium glutamicum

<400> 1170

```
Met Phe Tyr Phe Thr Val Asn Asn Pro Gln Asp Pro Leu Ser Thr Glu
  1               5                  10                  15

Ile Val Glu Thr Asn Arg Arg Asp Leu Ala Phe Trp His Arg Leu Arg
             20                  25                  30

Pro Lys Asp Asp Asp Asp Leu Ala Thr Ala Ile Asn Lys Ile Cys Val
         35                  40                  45

Arg Thr Gly Leu Ser Arg Lys Leu Ile Ala Ala Cys Leu Phe Ser Ile
     50                  55                  60

Cys Phe Leu Pro Tyr Leu Pro Asn Phe His Lys Leu Val Glu Lys Leu
 65                  70                  75                  80

Gly His Leu Asp Met Ala Arg Ile Asn Ala Ile Thr Lys Ala Gly Glu
                 85                  90                  95

Lys Val Pro Ser Glu Lys Arg Glu Leu Phe Asp Ala Tyr Leu Val Asp
            100                 105                 110

Tyr Leu Thr Pro Arg Ala Glu Ala Gln Cys Leu Pro Gln Ala Ser Ser
        115                 120                 125

Ile Ser Ala Met Met Arg Lys Phe Ile Ala Gln His Cys Pro Asp Asp
    130                 135                 140

Lys Ala Ser Ser Ala Thr Asn Asp Gly Ser Ile Arg Tyr Arg Arg Asn
145                 150                 155                 160

Asn Lys Gly Gly Ile Ser Ile Thr Val Asp Ala Thr Ala Ser Glu Val
                165                 170                 175

Thr Glu Ile Lys Ala Ala Leu Glu Gln Met Ser Lys Asp Lys Asp Cys
            180                 185                 190
```

```
Thr Pro Gly Thr Ser Leu Leu His Ile Ile Arg Gly Leu Pro Thr Lys
        195                 200                 205

Val Val Leu Asn Thr Tyr Gly Thr Lys Asp Ser Pro Glu Tyr Leu Glu
    210                 215                 220

Gly Gly Thr Trp Leu Ser Lys Glu Gln Ser Glu Phe Trp Lys Thr Arg
225                 230                 235                 240

Thr Thr Ser Ser Arg Asp Met Asp Ala Ala His Phe Ser Tyr Thr Thr
                245                 250                 255

Ala Tyr Ala Pro Thr Arg Glu Met Arg Val Tyr Ile Lys Gly Leu Arg
            260                 265                 270

Thr Thr Cys Ser Val Pro Gly Cys Ser Val Ala Val Glu Asn Cys Gln
        275                 280                 285

Leu Asp His Ile Ile Pro Trp Gly Glu Gly Gly Pro Thr Thr Pro Trp
    290                 295                 300

Asn Ile His Pro Leu Cys Val Phe His His Ile Gln Lys Thr Glu Gly
305                 310                 315                 320

Arg Leu Gln Cys Tyr Pro Leu Pro Asp Gly Thr Val Leu Phe Leu Val
                325                 330                 335

Asp Gly Ile Pro Val Phe Ser Ile Pro Asp Gly Pro Leu Ser Lys Ser
            340                 345                 350

Asn Lys Thr Trp Gly Thr Lys Phe Gly Lys Tyr Met Glu Arg Arg Ile
        355                 360                 365

Ala Ala
    370
```

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<210> 1171
<211> 1233
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1210)
<223> FRXA02457

<400> 1171
ctgtaaagcc acgtgagctg ttgcttagac tttactctac ccccgcgtgt ccaccacatc 60

agttagaaca tatgtaccac ttcaaatcta gggggaaaca atg ttc tac ttc acc 115
                                                Met Phe Tyr Phe Thr
                                                  1   5

gtc aat aat ccg cag gat cct tta agc acc gaa att gtt gag act aat 163
Val Asn Asn Pro Gln Asp Pro Leu Ser Thr Glu Ile Val Glu Thr Asn
                10   15   20

cgc cgt gac ctc gca ttt tgg cat cga tta cgc ccc aaa gat gac gat 211
Arg Arg Asp Leu Ala Phe Trp His Arg Leu Arg Pro Lys Asp Asp Asp
            25   30   35

```
gat tta gcc aca gcc atc aac aaa ata tgc gtg cgc aca ggc tta tcc   259
Asp Leu Ala Thr Ala Ile Asn Lys Ile Cys Val Arg Thr Gly Leu Ser
         40                  45                  50

cgc aaa ctg atc gcc gct tgt tta ttt agc atc tgc ttc ctg ccg tac   307
Arg Lys Leu Ile Ala Ala Cys Leu Phe Ser Ile Cys Phe Leu Pro Tyr
     55                  60                  65

tta ccc aac ttc cac aaa ctc gtc gaa aag ctt ggt cat ctc gac atg   355
Leu Pro Asn Phe His Lys Leu Val Glu Lys Leu Gly His Leu Asp Met
 70                  75                  80                  85

gcg cgc atc aac gcg atc act aaa gct ggc gaa aaa gtg cca agc gag   403
Ala Arg Ile Asn Ala Ile Thr Lys Ala Gly Glu Lys Val Pro Ser Glu
                 90                  95                 100

aag aga gag ctt ttc gac gcc tac ctc gtc gat tac ctg acg cct cga   451
Lys Arg Glu Leu Phe Asp Ala Tyr Leu Val Asp Tyr Leu Thr Pro Arg
            105                 110                 115

gcg gag gct cag tgc ttg ccc cag gca agc tca att tcc gca atg atg   499
Ala Glu Ala Gln Cys Leu Pro Gln Ala Ser Ser Ile Ser Ala Met Met
        120                 125                 130

cgg aaa ttt atc gca caa cac tgc ccc gac gac aag gcc tcc tca gcc   547
Arg Lys Phe Ile Ala Gln His Cys Pro Asp Asp Lys Ala Ser Ser Ala
    135                 140                 145

acc aat gat ggc tcc atc cgc tac cgc aga aac aac aaa ggc ggg atc   595
Thr Asn Asp Gly Ser Ile Arg Tyr Arg Arg Asn Asn Lys Gly Gly Ile
150                 155                 160                 165

agt atc acc gtc gat gcc acc gcc agc gaa gta aca gaa atc aaa gct   643
Ser Ile Thr Val Asp Ala Thr Ala Ser Glu Val Thr Glu Ile Lys Ala
                170                 175                 180

gcc ctg gaa caa atg tcc aaa gat aag gac tgc aca cca ggc act tcc   691
Ala Leu Glu Gln Met Ser Lys Asp Lys Asp Cys Thr Pro Gly Thr Ser
            185                 190                 195

cta ctc cac atc att cgt ggc ctg ccg aca aaa gtc gta ctc aac acc   739
Leu Leu His Ile Ile Arg Gly Leu Pro Thr Lys Val Val Leu Asn Thr
        200                 205                 210

tac ggc acc aaa gac agc cct gaa tac tta gaa gga gga acc tgg ctg   787
Tyr Gly Thr Lys Asp Ser Pro Glu Tyr Leu Glu Gly Gly Thr Trp Leu
    215                 220                 225

tca aag gaa cag tct gag ttc tgg aaa acc cga acc acg tcc agt cgg   835
Ser Lys Glu Gln Ser Glu Phe Trp Lys Thr Arg Thr Thr Ser Ser Arg
230                 235                 240                 245

gat atg gac gcc gcc cac ttc tct tac acc acc gcc tac gct cca acc   883
Asp Met Asp Ala Ala His Phe Ser Tyr Thr Thr Ala Tyr Ala Pro Thr
                250                 255                 260

cga gaa atg cgc gtc tac atc aaa ggt cta cgc acc acc tgt agc gtc   931
Arg Glu Met Arg Val Tyr Ile Lys Gly Leu Arg Thr Thr Cys Ser Val
            265                 270                 275
```

```
cct ggc tgc agt gta gcg gtc gaa aac tgc caa ctg gac cac atc atc   979
Pro Gly Cys Ser Val Ala Val Glu Asn Cys Gln Leu Asp His Ile Ile
        280                 285                 290

ccc tgg ggt gaa gga ggg ccg aca aca ccg tgg aat att cat ccc ctg   1027
Pro Trp Gly Glu Gly Gly Pro Thr Thr Pro Trp Asn Ile His Pro Leu
    295                 300                 305

tgt gtc ttc cac cac atc cag aag act gaa ggg agg ctc cag tgc tat   1075
Cys Val Phe His His Ile Gln Lys Thr Glu Gly Arg Leu Gln Cys Tyr
310                 315                 320                 325

cca cta ccg gac ggc acc gtc cta ttc cta gtg gat gga ata ccg gtg   1123
Pro Leu Pro Asp Gly Thr Val Leu Phe Leu Val Asp Gly Ile Pro Val
                330                 335                 340

ttc tcc atc ccc gac ggg cct tta tct aaa tcg aat aaa acc tgg ggg   1171
Phe Ser Ile Pro Asp Gly Pro Leu Ser Lys Ser Asn Lys Thr Trp Gly
            345                 350                 355

aca aag ttc ggc aaa tac atg gag cgt cga atc gcc gcc taatccagca    1220
Thr Lys Phe Gly Lys Tyr Met Glu Arg Arg Ile Ala Ala
        360                 365                 370

agccagcgtg atc                                                   1233
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<210> 1172
<211> 370
<212> PRT
<213> Corynebacterium glutamicum

<400> 1172

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Met Phe Tyr Phe Thr Val Asn Asn Pro Gln Asp Pro Leu Ser Thr Glu
  1               5                  10                  15

Ile Val Glu Thr Asn Arg Arg Asp Leu Ala Phe Trp His Arg Leu Arg
             20                  25                  30

Pro Lys Asp Asp Asp Asp Leu Ala Thr Ala Ile Asn Lys Ile Cys Val
         35                  40                  45

Arg Thr Gly Leu Ser Arg Lys Leu Ile Ala Ala Cys Leu Phe Ser Ile
     50                  55                  60

Cys Phe Leu Pro Tyr Leu Pro Asn Phe His Lys Leu Val Glu Lys Leu
 65                  70                  75                  80

Gly His Leu Asp Met Ala Arg Ile Asn Ala Ile Thr Lys Ala Gly Glu
                 85                  90                  95

Lys Val Pro Ser Glu Lys Arg Glu Leu Phe Asp Ala Tyr Leu Val Asp
            100                 105                 110

Tyr Leu Thr Pro Arg Ala Glu Ala Gln Cys Leu Pro Gln Ala Ser Ser
        115                 120                 125

Ile Ser Ala Met Met Arg Lys Phe Ile Ala Gln His Cys Pro Asp Asp
    130                 135                 140

Lys Ala Ser Ser Ala Thr Asn Asp Gly Ser Ile Arg Tyr Arg Arg Asn
```

```
145                 150                 155                 160

Asn Lys Gly Gly Ile Ser Ile Thr Val Asp Ala Thr Ala Ser Glu Val
                165                 170                 175

Thr Glu Ile Lys Ala Ala Leu Glu Gln Met Ser Lys Asp Lys Asp Cys
            180                 185                 190

Thr Pro Gly Thr Ser Leu Leu His Ile Ile Arg Gly Leu Pro Thr Lys
        195                 200                 205

Val Val Leu Asn Thr Tyr Gly Thr Lys Asp Ser Pro Glu Tyr Leu Glu
    210                 215                 220

Gly Gly Thr Trp Leu Ser Lys Glu Gln Ser Glu Phe Trp Lys Thr Arg
225                 230                 235                 240

Thr Thr Ser Ser Arg Asp Met Asp Ala Ala His Phe Ser Tyr Thr Thr
                245                 250                 255

Ala Tyr Ala Pro Thr Arg Glu Met Arg Val Tyr Ile Lys Gly Leu Arg
            260                 265                 270

Thr Thr Cys Ser Val Pro Gly Cys Ser Val Ala Val Glu Asn Cys Gln
        275                 280                 285

Leu Asp His Ile Ile Pro Trp Gly Glu Gly Gly Pro Thr Thr Pro Trp
    290                 295                 300

Asn Ile His Pro Leu Cys Val Phe His His Ile Gln Lys Thr Glu Gly
305                 310                 315                 320

Arg Leu Gln Cys Tyr Pro Leu Pro Asp Gly Thr Val Leu Phe Leu Val
                325                 330                 335

Asp Gly Ile Pro Val Phe Ser Ile Pro Asp Gly Pro Leu Ser Lys Ser
            340                 345                 350

Asn Lys Thr Trp Gly Thr Lys Phe Gly Lys Tyr Met Glu Arg Arg Ile
        355                 360                 365

Ala Ala
    370
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Application Filed with the Chinese Patent Office on 2008-12-29

<2105> 1173
<211> 627
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(604)
<223> RXN02460

<400> 1173
gcgccgtcga agccggactc gtaggcgtct actaccagca atttgaccgt gcagtcgtcg 60

aaatcgtcgg actgttcggg ctagaaggag aattctaatc ttg cgc gtc tac atc 115
                                                Leu Arg Val Tyr Ile
                                                  1   5

```
cca gca acg ttt tcc aca ctc cgc gga ctc aat gaa tcc cgc gtc atc   163
Pro Ala Thr Phe Ser Thr Leu Arg Gly Leu Asn Glu Ser Arg Val Ile
                10                  15                  20

aca gca cgc tcc gga tac ggt ttc gca gtc acc cca gca ctc ctt gac   211
Thr Ala Arg Ser Gly Tyr Gly Phe Ala Val Thr Pro Ala Leu Leu Asp
            25                  30                  35

ttc tac acc gac ggt gac gaa gaa gaa atc gca cat gca gcc ttc caa   259
Phe Tyr Thr Asp Gly Asp Glu Glu Glu Ile Ala His Ala Ala Phe Gln
        40                  45                  50

gac gcc gca gaa gcc tcc atc cga ctc ctc gca atc ggc gac gaa gaa   307
Asp Ala Ala Glu Ala Ser Ile Arg Leu Leu Ala Ile Gly Asp Glu Glu
    55                  60                  65

aca ttt ccc tac cgc aga gtc gtc gtc tca gta gat gtt gac gac tcc   355
Thr Phe Pro Tyr Arg Arg Val Val Val Ser Val Asp Val Asp Asp Ser
70                  75                  80                  85

gtg gtg acc tac cag cct gaa aac ggc gaa tcc gta gtc aaa ctc agc   403
Val Val Thr Tyr Gln Pro Glu Asn Gly Glu Ser Val Val Lys Leu Ser
                90                  95                  100

cca gcg cac atc aac ctc gac gac gtg gca gca atc cac atc gac gtt   451
Pro Ala His Ile Asn Leu Asp Asp Val Ala Ala Ile His Ile Asp Val
            105                 110                 115

gaa gcc tcc gaa gca gac acc aaa aaa gct atc gaa gtc atc gac gaa   499
Glu Ala Ser Glu Ala Asp Thr Lys Lys Ala Ile Glu Val Ile Asp Glu
        120                 125                 130

tcc gac ctc ggc gaa gaa gac gcc gaa ctc acc gtc gga gac gcc caa   547
Ser Asp Leu Gly Glu Glu Asp Ala Glu Leu Thr Val Gly Asp Ala Gln
    135                 140                 145

gac aac ttc atg gcc tgg tac gac cca gaa gag ctc ccc ttc cta gtc   595
Asp Asn Phe Met Ala Trp Tyr Asp Pro Glu Glu Leu Pro Phe Leu Val
150                 155                 160                 165

gag ctc ctc tagatcacat atcccacgcg tcg                            627
Glu Leu Leu
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<210> 1174
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 1174

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Leu Arg Val Tyr Ile Pro Ala Thr Phe Ser Thr Leu Arg Gly Leu Asn
  1               5                  10                  15

Glu Ser Arg Val Ile Thr Ala Arg Ser Gly Tyr Gly Phe Ala Val Thr
            20                  25                  30

Pro Ala Leu Leu Asp Phe Tyr Thr Asp Gly Asp Glu Glu Glu Ile Ala
        35                  40                  45
```

```
His Ala Ala Phe Gln Asp Ala Ala Glu Ala Ser Ile Arg Leu Leu Ala
     50                  55                  60

Ile Gly Asp Glu Glu Thr Phe Pro Tyr Arg Arg Val Val Val Ser Val
 65                  70                  75                  80

Asp Val Asp Asp Ser Val Val Thr Tyr Gln Pro Glu Asn Gly Glu Ser
                85                  90                  95

Val Val Lys Leu Ser Pro Ala His Ile Asn Leu Asp Asp Val Ala Ala
            100                 105                 110

Ile His Ile Asp Val Glu Ala Ser Glu Ala Asp Thr Lys Lys Ala Ile
        115                 120                 125

Glu Val Ile Asp Glu Ser Asp Leu Gly Glu Glu Asp Ala Glu Leu Thr
    130                 135                 140

Val Gly Asp Ala Gln Asp Asn Phe Met Ala Trp Tyr Asp Pro Glu Glu
145                 150                 155                 160

Leu Pro Phe Leu Val Glu Leu Leu
                165
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Application as filed - Sequence Listing

<210> 1175
<211> 627
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(604)
<223> FRXA02460

<400> 1175

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gcgccgtcga agccggactc gtaggcgtct actaccagca atttgaccgt gcagtcgtcg 60

aaatcgtcgg actgttcggg ctagaaggag aattctaatc ttg cgc gtc tac atc   115
                                               Leu Arg Val Tyr Ile
                                                 1               5

cca gca acg ttt tcc aca ctc cgc gga ctc aat gaa tcc cgc gtc atc   163
Pro Ala Thr Phe Ser Thr Leu Arg Gly Leu Asn Glu Ser Arg Val Ile
                10                  15                  20

aca gca cgc tcc gga tac ggt ttc gca gtc acc cca gca ctc ctt gac   211
Thr Ala Arg Ser Gly Tyr Gly Phe Ala Val Thr Pro Ala Leu Leu Asp
            25                  30                  35

ttc tac acc gac ggt gac gaa gaa gaa atc gca cat gca gcc ttc caa   259
Phe Tyr Thr Asp Gly Asp Glu Glu Glu Ile Ala His Ala Ala Phe Gln
        40                  45                  50

gac gcc gca gaa gcc tcc atc cga ctc ctc gca atc ggc gac gaa gaa   307
Asp Ala Ala Glu Ala Ser Ile Arg Leu Leu Ala Ile Gly Asp Glu Glu
    55                  60                  65

aca ttt ccc tac cgc aga gtc gtc gtc tca gta gat gtt gac gac tcc   355
Thr Phe Pro Tyr Arg Arg Val Val Val Ser Val Asp Val Asp Asp Ser
70                  75                  80                  85
```

```
gtg gtg acc tac cag cct gaa aac ggc gaa tcc gta gtc aaa ctc agc   403
Val Val Thr Tyr Gln Pro Glu Asn Gly Glu Ser Val Val Lys Leu Ser
                 90                  95                 100

cca gcg cac atc aac ctc gac gac gtg gca gca atc cac atc gac gtt   451
Pro Ala His Ile Asn Leu Asp Asp Val Ala Ala Ile His Ile Asp Val
            105                 110                 115

gaa gcc tcc gaa gca gac acc aaa aaa gct atc gaa gtc atc gac gaa   499
Glu Ala Ser Glu Ala Asp Thr Lys Lys Ala Ile Glu Val Ile Asp Glu
        120                 125                 130

tcc gac ctc ggc gaa gaa gac gcc gaa ctc acc gtc gga gac gcc caa   547
Ser Asp Leu Gly Glu Glu Asp Ala Glu Leu Thr Val Gly Asp Ala Gln
    135                 140                 145

gac aac ttc atg gcc tgg tac gac cca gaa gag ctc ccc ttc cta gtc   595
Asp Asn Phe Met Ala Trp Tyr Asp Pro Glu Glu Leu Pro Phe Leu Val
150                 155                 160                 165

gag ctc ctc tagatcacat atcccacgcg tcg                            627
Glu Leu Leu
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<210> 1176
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 1176

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Leu Arg Val Tyr Ile Pro Ala Thr Phe Ser Thr Leu Arg Gly Leu Asn
  1               5                  10                  15

Glu Ser Arg Val Ile Thr Ala Arg Ser Gly Tyr Gly Phe Ala Val Thr
             20                  25                  30

Pro Ala Leu Leu Asp Phe Tyr Thr Asp Gly Asp Glu Glu Glu Ile Ala
         35                  40                  45

His Ala Ala Phe Gln Asp Ala Ala Glu Ala Ser Ile Arg Leu Leu Ala
     50                  55                  60

Ile Gly Asp Glu Glu Thr Phe Pro Tyr Arg Arg Val Val Val Ser Val
 65                  70                  75                  80

Asp Val Asp Asp Ser Val Val Thr Tyr Gln Pro Glu Asn Gly Glu Ser
                 85                  90                  95

Val Val Lys Leu Ser Pro Ala His Ile Asn Leu Asp Asp Val Ala Ala
            100                 105                 110

Ile His Ile Asp Val Glu Ala Ser Glu Ala Asp Thr Lys Lys Ala Ile
        115                 120                 125

Glu Val Ile Asp Glu Ser Asp Leu Gly Glu Glu Asp Ala Glu Leu Thr
    130                 135                 140

Val Gly Asp Ala Gln Asp Asn Phe Met Ala Trp Tyr Asp Pro Glu Glu
145                 150                 155                 160
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Leu Pro Phe Leu Val Glu Leu Leu
165

<210> 1177
<211> 1323
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1300)
<223> RXN02464

<400> 1177
actcgacatc ccagaaggtg tcaccgaacg agtcggacca ccaaccaaag ttctaggcgg 60

aacagcccca cgaccaccac gccgcacccg gaaataactt atg gca gca aag ctt 115
Met Ala Ala Lys Leu
1 5

caa cca ctc aaa cgc acc aaa aaa gac ctc atc gca acc ggt gtc atc 163
Gln Pro Leu Lys Arg Thr Lys Lys Asp Leu Ile Ala Thr Gly Val Ile
10 15 20

aca gca cta gca gtc att ggc gtc ggc acg gtc tgg gca acc gca cca 211
Thr Ala Leu Ala Val Ile Gly Val Gly Thr Val Trp Ala Thr Ala Pro
25 30 35

ata cga gga tct gaa ctc acc ccc gcc gac gaa cca ttc att ggc tca 259
Ile Arg Gly Ser Glu Leu Thr Pro Ala Asp Glu Pro Phe Ile Gly Ser
40 45 50

acc aca ctg gac gcc atc ccc gaa aca ctc agc gaa cat tgg cga gcc 307
Thr Thr Leu Asp Ala Ile Pro Glu Thr Leu Ser Glu His Trp Arg Ala
55 60 65

acc gac acc tta aca aac cac aaa ccc ctc atc acc ggc gga gtc atc 355
Thr Asp Thr Leu Thr Asn His Lys Pro Leu Ile Thr Gly Gly Val Ile
70 75 80 85

ttc acc gcc gac ggc aac acc att aag acc tac acc ccc gac ggc gcc 403
Phe Thr Ala Asp Gly Asn Thr Ile Lys Thr Tyr Thr Pro Asp Gly Ala
90 95 100

ctc ctg tgg agc tac gaa cgc gac aaa gaa ctc tgc agc ctc tcc gta 451
Leu Leu Trp Ser Tyr Glu Arg Asp Lys Glu Leu Cys Ser Leu Ser Val
105 110 115

gga ttc gac gcc gcc gtc gcc acc tac aaa acc gga atc gga tgt ggc 499
Gly Phe Asp Ala Ala Val Ala Thr Tyr Lys Thr Gly Ile Gly Cys Gly
120 125 130

gac gtc acc gcc atc aac gcc aac gac ggc caa tac caa gca aca cgc 547
Asp Val Thr Ala Ile Asn Ala Asn Asp Gly Gln Tyr Gln Ala Thr Arg
135 140 145

agc gca atc tcc agc gac cac gta gca ccg atc tcc tcg aac gat cgg 595
Ser Ala Ile Ser Ser Asp His Val Ala Pro Ile Ser Ser Asn Asp Arg
150 155 160 165

```
atc ggt gtt ctc ggg aca gaa cgc ttg gag ctt tgg cga tcc gat ctg   643
Ile Gly Val Leu Gly Thr Glu Arg Leu Glu Leu Trp Arg Ser Asp Leu
                170                 175                 180

gtg cga acc atc gaa tac ggc gat gtg gaa gct cct caa gaa tct ggg   691
Val Arg Thr Ile Glu Tyr Gly Asp Val Glu Ala Pro Gln Glu Ser Gly
            185                 190                 195

caa caa cca cat ccg gaa tgc tcg att acg tcc gcc atg aca cgc aaa   739
Gln Gln Pro His Pro Glu Cys Ser Ile Thr Ser Ala Met Thr Arg Lys
        200                 205                 210

gat cta ttg gct atc acc gag gat tgc cct gac gga tct tct tac ttg   787
Asp Leu Leu Ala Ile Thr Glu Asp Cys Pro Asp Gly Ser Ser Tyr Leu
    215                 220                 225

agg ttc atg ggc aca aca cca gac gat tcc cga act cct gaa atc acc   835
Arg Phe Met Gly Thr Thr Pro Asp Asp Ser Arg Thr Pro Glu Ile Thr
230                 235                 240                 245

caa gac ata gaa ata acc gat ggc agg atc gtt gcc atc ggt caa tca   883
Gln Asp Ile Glu Ile Thr Asp Gly Arg Ile Val Ala Ile Gly Gln Ser
                250                 255                 260

gtg gct gcg gtg tat aca aac gat cct tcg cct cga atc gtc tcc tac   931
Val Ala Ala Val Tyr Thr Asn Asp Pro Ser Pro Arg Ile Val Ser Tyr
            265                 270                 275

aac gat gat ggt gaa cta gtt gga gaa caa gca gtc gat gag gtt gag   979
Asn Asp Asp Gly Glu Leu Val Gly Glu Gln Ala Val Asp Glu Val Glu
        280                 285                 290

ttc ccg gat ccg ccg ttt caa agc gcg acc gct gat ctt cca cac cat   1027
Phe Pro Asp Pro Pro Phe Gln Ser Ala Thr Ala Asp Leu Pro His His
    295                 300                 305

atg agt tgg ttc aac gga gac agc ctc gta ctg ttc tct ccc act cag   1075
Met Ser Trp Phe Asn Gly Asp Ser Leu Val Leu Phe Ser Pro Thr Gln
310                 315                 320                 325

ctc aat gta cga caa agc ttc aat gat gct tta gga acc ggc att gcg   1123
Leu Asn Val Arg Gln Ser Phe Asn Asp Ala Leu Gly Thr Gly Ile Ala
                330                 335                 340

ttg aac gga agt ctc ctc tac ccc acc gct gag ggc atc acg gta gct   1171
Leu Asn Gly Ser Leu Leu Tyr Pro Thr Ala Glu Gly Ile Thr Val Ala
            345                 350                 355

aat tgg gac acc gga gag gtg cag cgc acc att ccg gtg gac cgt gcg   1219
Asn Trp Asp Thr Gly Glu Val Gln Arg Thr Ile Pro Val Asp Arg Ala
        360                 365                 370

ggc tac gac ggt gaa gtt gcg ctc ggc gtt gta ggg cag gtg atc gtc   1267
Gly Tyr Asp Gly Glu Val Ala Leu Gly Val Val Gly Gln Val Ile Val
    375                 380                 385

gaa aag cgt ggc tct gag atc gtt gct cta ggc tagatctcgt tgttagccca 1320
Glu Lys Arg Gly Ser Glu Ile Val Ala Leu Gly
390                 395                 400
```

aag 1323

<210> 1178
<211> 400
<212> PRT
<213> Corynebacterium glutamicum

<400> 1178

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Met Ala Ala Lys Leu Gln Pro Leu Lys Arg Thr Lys Lys Asp Leu Ile
  1               5                  10                  15

Ala Thr Gly Val Ile Thr Ala Leu Ala Val Ile Gly Val Gly Thr Val
             20                  25                  30

Trp Ala Thr Ala Pro Ile Arg Gly Ser Glu Leu Thr Pro Ala Asp Glu
         35                  40                  45

Pro Phe Ile Gly Ser Thr Thr Leu Asp Ala Ile Pro Glu Thr Leu Ser
     50                  55                  60

Glu His Trp Arg Ala Thr Asp Thr Leu Thr Asn His Lys Pro Leu Ile
 65                  70                  75                  80

Thr Gly Gly Val Ile Phe Thr Ala Asp Gly Asn Thr Ile Lys Thr Tyr
                 85                  90                  95

Thr Pro Asp Gly Ala Leu Leu Trp Ser Tyr Glu Arg Asp Lys Glu Leu
            100                 105                 110

Cys Ser Leu Ser Val Gly Phe Asp Ala Ala Val Ala Thr Tyr Lys Thr
        115                 120                 125

Gly Ile Gly Cys Gly Asp Val Thr Ala Ile Asn Ala Asn Asp Gly Gln
    130                 135                 140

Tyr Gln Ala Thr Arg Ser Ala Ile Ser Ser Asp His Val Ala Pro Ile
145                 150                 155                 160

Ser Ser Asn Asp Arg Ile Gly Val Leu Gly Thr Glu Arg Leu Glu Leu
                165                 170                 175

Trp Arg Ser Asp Leu Val Arg Thr Ile Glu Tyr Gly Asp Val Glu Ala
            180                 185                 190

Pro Gln Glu Ser Gly Gln Gln Pro His Pro Glu Cys Ser Ile Thr Ser
        195                 200                 205

Ala Met Thr Arg Lys Asp Leu Leu Ala Ile Thr Glu Asp Cys Pro Asp
    210                 215                 220

Gly Ser Ser Tyr Leu Arg Phe Met Gly Thr Thr Pro Asp Asp Ser Arg
225                 230                 235                 240

Thr Pro Glu Ile Thr Gln Asp Ile Glu Ile Thr Asp Gly Arg Ile Val
                245                 250                 255

Ala Ile Gly Gln Ser Val Ala Ala Val Tyr Thr Asn Asp Pro Ser Pro
            260                 265                 270

Arg Ile Val Ser Tyr Asn Asp Asp Gly Glu Leu Val Gly Glu Gln Ala
```

```
        275                 280                 285

Val Asp Glu Val Glu Phe Pro Asp Pro Pro Phe Gln Ser Ala Thr Ala
    290                 295                 300

Asp Leu Pro His His Met Ser Trp Phe Asn Gly Asp Ser Leu Val Leu
305                 310                 315                 320

Phe Ser Pro Thr Gln Leu Asn Val Arg Gln Ser Phe Asn Asp Ala Leu
                325                 330                 335

Gly Thr Gly Ile Ala Leu Asn Gly Ser Leu Leu Tyr Pro Thr Ala Glu
            340                 345                 350

Gly Ile Thr Val Ala Asn Trp Asp Thr Gly Glu Val Gln Arg Thr Ile
        355                 360                 365

Pro Val Asp Arg Ala Gly Tyr Asp Gly Glu Val Ala Leu Gly Val Val
    370                 375                 380

Gly Gln Val Ile Val Glu Lys Arg Gly Ser Glu Ile Val Ala Leu Gly
385                 390                 395                 400
```

<210> 1179
<211> 630
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(607)
<223> FRXA02464

<400> 1179

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acaaccacat ccggaatgct cgattacgtc cgccatgaca cgcaaagatc tattggctat 60

caccgaggat tgccctgacg gatcttctta cttgaggttc atg ggc aca aca cca   115
                                            Met Gly Thr Thr Pro
                                              1               5

gac gat tcc cga act cct gaa atc acc caa gac ata gaa ata acc gat   163
Asp Asp Ser Arg Thr Pro Glu Ile Thr Gln Asp Ile Glu Ile Thr Asp
                 10                  15                  20

ggc agg atc gtt gcc atc ggt caa tca gtg gct gcg gtg tat aca aac   211
Gly Arg Ile Val Ala Ile Gly Gln Ser Val Ala Ala Val Tyr Thr Asn
             25                  30                  35

gat cct tcg cct cga atc gtc tcc tac aac gat gat ggt gaa cta gtt   259
Asp Pro Ser Pro Arg Ile Val Ser Tyr Asn Asp Asp Gly Glu Leu Val
         40                  45                  50

gga gaa caa gca gtc gat gag gtt gag ttc ccg gat ccg ccg ttt caa   307
Gly Glu Gln Ala Val Asp Glu Val Glu Phe Pro Asp Pro Pro Phe Gln
     55                  60                  65

agc gcg acc gct gat ctt cca cac cat atg agt tgg ttc aac gga gac   355
```

```
Ser Ala Thr Ala Asp Leu Pro His His Met Ser Trp Phe Asn Gly Asp
 70                  75                  80                  85

agc ctc gta ctg ttc tct ccc act cag ctc aat gta cga caa agc ttc   403
Ser Leu Val Leu Phe Ser Pro Thr Gln Leu Asn Val Arg Gln Ser Phe
                 90                  95                 100

aat gat gct tta gga acc ggc att gcg ttg aac gga agt ctc ctc tac   451
Asn Asp Ala Leu Gly Thr Gly Ile Ala Leu Asn Gly Ser Leu Leu Tyr
            105                 110                 115

ccc acc gct gag ggc atc acg gta gct aat tgg gac acc gga gag gtg   499
Pro Thr Ala Glu Gly Ile Thr Val Ala Asn Trp Asp Thr Gly Glu Val
        120                 125                 130

cag cgc acc att ccg gtg gac cgt gcg ggc tac gac ggt gaa gtt gcg   547
Gln Arg Thr Ile Pro Val Asp Arg Ala Gly Tyr Asp Gly Glu Val Ala
    135                 140                 145

ctc ggc gtt gta ggg cag gtg atc gtc gaa aag cgt ggc tct gag atc   595
Leu Gly Val Val Gly Gln Val Ile Val Glu Lys Arg Gly Ser Glu Ile
150                 155                 160                 165

gtt gct cta ggc tagatctcgt tgttagccca aag                        630
Val Ala Leu Gly
```

<210> 1180
<211> 169
<212> PRT
<213> Corynebacterium glutamicum

<400> 1180

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Met Gly Thr Thr Pro Asp Asp Ser Arg Thr Pro Glu Ile Thr Gln Asp
  1               5                  10                  15

Ile Glu Ile Thr Asp Gly Arg Ile Val Ala Ile Gly Gln Ser Val Ala
             20                  25                  30

Ala Val Tyr Thr Asn Asp Pro Ser Pro Arg Ile Val Ser Tyr Asn Asp
         35                  40                  45

Asp Gly Glu Leu Val Gly Glu Gln Ala Val Asp Glu Val Glu Phe Pro
     50                  55                  60

Asp Pro Pro Phe Gln Ser Ala Thr Ala Asp Leu Pro His His Met Ser
 65                  70                  75                  80

Trp Phe Asn Gly Asp Ser Leu Val Leu Phe Ser Pro Thr Gln Leu Asn
                 85                  90                  95

Val Arg Gln Ser Phe Asn Asp Ala Leu Gly Thr Gly Ile Ala Leu Asn
            100                 105                 110

Gly Ser Leu Leu Tyr Pro Thr Ala Glu Gly Ile Thr Val Ala Asn Trp
        115                 120                 125

Asp Thr Gly Glu Val Gln Arg Thr Ile Pro Val Asp Arg Ala Gly Tyr
    130                 135                 140
```

```
Asp Gly Glu Val Ala Leu Gly Val Val Gly Gln Val Ile Val Glu Lys
145                 150                 155                 160

Arg Gly Ser Glu Ile Val Ala Leu Gly
                165
```

<210> 1181
<211> 522
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(499)
<223> RXN02465

<400> 1181

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ctggtgcaat ataaaagtta accaaccagt catccaatat gtcgcctaag tagtcttccc 60

aaagttaaca gctagaatca tggccgtgac ttctccgaac atg cct gca tca att   115
                                            Met Pro Ala Ser Ile
                                              1               5

cgc tgg ggc ggc atc gtc gcc ctc att caa tcc acc atc gga ttc ggt   163
Arg Trp Gly Gly Ile Val Ala Leu Ile Gln Ser Thr Ile Gly Phe Gly
                10                  15                  20

tac gcc ttt ttc ctt att tac agg gaa gct acg ggc gag acg gat cca   211
Tyr Ala Phe Phe Leu Ile Tyr Arg Glu Ala Thr Gly Glu Thr Asp Pro
            25                  30                  35

agc atc gtc tac gaa acc gat aac gcc aac acg tgg gtt ggc tac ggt   259
Ser Ile Val Tyr Glu Thr Asp Asn Ala Asn Thr Trp Val Gly Tyr Gly
        40                  45                  50

acc gct gca ttc ttc atc att gtg ttc gga acg gtt gtt gca ggc gca   307
Thr Ala Ala Phe Phe Ile Ile Val Phe Gly Thr Val Val Ala Gly Ala
    55                  60                  65

atc aac atg atg aag ggg cat cgc tgg gga cgc gga gct gtc gtc atg   355
Ile Asn Met Met Lys Gly His Arg Trp Gly Arg Gly Ala Val Val Met
70                  75                  80                  85

ctg aat att att ttg ttg ccg gct gcg tat tac atg ttt atc gaa ggc   403
Leu Asn Ile Ile Leu Leu Pro Ala Ala Tyr Tyr Met Phe Ile Glu Gly
                90                  95                 100

cga ttc tcc tgg gcg atc gtc aca gga atc tca gct ctc ttc gtt ttg   451
Arg Phe Ser Trp Ala Ile Val Thr Gly Ile Ser Ala Leu Phe Val Leu
            105                 110                 115

ggc gca ctg ttt aat aag cgc gcc gtc ctt tgg gct aac aac gag atc   499
Gly Ala Leu Phe Asn Lys Arg Ala Val Leu Trp Ala Asn Asn Glu Ile
        120                 125                 130

tagcctagag caacgatctc aga                                       522
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<210> 1182
<211> 133

<212> PRT
<213> Corynebacterium glutamicum

<400> 1182
Met Pro Ala Ser Ile Arg Trp Gly Gly Ile Val Ala Leu Ile Gln Ser
1 5 10 15

Thr Ile Gly Phe Gly Tyr Ala Phe Phe Leu Ile Tyr Arg Glu Ala Thr
20 25 30

Gly Glu Thr Asp Pro Ser Ile Val Tyr Glu Thr Asp Asn Ala Asn Thr
35 40 45

Trp Val Gly Tyr Gly Thr Ala Ala Phe Phe Ile Ile Val Phe Gly Thr
50 55 60

Val Val Ala Gly Ala Ile Asn Met Met Lys Gly His Arg Trp Gly Arg
65 70 75 80

Gly Ala Val Val Met Leu Asn Ile Ile Leu Leu Pro Ala Ala Tyr Tyr
85 90 95

Met Phe Ile Glu Gly Arg Phe Ser Trp Ala Ile Val Thr Gly Ile Ser
100 105 110

Ala Leu Phe Val Leu Gly Ala Leu Phe Asn Lys Arg Ala Val Leu Trp
115 120 125

Ala Asn Asn Glu Ile
130

<210> 1183
<211> 522
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(499)
<223> FRXA02465

<400> 1183
ctggtgcaat ataaaagtta accaaccagt catccaatat gtcgcctaag tagtcttccc 60

aaagttaaca gctagaatca tggccgtgac ttctccgaac atg cct gca tca att 115
Met Pro Ala Ser Ile
1 5

cgc tgg ggc ggc atc gtc gcc ctc att caa tcc acc atc gga ttc ggt 163
Arg Trp Gly Gly Ile Val Ala Leu Ile Gln Ser Thr Ile Gly Phe Gly
10 15 20

tac gcc ttt ttc ctt att tac agg gaa gct acg ggc gag acg gat cca 211
Tyr Ala Phe Phe Leu Ile Tyr Arg Glu Ala Thr Gly Glu Thr Asp Pro
25 30 35

agc atc gtc tac gaa acc gat aac gcc aac acg tgg gtt ggc tac ggt 259
Ser Ile Val Tyr Glu Thr Asp Asn Ala Asn Thr Trp Val Gly Tyr Gly
40 45 50

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acc gct gca ttc ttc atc att gtg ttc gga acg gtt gtt gca ggc gca   307
Thr Ala Ala Phe Phe Ile Ile Val Phe Gly Thr Val Val Ala Gly Ala
     55                  60                  65

atc aac atg atg aag ggg cat cgc tgg gga cgc gga gct gtc gtc atg   355
Ile Asn Met Met Lys Gly His Arg Trp Gly Arg Gly Ala Val Val Met
 70                  75                  80                  85

ctg aat att att ttg ttg ccg gct gcg tat tac atg ttt atc gaa ggc   403
Leu Asn Ile Ile Leu Leu Pro Ala Ala Tyr Tyr Met Phe Ile Glu Gly
                 90                  95                 100

cga ttc tcc tgg gcg atc gtc aca gga atc tca gct ctc ttc gtt ttg   451
Arg Phe Ser Trp Ala Ile Val Thr Gly Ile Ser Ala Leu Phe Val Leu
            105                 110                 115

ggc gca ctg ttt aat aag cgc gcc gtc ctt tgg gct aac aac gag atc   499
Gly Ala Leu Phe Asn Lys Arg Ala Val Leu Trp Ala Asn Asn Glu Ile
        120                 125                 130

tagcctagag caacgatctc aga                                        522
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<210> 1184
<211> 133
<212> PRT
<213> Corynebacterium glutamicum

<400> 1184

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Met Pro Ala Ser Ile Arg Trp Gly Gly Ile Val Ala Leu Ile Gln Ser
  1               5                  10                  15

Thr Ile Gly Phe Gly Tyr Ala Phe Phe Leu Ile Tyr Arg Glu Ala Thr
             20                  25                  30

Gly Glu Thr Asp Pro Ser Ile Val Tyr Glu Thr Asp Asn Ala Asn Thr
         35                  40                  45

Trp Val Gly Tyr Gly Thr Ala Ala Phe Phe Ile Ile Val Phe Gly Thr
     50                  55                  60

Val Val Ala Gly Ala Ile Asn Met Met Lys Gly His Arg Trp Gly Arg
 65                  70                  75                  80

Gly Ala Val Val Met Leu Asn Ile Ile Leu Leu Pro Ala Ala Tyr Tyr
                 85                  90                  95

Met Phe Ile Glu Gly Arg Phe Ser Trp Ala Ile Val Thr Gly Ile Ser
            100                 105                 110

Ala Leu Phe Val Leu Gly Ala Leu Phe Asn Lys Arg Ala Val Leu Trp
        115                 120                 125

Ala Asn Asn Glu Ile
    130
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<210> 1185
<211> 187
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(187)
<223> RXN02466

<400> 1185
cgaaccgcaa agcgttccgc tgacggaact gccgcctggc ggcagctaca ccgaaaccgg 60

tgctggcact ttccgccagg tcggcgctgc tcttcctcgc gtg ggc gag ggg cag 115
Val Gly Glu Gly Gln
1 5

gaa caa act ttt acg tac gtc att gag att gag gat ggc gtc aac acg 163
Glu Gln Thr Phe Thr Tyr Val Ile Glu Ile Glu Asp Gly Val Asn Thr
10 15 20

gcc gct tat ggt ggc gac gat gcg 187
Ala Ala Tyr Gly Gly Asp Asp Ala
25

<210> 1186
<211> 29
<212> PRT
<213> Corynebacterium glutamicum

<400> 1186
Val Gly Glu Gly Gln Glu Gln Thr Phe Thr Tyr Val Ile Glu Ile Glu
1 5 10 15

Asp Gly Val Asn Thr Ala Ala Tyr Gly Gly Asp Asp Ala
20 25

<210> 1187
<211> 187
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(187)
<223> FRXA02466

<400> 1187
cgaaccgcaa agcgttccgc tgacggaact gccgcctggc ggcagctaca ccgaaaccgg 60

tgctggcact ttccgccagg tcggcgctgc tcttcctcgc gtg ggc gag ggg cag 115
Val Gly Glu Gly Gln
1 5

gaa caa act ttt acg tac gtc att gag att gag gat ggc gtc aac acg 163
Glu Gln Thr Phe Thr Tyr Val Ile Glu Ile Glu Asp Gly Val Asn Thr
10 15 20

gcc gct tat ggt ggc gac gat gcg 187
Ala Ala Tyr Gly Gly Asp Asp Ala
25

<210> 1188
<211> 29
<212> PRT
<213> Corynebacterium glutamicum

<400> 1188
Val Gly Glu Gly Gln Glu Gln Thr Phe Thr Tyr Val Ile Glu Ile Glu
1 5 10 15

Asp Gly Val Asn Thr Ala Ala Tyr Gly Gly Asp Asp Ala
20 25

<210> 1189
<211> 294
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(271)
<223> RXN02505

<400> 1189
tcggaaagca atccggaaca ttcaggttgt agacaatgtc atcagttcag ttgaccgtcc 60

cattaagcgc actggtcgtt tgcgtattcc gggggtcttt gtg gct ggc act cat 115
Val Ala Gly Thr His
1 5

gcg tat gtc aat gaa act ctt tcg gaa aat gag ttc agc atg tgc cga 163
Ala Tyr Val Asn Glu Thr Leu Ser Glu Asn Glu Phe Ser Met Cys Arg
10 15 20

aag aat gaa cct ggt ttg gtc att gag ctg gag aac atc agc atc gat 211
Lys Asn Glu Pro Gly Leu Val Ile Glu Leu Glu Asn Ile Ser Ile Asp
25 30 35

cgc att gtc att tcc aca cca gat gcc cac cgc tat gcg gat gag ctc 259
Arg Ile Val Ile Ser Thr Pro Asp Ala His Arg Tyr Ala Asp Glu Leu
40 45 50

atg gcg gct gtt tagaactcag tttccgtcaa taa 294
Met Ala Ala Val
55

<210> 1190
<211> 57
<212> PRT
<213> Corynebacterium glutamicum

<400> 1190
Val Ala Gly Thr His Ala Tyr Val Asn Glu Thr Leu Ser Glu Asn Glu
1 5 10 15

Phe Ser Met Cys Arg Lys Asn Glu Pro Gly Leu Val Ile Glu Leu Glu
20 25 30

Asn Ile Ser Ile Asp Arg Ile Val Ile Ser Thr Pro Asp Ala His Arg
35 40 45

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Tyr Ala Asp Glu Leu Met Ala Ala Val
     50                  55


<210> 1191
<211> 294
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(271)
<223> FRXA02505

<400> 1191
tcggaaagca atccggaaca ttcaggttgt agacaatgtc atcagttcag ttgaccgtcc 60

cattaagcgc actggtcgtt tgcgtattcc gggggtcttt gtg gct ggc act cat   115
                                              Val Ala Gly Thr His
                                                1               5

gcg tat gtc aat gaa act ctt tcg gaa aat gag ttc agc atg tgc cga   163
Ala Tyr Val Asn Glu Thr Leu Ser Glu Asn Glu Phe Ser Met Cys Arg
               10                  15                  20

aag aat gaa cct ggt ttg gtc att gag ctg gag aac atc agc atc gat   211
Lys Asn Glu Pro Gly Leu Val Ile Glu Leu Glu Asn Ile Ser Ile Asp
            25                  30                  35

cgc att gtc att tcc aca cca gat gcc cac cgc tat gcg gat gag ctc   259
Arg Ile Val Ile Ser Thr Pro Asp Ala His Arg Tyr Ala Asp Glu Leu
         40                  45                  50

atg gcg gct gtt tagaactcag tttccgtcaa taa                        294
Met Ala Ala Val
     55


<210> 1192
<211> 57
<212> PRT
<213> Corynebacterium glutamicum

<400> 1192
Val Ala Gly Thr His Ala Tyr Val Asn Glu Thr Leu Ser Glu Asn Glu
  1               5                  10                  15

Phe Ser Met Cys Arg Lys Asn Glu Pro Gly Leu Val Ile Glu Leu Glu
            20                  25                  30

Asn Ile Ser Ile Asp Arg Ile Val Ile Ser Thr Pro Asp Ala His Arg
         35                  40                  45

Tyr Ala Asp Glu Leu Met Ala Ala Val
     50                  55


<210> 1193
<211> 759
<212> DNA
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<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(736)
<223> RXN02510

<400> 1193
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ccgagcgagg actccattgc agctcgcagg tagccctgag atg gac tca tct gac 115
Met Asp Ser Ser Asp
1 5

agc cac gtt ggt cag gat gta tat gtt gat caa ggt cta ggg gag ccc 163
Ser His Val Gly Gln Asp Val Tyr Val Asp Gln Gly Leu Gly Glu Pro
10 15 20

gac aga ctg gaa cgt ctg tgg gcg ccc tac cgg atg agc tac atc aac 211
Asp Arg Leu Glu Arg Leu Trp Ala Pro Tyr Arg Met Ser Tyr Ile Asn
25 30 35

act cga tct ggc ggt aag caa tca act acc gcc aag cgg gac ccc ttc 259
Thr Arg Ser Gly Gly Lys Gln Ser Thr Thr Ala Lys Arg Asp Pro Phe
40 45 50

att gag gtt ccc aaa atg agt gat gag gac ggc ctg atc gtt gcg cgg 307
Ile Glu Val Pro Lys Met Ser Asp Glu Asp Gly Leu Ile Val Ala Arg
55 60 65

ggt gag ctg gtg tat tgc gta ctc aac ttg tat ccc tac aac gct gga 355
Gly Glu Leu Val Tyr Cys Val Leu Asn Leu Tyr Pro Tyr Asn Ala Gly
70 75 80 85

cac atg atg gtg atc cca ttc cgt aag gaa aag aat cta gag gat ttg 403
His Met Met Val Ile Pro Phe Arg Lys Glu Lys Asn Leu Glu Asp Leu
90 95 100

agc ttg gca gaa tct gcg gag ttg atg ctc ttt acc caa acg gcc atc 451
Ser Leu Ala Glu Ser Ala Glu Leu Met Leu Phe Thr Gln Thr Ala Ile
105 110 115

aag gcg ctg aag cag gtg tca aac cct gat gct gtc aat gtt ggt tta 499
Lys Ala Leu Lys Gln Val Ser Asn Pro Asp Ala Val Asn Val Gly Leu
120 125 130

aac ctt ggc aaa gca tcg ggt ggc tca gtg gga gat cac ctt cat gtc 547
Asn Leu Gly Lys Ala Ser Gly Gly Ser Val Gly Asp His Leu His Val
135 140 145

cat gtg gtg cct agg tgg tcg ggt gat gct aat ttc atg act gtg att 595
His Val Val Pro Arg Trp Ser Gly Asp Ala Asn Phe Met Thr Val Ile
150 155 160 165

gac ggt gtc aaa gtg cta ccg cag acc ctg cgt caa acc agg gcc atg 643
Asp Gly Val Lys Val Leu Pro Gln Thr Leu Arg Gln Thr Arg Ala Met
170 175 180

ctt gcg caa gca tgg ggc acc att gat ggg gca cca ggc act gtc gac 691
Leu Ala Gln Ala Trp Gly Thr Ile Asp Gly Ala Pro Gly Thr Val Asp
185 190 195

```
cca acg ctg act tca gcg atc cgt acc gca gca ccg aag gag cac       736
Pro Thr Leu Thr Ser Ala Ile Arg Thr Ala Ala Pro Lys Glu His
        200                 205                 210

tgatgctggg acttcatgga cgt                                         759
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<210> 1194
<211> 212
<212> PRT
<213> Corynebacterium glutamicum

<400> 1194

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Met Asp Ser Ser Asp Ser His Val Gly Gln Asp Val Tyr Val Asp Gln
  1               5                  10                  15

Gly Leu Gly Glu Pro Asp Arg Leu Glu Arg Leu Trp Ala Pro Tyr Arg
             20                  25                  30

Met Ser Tyr Ile Asn Thr Arg Ser Gly Gly Lys Gln Ser Thr Thr Ala
         35                  40                  45

Lys Arg Asp Pro Phe Ile Glu Val Pro Lys Met Ser Asp Glu Asp Gly
     50                  55                  60

Leu Ile Val Ala Arg Gly Glu Leu Val Tyr Cys Val Leu Asn Leu Tyr
 65                  70                  75                  80

Pro Tyr Asn Ala Gly His Met Met Val Ile Pro Phe Arg Lys Glu Lys
                 85                  90                  95

Asn Leu Glu Asp Leu Ser Leu Ala Glu Ser Ala Glu Leu Met Leu Phe
            100                 105                 110

Thr Gln Thr Ala Ile Lys Ala Leu Lys Gln Val Ser Asn Pro Asp Ala
        115                 120                 125

Val Asn Val Gly Leu Asn Leu Gly Lys Ala Ser Gly Gly Ser Val Gly
    130                 135                 140

Asp His Leu His Val His Val Val Pro Arg Trp Ser Gly Asp Ala Asn
145                 150                 155                 160

Phe Met Thr Val Ile Asp Gly Val Lys Val Leu Pro Gln Thr Leu Arg
                165                 170                 175

Gln Thr Arg Ala Met Leu Ala Gln Ala Trp Gly Thr Ile Asp Gly Ala
            180                 185                 190

Pro Gly Thr Val Asp Pro Thr Leu Thr Ser Ala Ile Arg Thr Ala Ala
        195                 200                 205

Pro Lys Glu His
    210
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<210> 1195
<211> 759
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(736)
<223> FRXA02510

<400> 1195
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ccgagcgagg actccattgc agctcgcagg tagccctgag atg gac tca tct gac 115
Met Asp Ser Ser Asp
1 5

agc cac gtt ggt cag gat gta tat gtt gat caa ggt cta ggg gag ccc 163
Ser His Val Gly Gln Asp Val Tyr Val Asp Gln Gly Leu Gly Glu Pro
10 15 20

gac aga ctg gaa cgt ctg tgg gcg ccc tac cgg atg agc tac atc aac 211
Asp Arg Leu Glu Arg Leu Trp Ala Pro Tyr Arg Met Ser Tyr Ile Asn
25 30 35

act cga tct ggc ggt aag caa tca act acc gcc aag cgg gac ccc ttc 259
Thr Arg Ser Gly Gly Lys Gln Ser Thr Thr Ala Lys Arg Asp Pro Phe
40 45 50

att gag gtt ccc aaa atg agt gat gag gac ggc ctg atc gtt gcg cgg 307
Ile Glu Val Pro Lys Met Ser Asp Glu Asp Gly Leu Ile Val Ala Arg
55 60 65

ggt gag ctg gtg tat tgc gta ctc aac ttg tat ccc tac aac gct gga 355
Gly Glu Leu Val Tyr Cys Val Leu Asn Leu Tyr Pro Tyr Asn Ala Gly
70 75 80 85

cac atg atg gtg atc cca ttc cgt aag gaa aag aat cta gag gat ttg 403
His Met Met Val Ile Pro Phe Arg Lys Glu Lys Asn Leu Glu Asp Leu
90 95 100

agc ttg gca gaa tct gcg gag ttg atg ctc ttt acc caa acg gcc atc 451
Ser Leu Ala Glu Ser Ala Glu Leu Met Leu Phe Thr Gln Thr Ala Ile
105 110 115

aag gcg ctg aag cag gtg tca aac cct gat gct gtc aat gtt ggt tta 499
Lys Ala Leu Lys Gln Val Ser Asn Pro Asp Ala Val Asn Val Gly Leu
120 125 130

aac ctt ggc aaa gca tcg ggt ggc tca gtg gga gat cac ctt cat gtc 547
Asn Leu Gly Lys Ala Ser Gly Gly Ser Val Gly Asp His Leu His Val
135 140 145

cat gtg gtg cct agg tgg tcg ggt gat gct aat ttc atg act gtg att 595
His Val Val Pro Arg Trp Ser Gly Asp Ala Asn Phe Met Thr Val Ile
150 155 160 165

gac ggt gtc aaa gtg cta ccg cag acc ctg cgt caa acc agg gcc atg 643
Asp Gly Val Lys Val Leu Pro Gln Thr Leu Arg Gln Thr Arg Ala Met
170 175 180

ctt gcg caa gca tgg ggc acc att gat ggg gca cca ggc act gtc gac 691
Leu Ala Gln Ala Trp Gly Thr Ile Asp Gly Ala Pro Gly Thr Val Asp
185 190 195

```
cca acg ctg act tca gcg atc cgt acc gca gca ccg aag gag cac       736
Pro Thr Leu Thr Ser Ala Ile Arg Thr Ala Ala Pro Lys Glu His
        200                 205                 210

tgatgctggg acttcatgga cgt                                         759


<210> 1196
<211> 212
<212> PRT
<213> Corynebacterium glutamicum

<400> 1196
Met Asp Ser Ser Asp Ser His Val Gly Gln Asp Val Tyr Val Asp Gln
  1               5                  10                  15

Gly Leu Gly Glu Pro Asp Arg Leu Glu Arg Leu Trp Ala Pro Tyr Arg
             20                  25                  30

Met Ser Tyr Ile Asn Thr Arg Ser Gly Gly Lys Gln Ser Thr Thr Ala
         35                  40                  45

Lys Arg Asp Pro Phe Ile Glu Val Pro Lys Met Ser Asp Glu Asp Gly
     50                  55                  60

Leu Ile Val Ala Arg Gly Glu Leu Val Tyr Cys Val Leu Asn Leu Tyr
 65                  70                  75                  80

Pro Tyr Asn Ala Gly His Met Met Val Ile Pro Phe Arg Lys Glu Lys
                 85                  90                  95

Asn Leu Glu Asp Leu Ser Leu Ala Glu Ser Ala Glu Leu Met Leu Phe
            100                 105                 110

Thr Gln Thr Ala Ile Lys Ala Leu Lys Gln Val Ser Asn Pro Asp Ala
        115                 120                 125

Val Asn Val Gly Leu Asn Leu Gly Lys Ala Ser Gly Gly Ser Val Gly
    130                 135                 140

Asp His Leu His Val His Val Val Pro Arg Trp Ser Gly Asp Ala Asn
145                 150                 155                 160

Phe Met Thr Val Ile Asp Gly Val Lys Val Leu Pro Gln Thr Leu Arg
                165                 170                 175

Gln Thr Arg Ala Met Leu Ala Gln Ala Trp Gly Thr Ile Asp Gly Ala
            180                 185                 190

Pro Gly Thr Val Asp Pro Thr Leu Thr Ser Ala Ile Arg Thr Ala Ala
        195                 200                 205

Pro Lys Glu His
    210


<210> 1197
<211> 1752
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1729)
<223> RXN02519

<400> 1197
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gcgcatcggc accgctggtt ccagatcagc gaccctccac gtg gaa gac gag cag 115
Val Glu Asp Glu Gln
1 5

agc cct tta ggg gca acg ctt ttc gac gtc gcg acc ggc gcg agc tcc 163
Ser Pro Leu Gly Ala Thr Leu Phe Asp Val Ala Thr Gly Ala Ser Ser
10 15 20

atc aac gac cgc gat acc gac gcc tca ggg ctt gag cct gaa aag att 211
Ile Asn Asp Arg Asp Thr Asp Ala Ser Gly Leu Glu Pro Glu Lys Ile
25 30 35

cgc cga ttt gca tgg ctg cgc ctg atc ggc acc atg ggt gcg tta atg 259
Arg Arg Phe Ala Trp Leu Arg Leu Ile Gly Thr Met Gly Ala Leu Met
40 45 50

atc gcg ttt ggt gcg ctg ggc gcg ggt gca ctt ccg gtg gtg aat aat 307
Ile Ala Phe Gly Ala Leu Gly Ala Gly Ala Leu Pro Val Val Asn Asn
55 60 65

ccg tat gtg gat ttc cct ggc gga aac ttc atg agc cga atg ctg cag 355
Pro Tyr Val Asp Phe Pro Gly Gly Asn Phe Met Ser Arg Met Leu Gln
70 75 80 85

acc tct tcc atg atc gtg ctc atc ggc gtg gga ttt ttg gtg ctg gcg 403
Thr Ser Ser Met Ile Val Leu Ile Gly Val Gly Phe Leu Val Leu Ala
90 95 100

tgg gtg tta atg gca ccg ctg gtg ggt att cct ttt aaa cgc agc gga 451
Trp Val Leu Met Ala Pro Leu Val Gly Ile Pro Phe Lys Arg Ser Gly
105 110 115

aac aga aca gcc agc gtg agt ttg tcc atg ctg cgc cgc aca ttt ggc 499
Asn Arg Thr Ala Ser Val Ser Leu Ser Met Leu Arg Arg Thr Phe Gly
120 125 130

gcc tgg gta gcg ccc atc atg ctc acc gcc cca ctg ttt act caa gac 547
Ala Trp Val Ala Pro Ile Met Leu Thr Ala Pro Leu Phe Thr Gln Asp
135 140 145

att tat tct tat ctg gca caa ggc tct gtg acc gcg cag gga atg gat 595
Ile Tyr Ser Tyr Leu Ala Gln Gly Ser Val Thr Ala Gln Gly Met Asp
150 155 160 165

gcc tac gcc ggt gga ccg ctt gaa cta ttg ggg ccc gat aat cat ctg 643
Ala Tyr Ala Gly Gly Pro Leu Glu Leu Leu Gly Pro Asp Asn His Leu
170 175 180

gca cgg tcc gtg ccc ttt att tgg gcc cag tcg ccc tcg ccc tac ggc 691
Ala Arg Ser Val Pro Phe Ile Trp Ala Gln Ser Pro Ser Pro Tyr Gly
185 190 195

cct gtt gcg ctg agc atc gcg gcg tcg ata agc gtt att act aat gac 739

```
Pro Val Ala Leu Ser Ile Ala Ala Ser Ile Ser Val Ile Thr Asn Asp
        200                 205                 210

agc atc gtt gga ggc gtg ctg gcg cac cgt att gcg tcg ctg ctg ggc   787
Ser Ile Val Gly Gly Val Leu Ala His Arg Ile Ala Ser Leu Leu Gly
    215                 220                 225

gtt gtg gct gca ggc tgg gcg atc acc atg ctg gcc agg cgc tgt cgg   835
Val Val Ala Ala Gly Trp Ala Ile Thr Met Leu Ala Arg Arg Cys Arg
230                 235                 240                 245

gta tct gaa gaa gcg tcc ttt tac ctg ggc gta ctt aat ccg ctg ctg   883
Val Ser Glu Glu Ala Ser Phe Tyr Leu Gly Val Leu Asn Pro Leu Leu
                250                 255                 260

att ctg cac ctg atc ggc ggt att cac aac gaa tcc atc ctg ctg gga   931
Ile Leu His Leu Ile Gly Gly Ile His Asn Glu Ser Ile Leu Leu Gly
            265                 270                 275

ttt tta ctt gtt ggc ctg gaa ctc gga ctg cgt ggc acc gac cgg att   979
Phe Leu Leu Val Gly Leu Glu Leu Gly Leu Arg Gly Thr Asp Arg Ile
        280                 285                 290

caa aca ggg ctg tgg ggg cct gcg tgg aca tat att gca ctg agt ggc   1027
Gln Thr Gly Leu Trp Gly Pro Ala Trp Thr Tyr Ile Ala Leu Ser Gly
    295                 300                 305

gta ttg att tct tgc gca ggc ctg gtc aag gtg acc ggc ttt att ggg   1075
Val Leu Ile Ser Cys Ala Gly Leu Val Lys Val Thr Gly Phe Ile Gly
310                 315                 320                 325

ctc ggt ttt gtg ggc atg gcc ttg gcc agg gcg ttt cat gca cgt gga   1123
Leu Gly Phe Val Gly Met Ala Leu Ala Arg Ala Phe His Ala Arg Gly
                330                 335                 340

cat cga cac gtc gtt gcg atc ggc gtt gca ggc ctc gtt caa gta gca   1171
His Arg His Val Val Ala Ile Gly Val Ala Gly Leu Val Gln Val Ala
            345                 350                 355

gcc ctg gtg atc acc gtg gtt gtt ctc agt gtg att acc gga atc agt   1219
Ala Leu Val Ile Thr Val Val Val Leu Ser Val Ile Thr Gly Ile Ser
        360                 365                 370

ttg ggg tgg atc aca ggt caa ggt ggc gct gcg acg atc cga agc tgg   1267
Leu Gly Trp Ile Thr Gly Gln Gly Gly Ala Ala Thr Ile Arg Ser Trp
    375                 380                 385

atg tct atg acc acc aac att ggc gtt att tct gga ttc atc gga atg   1315
Met Ser Met Thr Thr Asn Ile Gly Val Ile Ser Gly Phe Ile Gly Met
390                 395                 400                 405

aat ttg ggg cta ggc gac cac acc gca gcc atg ctc gtt gtg acc cgt   1363
Asn Leu Gly Leu Gly Asp His Thr Ala Ala Met Leu Val Val Thr Arg
                410                 415                 420

gca gcc gga atc gcg gta gct gcc gcc ttc atg gtt cgt atg ttg ttt   1411
Ala Ala Gly Ile Ala Val Ala Ala Ala Phe Met Val Arg Met Leu Phe
            425                 430                 435

gcc aca tat aga ggt cac att cac gct gtg ggc gga ctg ggc gtg gcg   1459
Ala Thr Tyr Arg Gly His Ile His Ala Val Gly Gly Leu Gly Val Ala
```

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        440                 445                 450

act ttc gtc ctc gtt atc ctc ttc ccc gtg gtg cat ccg tgg tac atg   1507
Thr Phe Val Leu Val Ile Leu Phe Pro Val Val His Pro Trp Tyr Met
    455                 460                 465

ctg tgg gct atc gtg ccg cta gct tcc tgg gca aat aga ctg ttc ttc   1555
Leu Trp Ala Ile Val Pro Leu Ala Ser Trp Ala Asn Arg Leu Phe Phe
470                 475                 480                 485

cag ctc gga gtg att gcc tac tcc act gcc ttc agt ttc ttt gtg ctg   1603
Gln Leu Gly Val Ile Ala Tyr Ser Thr Ala Phe Ser Phe Phe Val Leu
                490                 495                 500

cct cgc ggg ctt gca ctt cca gtc gga act gtc ttt tcc atc tac ttc   1651
Pro Arg Gly Leu Ala Leu Pro Val Gly Thr Val Phe Ser Ile Tyr Phe
            505                 510                 515

ggc gca gcg ctc gga ttc agc att ctc cta tta gtt gga tgg tgg agt   1699
Gly Ala Ala Leu Gly Phe Ser Ile Leu Leu Leu Val Gly Trp Trp Ser
        520                 525                 530

ttg agg cgg aat cca acc ttt ggt tta cac tgatcaactg tgactactga     1749
Leu Arg Arg Asn Pro Thr Phe Gly Leu His
    535                 540

ttt                                                               1752


<210> 1198
<211> 543
<212> PRT
<213> Corynebacterium glutamicum

<400> 1198
Val Glu Asp Glu Gln Ser Pro Leu Gly Ala Thr Leu Phe Asp Val Ala
  1               5                  10                  15

Thr Gly Ala Ser Ser Ile Asn Asp Arg Asp Thr Asp Ala Ser Gly Leu
             20                  25                  30

Glu Pro Glu Lys Ile Arg Arg Phe Ala Trp Leu Arg Leu Ile Gly Thr
         35                  40                  45

Met Gly Ala Leu Met Ile Ala Phe Gly Ala Leu Gly Ala Gly Ala Leu
     50                  55                  60

Pro Val Val Asn Asn Pro Tyr Val Asp Phe Pro Gly Gly Asn Phe Met
 65                  70                  75                  80

Ser Arg Met Leu Gln Thr Ser Ser Met Ile Val Leu Ile Gly Val Gly
                 85                  90                  95

Phe Leu Val Leu Ala Trp Val Leu Met Ala Pro Leu Val Gly Ile Pro
            100                 105                 110

Phe Lys Arg Ser Gly Asn Arg Thr Ala Ser Val Ser Leu Ser Met Leu
        115                 120                 125

Arg Arg Thr Phe Gly Ala Trp Val Ala Pro Ile Met Leu Thr Ala Pro
    130                 135                 140
```

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Leu Phe Thr Gln Asp Ile Tyr Ser Tyr Leu Ala Gln Gly Ser Val Thr
145                 150                 155                 160

Ala Gln Gly Met Asp Ala Tyr Ala Gly Gly Pro Leu Glu Leu Leu Gly
                165                 170                 175

Pro Asp Asn His Leu Ala Arg Ser Val Pro Phe Ile Trp Ala Gln Ser
            180                 185                 190

Pro Ser Pro Tyr Gly Pro Val Ala Leu Ser Ile Ala Ala Ser Ile Ser
        195                 200                 205

Val Ile Thr Asn Asp Ser Ile Val Gly Gly Val Leu Ala His Arg Ile
    210                 215                 220

Ala Ser Leu Leu Gly Val Val Ala Ala Gly Trp Ala Ile Thr Met Leu
225                 230                 235                 240

Ala Arg Arg Cys Arg Val Ser Glu Glu Ala Ser Phe Tyr Leu Gly Val
                245                 250                 255

Leu Asn Pro Leu Leu Ile Leu His Leu Ile Gly Gly Ile His Asn Glu
            260                 265                 270

Ser Ile Leu Leu Gly Phe Leu Leu Val Gly Leu Glu Leu Gly Leu Arg
        275                 280                 285

Gly Thr Asp Arg Ile Gln Thr Gly Leu Trp Gly Pro Ala Trp Thr Tyr
    290                 295                 300

Ile Ala Leu Ser Gly Val Leu Ile Ser Cys Ala Gly Leu Val Lys Val
305                 310                 315                 320

Thr Gly Phe Ile Gly Leu Gly Phe Val Gly Met Ala Leu Ala Arg Ala
                325                 330                 335

Phe His Ala Arg Gly His Arg His Val Val Ala Ile Gly Val Ala Gly
            340                 345                 350

Leu Val Gln Val Ala Ala Leu Val Ile Thr Val Val Val Leu Ser Val
        355                 360                 365

Ile Thr Gly Ile Ser Leu Gly Trp Ile Thr Gly Gln Gly Gly Ala Ala
    370                 375                 380

Thr Ile Arg Ser Trp Met Ser Met Thr Thr Asn Ile Gly Val Ile Ser
385                 390                 395                 400

Gly Phe Ile Gly Met Asn Leu Gly Leu Gly Asp His Thr Ala Ala Met
                405                 410                 415

Leu Val Val Thr Arg Ala Ala Gly Ile Ala Val Ala Ala Ala Phe Met
            420                 425                 430

Val Arg Met Leu Phe Ala Thr Tyr Arg Gly His Ile His Ala Val Gly
        435                 440                 445

Gly Leu Gly Val Ala Thr Phe Val Leu Val Ile Leu Phe Pro Val Val
    450                 455                 460
```

```
His Pro Trp Tyr Met Leu Trp Ala Ile Val Pro Leu Ala Ser Trp Ala
465                 470                 475                 480

Asn Arg Leu Phe Phe Gln Leu Gly Val Ile Ala Tyr Ser Thr Ala Phe
                485                 490                 495

Ser Phe Phe Val Leu Pro Arg Gly Leu Ala Leu Pro Val Gly Thr Val
            500                 505                 510

Phe Ser Ile Tyr Phe Gly Ala Ala Leu Gly Phe Ser Ile Leu Leu Leu
        515                 520                 525

Val Gly Trp Trp Ser Leu Arg Arg Asn Pro Thr Phe Gly Leu His
    530                 535                 540


<210> 1199
<211> 1929
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1906)
<223> FRXA02519

<400> 1199
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atccccccttc gggtcaccac cagactctga tgcgaggtaa atg ttc tcc gct ccc   115
                                            Met Phe Ser Ala Pro
                                              1               5

ttg cgt aga atg atg cga gtg acg aag gac gag cag att caa ccc aat   163
Leu Arg Arg Met Met Arg Val Thr Lys Asp Glu Gln Ile Gln Pro Asn
                10                  15                  20

tcg aac gcc cct gaa aac aga aaa tgg ttt cct cgg gca cct cgt ccc   211
Ser Asn Ala Pro Glu Asn Arg Lys Trp Phe Pro Arg Ala Pro Arg Pro
            25                  30                  35

cta cgc caa ttt ctc gac act ttg ccg cgc atc ggc acc gct ggt tcc   259
Leu Arg Gln Phe Leu Asp Thr Leu Pro Arg Ile Gly Thr Ala Gly Ser
        40                  45                  50

aga tca gcg acc ctc cac gtg gaa gac gag cag agc cct tta ggg gca   307
Arg Ser Ala Thr Leu His Val Glu Asp Glu Gln Ser Pro Leu Gly Ala
    55                  60                  65

acg ctt ttc gac gtc gcg acc ggc gcg agc tcc atc aac gac cgc gat   355
Thr Leu Phe Asp Val Ala Thr Gly Ala Ser Ser Ile Asn Asp Arg Asp
70                  75                  80                  85

acc gac gcc tca ggg ctt gag cct gaa aag att cgc cga ttt gca tgg   403
Thr Asp Ala Ser Gly Leu Glu Pro Glu Lys Ile Arg Arg Phe Ala Trp
                90                  95                  100

ctg cgc ctg atc ggc acc atg ggt gcg tta atg atc gcg ttt ggt gcg   451
Leu Arg Leu Ile Gly Thr Met Gly Ala Leu Met Ile Ala Phe Gly Ala
            105                 110                 115
```

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ctg ggc gcg ggt gca ctt ccg gtg gtg aat aat ccg tat gtg gat ttc   499
Leu Gly Ala Gly Ala Leu Pro Val Val Asn Asn Pro Tyr Val Asp Phe
        120                 125                 130

cct ggc gga aac ttc atg agc cga atg ctg cag acc tct tcc atg atc   547
Pro Gly Gly Asn Phe Met Ser Arg Met Leu Gln Thr Ser Ser Met Ile
    135                 140                 145

gtg ctc atc ggc gtg gga ttt ttg gtg ctg gcg tgg gtg tta atg gca   595
Val Leu Ile Gly Val Gly Phe Leu Val Leu Ala Trp Val Leu Met Ala
150                 155                 160                 165

ccg ctg gtg ggt att cct ttt aaa cgc agc gga aac aga aca gcc agc   643
Pro Leu Val Gly Ile Pro Phe Lys Arg Ser Gly Asn Arg Thr Ala Ser
                170                 175                 180

gtg agt ttg tcc atg ctg cgc cgc aca ttt ggc gcc tgg gta gcg ccc   691
Val Ser Leu Ser Met Leu Arg Arg Thr Phe Gly Ala Trp Val Ala Pro
            185                 190                 195

atc atg ctc acc gcc cca ctg ttt act caa gac att tat tct tat ctg   739
Ile Met Leu Thr Ala Pro Leu Phe Thr Gln Asp Ile Tyr Ser Tyr Leu
        200                 205                 210

gca caa ggc tct gtg acc gcg cag gga atg gat gcc tac gcc ggt gga   787
Ala Gln Gly Ser Val Thr Ala Gln Gly Met Asp Ala Tyr Ala Gly Gly
    215                 220                 225

ccg ctt gaa cta ttg ggg ccc gat aat cat ctg gca cgg tcc gtg ccc   835
Pro Leu Glu Leu Leu Gly Pro Asp Asn His Leu Ala Arg Ser Val Pro
230                 235                 240                 245

ttt att tgg gcc cag tcg ccc tcg ccc tac ggc cct gtt gcg ctg agc   883
Phe Ile Trp Ala Gln Ser Pro Ser Pro Tyr Gly Pro Val Ala Leu Ser
                250                 255                 260

atc gcg gcg tcg ata agc gtt att act aat gac agc atc gtt gga ggc   931
Ile Ala Ala Ser Ile Ser Val Ile Thr Asn Asp Ser Ile Val Gly Gly
            265                 270                 275

gtg ctg gcg cac cgt att gcg tcg ctg ctg ggc gtt gtg gct gca ggc   979
Val Leu Ala His Arg Ile Ala Ser Leu Leu Gly Val Val Ala Ala Gly
        280                 285                 290

tgg gcg atc acc atg ctg gcc agg cgc tgt cgg gta tct gaa gaa gcg   1027
Trp Ala Ile Thr Met Leu Ala Arg Arg Cys Arg Val Ser Glu Glu Ala
    295                 300                 305

tcc ttt tac ctg ggc gta ctt aat ccg ctg ctg att ctg cac ctg atc   1075
Ser Phe Tyr Leu Gly Val Leu Asn Pro Leu Leu Ile Leu His Leu Ile
310                 315                 320                 325

ggc ggt att cac aac gaa tcc atc ctg ctg gga ttt tta ctt gtt ggc   1123
Gly Gly Ile His Asn Glu Ser Ile Leu Leu Gly Phe Leu Leu Val Gly
                330                 335                 340

ctg gaa ctc gga ctg cgt ggc acc gac cgg att caa aca ggg ctg tgg   1171
Leu Glu Leu Gly Leu Arg Gly Thr Asp Arg Ile Gln Thr Gly Leu Trp
            345                 350                 355

ggg cct gcg tgg aca tat att gca ctg agt ggc gta ttg att tct tgc   1219
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Gly Pro Ala Trp Thr Tyr Ile Ala Leu Ser Gly Val Leu Ile Ser Cys
        360                 365                 370

gca ggc ctg gtc aag gtg acc ggc ttt att ggg ctc ggt ttt gtg ggc   1267
Ala Gly Leu Val Lys Val Thr Gly Phe Ile Gly Leu Gly Phe Val Gly
    375                 380                 385

atg gcc ttg gcc agg gcg ttt cat gca cgt gga cat cga cac gtc gtt   1315
Met Ala Leu Ala Arg Ala Phe His Ala Arg Gly His Arg His Val Val
390                 395                 400                 405

gcg atc ggc gtt gca ggc ctc gtt caa gta gca gcc ctg gtg atc acc   1363
Ala Ile Gly Val Ala Gly Leu Val Gln Val Ala Ala Leu Val Ile Thr
                410                 415                 420

gtg gtt gtt ctc agt gtg att acc gga atc agt ttg ggg tgg atc aca   1411
Val Val Val Leu Ser Val Ile Thr Gly Ile Ser Leu Gly Trp Ile Thr
            425                 430                 435

ggt caa ggt ggc gct gcg acg atc cga agc tgg atg tct atg acc acc   1459
Gly Gln Gly Gly Ala Ala Thr Ile Arg Ser Trp Met Ser Met Thr Thr
        440                 445                 450

aac att ggc gtt att tct gga ttc atc gga atg aat ttg ggg cta ggc   1507
Asn Ile Gly Val Ile Ser Gly Phe Ile Gly Met Asn Leu Gly Leu Gly
    455                 460                 465

gac cac acc gca gcc atg ctc gtt gtg acc cgt gca gcc gga atc gcg   1555
Asp His Thr Ala Ala Met Leu Val Val Thr Arg Ala Ala Gly Ile Ala
470                 475                 480                 485

gta gct gcc gcc ttc atg gtt cgt atg ttg ttt gcc aca tat aga ggt   1603
Val Ala Ala Ala Phe Met Val Arg Met Leu Phe Ala Thr Tyr Arg Gly
                490                 495                 500

cac att cac gct gtg ggc gga ctg ggc gtg gcg act ttc gtc ctc gtt   1651
His Ile His Ala Val Gly Gly Leu Gly Val Ala Thr Phe Val Leu Val
            505                 510                 515

atc ctc ttc ccc gtg gtg cat ccg tgg tac atg ctg tgg gct atc gtg   1699
Ile Leu Phe Pro Val Val His Pro Trp Tyr Met Leu Trp Ala Ile Val
        520                 525                 530

ccg cta gct tcc tgg gca aat aga ctg ttc ttc cag ctc gga gtg att   1747
Pro Leu Ala Ser Trp Ala Asn Arg Leu Phe Phe Gln Leu Gly Val Ile
    535                 540                 545

gcc tac tcc act gcc ttc agt ttc ttt gtg ctg cct cgc ggg ctt gca   1795
Ala Tyr Ser Thr Ala Phe Ser Phe Phe Val Leu Pro Arg Gly Leu Ala
550                 555                 560                 565

ctt cca gtc gga act gtc ttt tcc atc tac ttc ggc gca gcg ctc gga   1843
Leu Pro Val Gly Thr Val Phe Ser Ile Tyr Phe Gly Ala Ala Leu Gly
                570                 575                 580

ttc agc att ctc cta tta gtt gga tgg tgg agt ttg agg cgg aat cca   1891
Phe Ser Ile Leu Leu Leu Val Gly Trp Trp Ser Leu Arg Arg Asn Pro
            585                 590                 595

acc ttt ggt tta cac tgatcaactg tgactactga ttt                    1929
Thr Phe Gly Leu His
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600

<210> 1200
<211> 602
<212> PRT
<213> Corynebacterium glutamicum

<400> 1200

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Met Phe Ser Ala Pro Leu Arg Arg Met Met Arg Val Thr Lys Asp Glu
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Gln Ile Gln Pro Asn Ser Asn Ala Pro Glu Asn Arg Lys Trp Phe Pro
             20                  25                  30

Arg Ala Pro Arg Pro Leu Arg Gln Phe Leu Asp Thr Leu Pro Arg Ile
         35                  40                  45

Gly Thr Ala Gly Ser Arg Ser Ala Thr Leu His Val Glu Asp Glu Gln
     50                  55                  60

Ser Pro Leu Gly Ala Thr Leu Phe Asp Val Ala Thr Gly Ala Ser Ser
 65                  70                  75                  80

Ile Asn Asp Arg Asp Thr Asp Ala Ser Gly Leu Glu Pro Glu Lys Ile
                 85                  90                  95

Arg Arg Phe Ala Trp Leu Arg Leu Ile Gly Thr Met Gly Ala Leu Met
            100                 105                 110

Ile Ala Phe Gly Ala Leu Gly Ala Gly Ala Leu Pro Val Val Asn Asn
        115                 120                 125

Pro Tyr Val Asp Phe Pro Gly Gly Asn Phe Met Ser Arg Met Leu Gln
    130                 135                 140

Thr Ser Ser Met Ile Val Leu Ile Gly Val Gly Phe Leu Val Leu Ala
145                 150                 155                 160

Trp Val Leu Met Ala Pro Leu Val Gly Ile Pro Phe Lys Arg Ser Gly
                165                 170                 175

Asn Arg Thr Ala Ser Val Ser Leu Ser Met Leu Arg Arg Thr Phe Gly
            180                 185                 190

Ala Trp Val Ala Pro Ile Met Leu Thr Ala Pro Leu Phe Thr Gln Asp
        195                 200                 205

Ile Tyr Ser Tyr Leu Ala Gln Gly Ser Val Thr Ala Gln Gly Met Asp
    210                 215                 220

Ala Tyr Ala Gly Gly Pro Leu Glu Leu Leu Gly Pro Asp Asn His Leu
225                 230                 235                 240

Ala Arg Ser Val Pro Phe Ile Trp Ala Gln Ser Pro Ser Pro Tyr Gly
                245                 250                 255

Pro Val Ala Leu Ser Ile Ala Ala Ser Ile Ser Val Ile Thr Asn Asp
            260                 265                 270

Ser Ile Val Gly Gly Val Leu Ala His Arg Ile Ala Ser Leu Leu Gly
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        275                 280                 285

Val Val Ala Ala Gly Trp Ala Ile Thr Met Leu Ala Arg Arg Cys Arg
    290                 295                 300

Val Ser Glu Glu Ala Ser Phe Tyr Leu Gly Val Leu Asn Pro Leu Leu
305                 310                 315                 320

Ile Leu His Leu Ile Gly Gly Ile His Asn Glu Ser Ile Leu Leu Gly
                325                 330                 335

Phe Leu Leu Val Gly Leu Glu Leu Gly Leu Arg Gly Thr Asp Arg Ile
            340                 345                 350

Gln Thr Gly Leu Trp Gly Pro Ala Trp Thr Tyr Ile Ala Leu Ser Gly
        355                 360                 365

Val Leu Ile Ser Cys Ala Gly Leu Val Lys Val Thr Gly Phe Ile Gly
    370                 375                 380

Leu Gly Phe Val Gly Met Ala Leu Ala Arg Ala Phe His Ala Arg Gly
385                 390                 395                 400

His Arg His Val Val Ala Ile Gly Val Ala Gly Leu Val Gln Val Ala
                405                 410                 415

Ala Leu Val Ile Thr Val Val Val Leu Ser Val Ile Thr Gly Ile Ser
            420                 425                 430

Leu Gly Trp Ile Thr Gly Gln Gly Gly Ala Ala Thr Ile Arg Ser Trp
        435                 440                 445

Met Ser Met Thr Thr Asn Ile Gly Val Ile Ser Gly Phe Ile Gly Met
    450                 455                 460

Asn Leu Gly Leu Gly Asp His Thr Ala Ala Met Leu Val Val Thr Arg
465                 470                 475                 480

Ala Ala Gly Ile Ala Val Ala Ala Ala Phe Met Val Arg Met Leu Phe
                485                 490                 495

Ala Thr Tyr Arg Gly His Ile His Ala Val Gly Gly Leu Gly Val Ala
            500                 505                 510

Thr Phe Val Leu Val Ile Leu Phe Pro Val Val His Pro Trp Tyr Met
        515                 520                 525

Leu Trp Ala Ile Val Pro Leu Ala Ser Trp Ala Asn Arg Leu Phe Phe
    530                 535                 540

Gln Leu Gly Val Ile Ala Tyr Ser Thr Ala Phe Ser Phe Phe Val Leu
545                 550                 555                 560

Pro Arg Gly Leu Ala Leu Pro Val Gly Thr Val Phe Ser Ile Tyr Phe
                565                 570                 575

Gly Ala Ala Leu Gly Phe Ser Ile Leu Leu Leu Val Gly Trp Trp Ser
            580                 585                 590

Leu Arg Arg Asn Pro Thr Phe Gly Leu His
        595                 600
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<210> 1201
<211> 807
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(784)
<223> RXN02520

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gtctaaaggt gaaagctaaa tcaagcagga ggtgacacca gtg gga gat gtt gta 115
Val Gly Asp Val Val
1 5

aaa ggc aac gac gcg cac acc gga gac ggt gat acg cgc cga aaa att 163
Lys Gly Asn Asp Ala His Thr Gly Asp Gly Asp Thr Arg Arg Lys Ile
10 15 20

ctt ctc atc ctg ttg gaa cgt gca ccg gtg atc gct tca gat att gct 211
Leu Leu Ile Leu Leu Glu Arg Ala Pro Val Ile Ala Ser Asp Ile Ala
25 30 35

gaa cag ctt cag ctt tca act gtg gga gtg cgc agg cac cta gac aac 259
Glu Gln Leu Gln Leu Ser Thr Val Gly Val Arg Arg His Leu Asp Asn
40 45 50

ttg gtt gaa gaa aat ctg gcg gag gcg gca aat ccg cgc cag aac cca 307
Leu Val Glu Glu Asn Leu Ala Glu Ala Ala Asn Pro Arg Gln Asn Pro
55 60 65

tat gag ccc aaa atg cgc ggt agg cca gca aaa act tat cgg ctt act 355
Tyr Glu Pro Lys Met Arg Gly Arg Pro Ala Lys Thr Tyr Arg Leu Thr
70 75 80 85

gat aaa ggt cgc tca atc ttc ggc cac gaa tat gat tcc ctt gct gcg 403
Asp Lys Gly Arg Ser Ile Phe Gly His Glu Tyr Asp Ser Leu Ala Ala
90 95 100

gca gct cta gcc act ctt cga gag gtc ggc gga gat gat gca gta agg 451
Ala Ala Leu Ala Thr Leu Arg Glu Val Gly Gly Asp Asp Ala Val Arg
105 110 115

caa ttt gct aga aag cgg atc gaa aca att gtt gag ggt att acc cca 499
Gln Phe Ala Arg Lys Arg Ile Glu Thr Ile Val Glu Gly Ile Thr Pro
120 125 130

gca gat gtc aca gat caa tca atc gaa gat aca gcc aaa tct tta gtt 547
Ala Asp Val Thr Asp Gln Ser Ile Glu Asp Thr Ala Lys Ser Leu Val
135 140 145

gaa gct ttt agt cgg cat ggt tat gca gca act gtc gat gcc act cga 595
Glu Ala Phe Ser Arg His Gly Tyr Ala Ala Thr Val Asp Ala Thr Arg
150 155 160 165

aac ggg ttg caa ctc tgc cag cat cac tgt cca ata tct aca gtc gcc 643
Asn Gly Leu Gln Leu Cys Gln His His Cys Pro Ile Ser Thr Val Ala

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                170                 175                 180

acg gaa ttt ccg gaa ctg tgt gag gca gag cat caa gca gtc tca gaa   691
Thr Glu Phe Pro Glu Leu Cys Glu Ala Glu His Gln Ala Val Ser Glu
            185                 190                 195

ctt ttg ggg cag cac acg caa cca ttg gca aca atc gcg gac ggc cac   739
Leu Leu Gly Gln His Thr Gln Pro Leu Ala Thr Ile Ala Asp Gly His
        200                 205                 210

ggc atc tgc aca aca aat att gca ttg aca ccc atc aaa cac tcc       784
Gly Ile Cys Thr Thr Asn Ile Ala Leu Thr Pro Ile Lys His Ser
    215                 220                 225

tgatgaaagg agcggatcat gac                                        807


<210> 1202
<211> 228
<212> PRT
<213> Corynebacterium glutamicum

<400> 1202
Val Gly Asp Val Val Lys Gly Asn Asp Ala His Thr Gly Asp Gly Asp
  1               5                  10                  15

Thr Arg Arg Lys Ile Leu Leu Ile Leu Leu Glu Arg Ala Pro Val Ile
             20                  25                  30

Ala Ser Asp Ile Ala Glu Gln Leu Gln Leu Ser Thr Val Gly Val Arg
         35                  40                  45

Arg His Leu Asp Asn Leu Val Glu Glu Asn Leu Ala Glu Ala Ala Asn
     50                  55                  60

Pro Arg Gln Asn Pro Tyr Glu Pro Lys Met Arg Gly Arg Pro Ala Lys
 65                  70                  75                  80

Thr Tyr Arg Leu Thr Asp Lys Gly Arg Ser Ile Phe Gly His Glu Tyr
                 85                  90                  95

Asp Ser Leu Ala Ala Ala Ala Leu Ala Thr Leu Arg Glu Val Gly Gly
            100                 105                 110

Asp Asp Ala Val Arg Gln Phe Ala Arg Lys Arg Ile Glu Thr Ile Val
        115                 120                 125

Glu Gly Ile Thr Pro Ala Asp Val Thr Asp Gln Ser Ile Glu Asp Thr
    130                 135                 140

Ala Lys Ser Leu Val Glu Ala Phe Ser Arg His Gly Tyr Ala Ala Thr
145                 150                 155                 160

Val Asp Ala Thr Arg Asn Gly Leu Gln Leu Cys Gln His His Cys Pro
                165                 170                 175

Ile Ser Thr Val Ala Thr Glu Phe Pro Glu Leu Cys Glu Ala Glu His
            180                 185                 190

Gln Ala Val Ser Glu Leu Leu Gly Gln His Thr Gln Pro Leu Ala Thr
        195                 200                 205
```

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Ile Ala Asp Gly His Gly Ile Cys Thr Thr Asn Ile Ala Leu Thr Pro
    210                 215                 220

Ile Lys His Ser
225


<210> 1203
<211> 807
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(784)
<223> FRXA02520

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gtctaaaggt gaaagctaaa tcaagcagga ggtgacacca gtg gga gat gtt gta   115
                                              Val Gly Asp Val Val
                                                1               5

aaa ggc aac gac gcg cac acc gga gac ggt gat acg cgc cga aaa att   163
Lys Gly Asn Asp Ala His Thr Gly Asp Gly Asp Thr Arg Arg Lys Ile
                10                  15                  20

ctt ctc atc ctg ttg gaa cgt gca ccg gtg atc gct tca gat att gct   211
Leu Leu Ile Leu Leu Glu Arg Ala Pro Val Ile Ala Ser Asp Ile Ala
            25                  30                  35

gaa cag ctt cag ctt tca act gtg gga gtg cgc agg cac cta gac aac   259
Glu Gln Leu Gln Leu Ser Thr Val Gly Val Arg Arg His Leu Asp Asn
        40                  45                  50

ttg gtt gaa gaa aat ctg gcg gag gcg gca aat ccg cgc cag aac cca   307
Leu Val Glu Glu Asn Leu Ala Glu Ala Ala Asn Pro Arg Gln Asn Pro
    55                  60                  65

tat gag ccc aaa atg cgc ggt agg cca gca aaa act tat cgg ctt act   355
Tyr Glu Pro Lys Met Arg Gly Arg Pro Ala Lys Thr Tyr Arg Leu Thr
70                  75                  80                  85

gat aaa ggt cgc tca atc ttc ggc cac gaa tat gat tcc ctt gct gcg   403
Asp Lys Gly Arg Ser Ile Phe Gly His Glu Tyr Asp Ser Leu Ala Ala
                90                  95                  100

gca gct cta gcc act ctt cga gag gtc ggc gga gat gat gca gta agg   451
Ala Ala Leu Ala Thr Leu Arg Glu Val Gly Gly Asp Asp Ala Val Arg
            105                 110                 115

caa ttt gct aga aag cgg atc gaa aca att gtt gag ggt att acc cca   499
Gln Phe Ala Arg Lys Arg Ile Glu Thr Ile Val Glu Gly Ile Thr Pro
        120                 125                 130

gca gat gtc aca gat caa tca atc gaa gat aca gcc aaa tct tta gtt   547
Ala Asp Val Thr Asp Gln Ser Ile Glu Asp Thr Ala Lys Ser Leu Val
    135                 140                 145
```

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gaa gct ttt agt cgg cat ggt tat gca gca act gtc gat gcc act cga   595
Glu Ala Phe Ser Arg His Gly Tyr Ala Ala Thr Val Asp Ala Thr Arg
150                 155                 160                 165

aac ggg ttg caa ctc tgc cag cat cac tgt cca ata tct aca gtc gcc   643
Asn Gly Leu Gln Leu Cys Gln His His Cys Pro Ile Ser Thr Val Ala
                170                 175                 180

acg gaa ttt ccg gaa ctg tgt gag gca gag cat caa gca gtc tca gaa   691
Thr Glu Phe Pro Glu Leu Cys Glu Ala Glu His Gln Ala Val Ser Glu
            185                 190                 195

ctt ttg ggg cag cac acg caa cca ttg gca aca atc gcg gac ggc cac   739
Leu Leu Gly Gln His Thr Gln Pro Leu Ala Thr Ile Ala Asp Gly His
        200                 205                 210

ggc atc tgc aca aca aat att gca ttg aca ccc atc aaa cac tcc       784
Gly Ile Cys Thr Thr Asn Ile Ala Leu Thr Pro Ile Lys His Ser
    215                 220                 225

tgatgaaagg agcggatcat gac                                        807
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<210> 1204
<211> 228
<212> PRT
<213> Corynebacterium glutamicum

<400> 1204

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Val Gly Asp Val Val Lys Gly Asn Asp Ala His Thr Gly Asp Gly Asp
  1               5                  10                  15

Thr Arg Arg Lys Ile Leu Leu Ile Leu Leu Glu Arg Ala Pro Val Ile
             20                  25                  30

Ala Ser Asp Ile Ala Glu Gln Leu Gln Leu Ser Thr Val Gly Val Arg
         35                  40                  45

Arg His Leu Asp Asn Leu Val Glu Glu Asn Leu Ala Glu Ala Ala Asn
     50                  55                  60

Pro Arg Gln Asn Pro Tyr Glu Pro Lys Met Arg Gly Arg Pro Ala Lys
 65                  70                  75                  80

Thr Tyr Arg Leu Thr Asp Lys Gly Arg Ser Ile Phe Gly His Glu Tyr
                 85                  90                  95

Asp Ser Leu Ala Ala Ala Ala Leu Ala Thr Leu Arg Glu Val Gly Gly
            100                 105                 110

Asp Asp Ala Val Arg Gln Phe Ala Arg Lys Arg Ile Glu Thr Ile Val
        115                 120                 125

Glu Gly Ile Thr Pro Ala Asp Val Thr Asp Gln Ser Ile Glu Asp Thr
    130                 135                 140

Ala Lys Ser Leu Val Glu Ala Phe Ser Arg His Gly Tyr Ala Ala Thr
145                 150                 155                 160

Val Asp Ala Thr Arg Asn Gly Leu Gln Leu Cys Gln His His Cys Pro
                165                 170                 175
```

```
Ile Ser Thr Val Ala Thr Glu Phe Pro Glu Leu Cys Glu Ala Glu His
            180                 185                 190

Gln Ala Val Ser Glu Leu Leu Gly Gln His Thr Gln Pro Leu Ala Thr
        195                 200                 205

Ile Ala Asp Gly His Gly Ile Cys Thr Thr Asn Ile Ala Leu Thr Pro
    210                 215                 220

Ile Lys His Ser
225
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<210> 1205
<211> 927
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(904)
<223> RXN02534

<400> 1205

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ttaccagtaa tctatgcaga tttactgtcc gttggggatc cgcgcctatc ggaagttgcc 60

tacattataa aaactcagat tcaggaatac acagaccatg atg aat tca ccg aac   115
                                          Met Asn Ser Pro Asn
                                            1               5

gcg gac att att tta gta gtt aac aag ctg tcc aag ttt att gat atc   163
Ala Asp Ile Ile Leu Val Val Asn Lys Leu Ser Lys Phe Ile Asp Ile
                10                  15                  20

gaa aat att atg ctc gtt gga gca cga tgt aga gac att cac cag caa   211
Glu Asn Ile Met Leu Val Gly Ala Arg Cys Arg Asp Ile His Gln Gln
            25                  30                  35

aaa tat cgc gat caa aca gcg ggt aga aga act aag gat gtt gac ttc   259
Lys Tyr Arg Asp Gln Thr Ala Gly Arg Arg Thr Lys Asp Val Asp Phe
        40                  45                  50

gct tta gct tta gaa agc tgg gac gac ttc aat cta tta aag caa caa   307
Ala Leu Ala Leu Glu Ser Trp Asp Asp Phe Asn Leu Leu Lys Gln Gln
    55                  60                  65

ttc tca ccg act ggt aac gca tgg caa gga atc acc att gga aat att   355
Phe Ser Pro Thr Gly Asn Ala Trp Gln Gly Ile Thr Ile Gly Asn Ile
70                  75                  80                  85

cca gta gat ctc gtg cca ttc gga aat att gaa aac cca ccc ggt gaa   403
Pro Val Asp Leu Val Pro Phe Gly Asn Ile Glu Asn Pro Pro Gly Glu
                90                  95                  100

gtc ttg tcc aga aaa ggt cat cta ctt aat gtc gct ggg ttc aag gaa   451
Val Leu Ser Arg Lys Gly His Leu Leu Asn Val Ala Gly Phe Lys Glu
            105                 110                 115

gta ttc gag caa gct gag cta tat ccc cta aat gat gcg ata gac att   499
Val Phe Glu Gln Ala Glu Leu Tyr Pro Leu Asn Asp Ala Ile Asp Ile
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```
        120                 125                 130

aag ttg tct aca gtt ccc gga ctt act gcg cta aag cta cat gca tgg   547
Lys Leu Ser Thr Val Pro Gly Leu Thr Ala Leu Lys Leu His Ala Trp
    135                 140                 145

ctc gac cgt aaa gaa aat aac atc aaa gat gca agc gat cta gca tta   595
Leu Asp Arg Lys Glu Asn Asn Ile Lys Asp Ala Ser Asp Leu Ala Leu
150                 155                 160                 165

atc ttg tcg tgg tac gaa gag gat gta gaa act tta tgg aat cgc tat   643
Ile Leu Ser Trp Tyr Glu Glu Asp Val Glu Thr Leu Trp Asn Arg Tyr
                170                 175                 180

ttt gcc ctg gaa aat caa gga tac ata ggt gaa cca gag gca atg gca   691
Phe Ala Leu Glu Asn Gln Gly Tyr Ile Gly Glu Pro Glu Ala Met Ala
            185                 190                 195

gct gaa tta cta gga ctt gac act gga aga ata ctc ggc cac aag gaa   739
Ala Glu Leu Leu Gly Leu Asp Thr Gly Arg Ile Leu Gly His Lys Glu
        200                 205                 210

act caa gcc ctc ctt gat cga ttt aat gaa cag tct cct cct gag cta   787
Thr Gln Ala Leu Leu Asp Arg Phe Asn Glu Gln Ser Pro Pro Glu Leu
    215                 220                 225

aac caa ttt gct gaa tca ctt gaa gcc cct cct gaa cac agt cac cca   835
Asn Gln Phe Ala Glu Ser Leu Glu Ala Pro Pro Glu His Ser His Pro
230                 235                 240                 245

tta gaa cgg cgt cgt atc cag gtc gag gca ctg tta ggt gga ctt aga   883
Leu Glu Arg Arg Arg Ile Gln Val Glu Ala Leu Leu Gly Gly Leu Arg
                250                 255                 260

gat tcc ctc ggt tac gat gaa tagcttccaa tcccgcattg ttc            927
Asp Ser Leu Gly Tyr Asp Glu
            265
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<210> 1206
<211> 268
<212> PRT
<213> Corynebacterium glutamicum

<400> 1206

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Met Asn Ser Pro Asn Ala Asp Ile Ile Leu Val Val Asn Lys Leu Ser
  1               5                  10                  15

Lys Phe Ile Asp Ile Glu Asn Ile Met Leu Val Gly Ala Arg Cys Arg
             20                  25                  30

Asp Ile His Gln Gln Lys Tyr Arg Asp Gln Thr Ala Gly Arg Arg Thr
         35                  40                  45

Lys Asp Val Asp Phe Ala Leu Ala Leu Glu Ser Trp Asp Asp Phe Asn
     50                  55                  60

Leu Leu Lys Gln Gln Phe Ser Pro Thr Gly Asn Ala Trp Gln Gly Ile
 65                  70                  75                  80

Thr Ile Gly Asn Ile Pro Val Asp Leu Val Pro Phe Gly Asn Ile Glu
```

```
                85                  90                  95

Asn Pro Pro Gly Glu Val Leu Ser Arg Lys Gly His Leu Leu Asn Val
            100                 105                 110

Ala Gly Phe Lys Glu Val Phe Glu Gln Ala Glu Leu Tyr Pro Leu Asn
        115                 120                 125

Asp Ala Ile Asp Ile Lys Leu Ser Thr Val Pro Gly Leu Thr Ala Leu
    130                 135                 140

Lys Leu His Ala Trp Leu Asp Arg Lys Glu Asn Asn Ile Lys Asp Ala
145                 150                 155                 160

Ser Asp Leu Ala Leu Ile Leu Ser Trp Tyr Glu Glu Asp Val Glu Thr
                165                 170                 175

Leu Trp Asn Arg Tyr Phe Ala Leu Glu Asn Gln Gly Tyr Ile Gly Glu
            180                 185                 190

Pro Glu Ala Met Ala Ala Glu Leu Leu Gly Leu Asp Thr Gly Arg Ile
        195                 200                 205

Leu Gly His Lys Glu Thr Gln Ala Leu Leu Asp Arg Phe Asn Glu Gln
    210                 215                 220

Ser Pro Pro Glu Leu Asn Gln Phe Ala Glu Ser Leu Glu Ala Pro Pro
225                 230                 235                 240

Glu His Ser His Pro Leu Glu Arg Arg Arg Ile Gln Val Glu Ala Leu
                245                 250                 255

Leu Gly Gly Leu Arg Asp Ser Leu Gly Tyr Asp Glu
            260                 265


<210> 1207
<211> 927
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(904)
<223> FRXA02534

<400> 1207
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tacattataa aaactcagat tcaggaatac acagaccatg atg aat tca ccg aac   115
                                        Met Asn Ser Pro Asn
                                          1               5

gcg gac att att tta gta gtt aac aag ctg tcc aag ttt att gat atc   163
Ala Asp Ile Ile Leu Val Val Asn Lys Leu Ser Lys Phe Ile Asp Ile
                  10                  15                  20

gaa aat att atg ctc gtt gga gca cga tgt aga gac att cac cag caa   211
Glu Asn Ile Met Leu Val Gly Ala Arg Cys Arg Asp Ile His Gln Gln
              25                  30                  35
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```
aaa tat cgc gat caa aca gcg ggt aga aga act aag gat gtt gac ttc   259
Lys Tyr Arg Asp Gln Thr Ala Gly Arg Arg Thr Lys Asp Val Asp Phe
         40                  45                  50

gct tta gct tta gaa agc tgg gac gac ttc aat cta tta aag caa caa   307
Ala Leu Ala Leu Glu Ser Trp Asp Asp Phe Asn Leu Leu Lys Gln Gln
     55                  60                  65

ttc tca ccg act ggt aac gca tgg caa gga atc acc att gga aat att   355
Phe Ser Pro Thr Gly Asn Ala Trp Gln Gly Ile Thr Ile Gly Asn Ile
 70                  75                  80                  85

cca gta gat ctc gtg cca ttc gga aat att gaa aac cca ccc ggt gaa   403
Pro Val Asp Leu Val Pro Phe Gly Asn Ile Glu Asn Pro Pro Gly Glu
                 90                  95                 100

gtc ttg tcc aga aaa ggt cat cta ctt aat gtc gct ggg ttc aag gaa   451
Val Leu Ser Arg Lys Gly His Leu Leu Asn Val Ala Gly Phe Lys Glu
            105                 110                 115

gta ttc gag caa gct gag cta tat ccc cta aat gat gcg ata gac att   499
Val Phe Glu Gln Ala Glu Leu Tyr Pro Leu Asn Asp Ala Ile Asp Ile
        120                 125                 130

aag ttg tct aca gtt ccc gga ctt act gcg cta aag cta cat gca tgg   547
Lys Leu Ser Thr Val Pro Gly Leu Thr Ala Leu Lys Leu His Ala Trp
    135                 140                 145

ctc gac cgt aaa gaa aat aac atc aaa gat gca agc gat cta gca tta   595
Leu Asp Arg Lys Glu Asn Asn Ile Lys Asp Ala Ser Asp Leu Ala Leu
150                 155                 160                 165

atc ttg tcg tgg tac gaa gag gat gta gaa act tta tgg aat cgc tat   643
Ile Leu Ser Trp Tyr Glu Glu Asp Val Glu Thr Leu Trp Asn Arg Tyr
                170                 175                 180

ttt gcc ctg gaa aat caa gga tac ata ggt gaa cca gag gca atg gca   691
Phe Ala Leu Glu Asn Gln Gly Tyr Ile Gly Glu Pro Glu Ala Met Ala
            185                 190                 195

gct gaa tta cta gga ctt gac act gga aga ata ctc ggc cac aag gaa   739
Ala Glu Leu Leu Gly Leu Asp Thr Gly Arg Ile Leu Gly His Lys Glu
        200                 205                 210

act caa gcc ctc ctt gat cga ttt aat gaa cag tct cct cct gag cta   787
Thr Gln Ala Leu Leu Asp Arg Phe Asn Glu Gln Ser Pro Pro Glu Leu
    215                 220                 225

aac caa ttt gct gaa tca ctt gaa gcc cct cct gaa cac agt cac cca   835
Asn Gln Phe Ala Glu Ser Leu Glu Ala Pro Pro Glu His Ser His Pro
230                 235                 240                 245

tta gaa cgg cgt cgt atc cag gtc gag gca ctg tta ggt gga ctt aga   883
Leu Glu Arg Arg Arg Ile Gln Val Glu Ala Leu Leu Gly Gly Leu Arg
                250                 255                 260

gat tcc ctc ggt tac gat gaa tagcttccaa tcccgcattg ttc            927
Asp Ser Leu Gly Tyr Asp Glu
            265
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<210> 1208
<211> 268
<212> PRT
<213> Corynebacterium glutamicum

<400> 1208
Met Asn Ser Pro Asn Ala Asp Ile Ile Leu Val Val Asn Lys Leu Ser
1 5 10 15

Lys Phe Ile Asp Ile Glu Asn Ile Met Leu Val Gly Ala Arg Cys Arg
20 25 30

Asp Ile His Gln Gln Lys Tyr Arg Asp Gln Thr Ala Gly Arg Arg Thr
35 40 45

Lys Asp Val Asp Phe Ala Leu Ala Leu Glu Ser Trp Asp Asp Phe Asn
50 55 60

Leu Leu Lys Gln Gln Phe Ser Pro Thr Gly Asn Ala Trp Gln Gly Ile
65 70 75 80

Thr Ile Gly Asn Ile Pro Val Asp Leu Val Pro Phe Gly Asn Ile Glu
85 90 95

Asn Pro Pro Gly Glu Val Leu Ser Arg Lys Gly His Leu Leu Asn Val
100 105 110

Ala Gly Phe Lys Glu Val Phe Glu Gln Ala Glu Leu Tyr Pro Leu Asn
115 120 125

Asp Ala Ile Asp Ile Lys Leu Ser Thr Val Pro Gly Leu Thr Ala Leu
130 135 140

Lys Leu His Ala Trp Leu Asp Arg Lys Glu Asn Asn Ile Lys Asp Ala
145 150 155 160

Ser Asp Leu Ala Leu Ile Leu Ser Trp Tyr Glu Glu Asp Val Glu Thr
165 170 175

Leu Trp Asn Arg Tyr Phe Ala Leu Glu Asn Gln Gly Tyr Ile Gly Glu
180 185 190

Pro Glu Ala Met Ala Ala Glu Leu Leu Gly Leu Asp Thr Gly Arg Ile
195 200 205

Leu Gly His Lys Glu Thr Gln Ala Leu Leu Asp Arg Phe Asn Glu Gln
210 215 220

Ser Pro Pro Glu Leu Asn Gln Phe Ala Glu Ser Leu Glu Ala Pro Pro
225 230 235 240

Glu His Ser His Pro Leu Glu Arg Arg Arg Ile Gln Val Glu Ala Leu
245 250 255

Leu Gly Gly Leu Arg Asp Ser Leu Gly Tyr Asp Glu
260 265

<210> 1209
<211> 585
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(562)
<223> RXN02537

<400> 1209
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tagacgtcga tcttggccac acactgaata agttgcactg atg ctc gcc ctc aaa 115
Met Leu Ala Leu Lys
1 5

agt tca gaa tta gaa ggc ata gcc aca tca ctc acc gcc gtg gcg ggt 163
Ser Ser Glu Leu Glu Gly Ile Ala Thr Ser Leu Thr Ala Val Ala Gly
10 15 20

gcg ctc cac gaa tca aac act gac cgg ttg cag tcc tgg cag cag ctc 211
Ala Leu His Glu Ser Asn Thr Asp Arg Leu Gln Ser Trp Gln Gln Leu
25 30 35

gaa acg atg acc tct gcc agc tcc ctt atc cag ggc ttt atc aag ctt 259
Glu Thr Met Thr Ser Ala Ser Ser Leu Ile Gln Gly Phe Ile Lys Leu
40 45 50

gtc gat tac aac cga ccc aca gtg aat atc gtg gaa caa atg cac aaa 307
Val Asp Tyr Asn Arg Pro Thr Val Asn Ile Val Glu Gln Met His Lys
55 60 65

acc gca tcc acg ctt ttc aac acc gct gat ttc cta cgc act ttg gaa 355
Thr Ala Ser Thr Leu Phe Asn Thr Ala Asp Phe Leu Arg Thr Leu Glu
70 75 80 85

ggc tat gtt gat gta ctg gaa aaa caa gcc gat aaa tct ata acg ctc 403
Gly Tyr Val Asp Val Leu Glu Lys Gln Ala Asp Lys Ser Ile Thr Leu
90 95 100

acc gtc atg ctt cga tat att gcc agc ttg agt agc ctt tta gac ctc 451
Thr Val Met Leu Arg Tyr Ile Ala Ser Leu Ser Ser Leu Leu Asp Leu
105 110 115

atg tgt gca cgc gag atc aac gcg ttg tgc aca gcg att act cca gaa 499
Met Cys Ala Arg Glu Ile Asn Ala Leu Cys Thr Ala Ile Thr Pro Glu
120 125 130

cca ttg aag cat ctg ggc gat ttt ggc act cta ccg cct cag caa tcc 547
Pro Leu Lys His Leu Gly Asp Phe Gly Thr Leu Pro Pro Gln Gln Ser
135 140 145

acg agt ttc att tgg tgaatgcccc accagaaatc cgt 585
Thr Ser Phe Ile Trp
150

<210> 1210
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 1210

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Met Leu Ala Leu Lys Ser Ser Glu Leu Glu Gly Ile Ala Thr Ser Leu
  1               5                  10                  15

Thr Ala Val Ala Gly Ala Leu His Glu Ser Asn Thr Asp Arg Leu Gln
             20                  25                  30

Ser Trp Gln Gln Leu Glu Thr Met Thr Ser Ala Ser Ser Leu Ile Gln
         35                  40                  45

Gly Phe Ile Lys Leu Val Asp Tyr Asn Arg Pro Thr Val Asn Ile Val
     50                  55                  60

Glu Gln Met His Lys Thr Ala Ser Thr Leu Phe Asn Thr Ala Asp Phe
 65                  70                  75                  80

Leu Arg Thr Leu Glu Gly Tyr Val Asp Val Leu Glu Lys Gln Ala Asp
                 85                  90                  95

Lys Ser Ile Thr Leu Thr Val Met Leu Arg Tyr Ile Ala Ser Leu Ser
            100                 105                 110

Ser Leu Leu Asp Leu Met Cys Ala Arg Glu Ile Asn Ala Leu Cys Thr
        115                 120                 125

Ala Ile Thr Pro Glu Pro Leu Lys His Leu Gly Asp Phe Gly Thr Leu
    130                 135                 140

Pro Pro Gln Gln Ser Thr Ser Phe Ile Trp
145                 150
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Application Number 10/588,377 Filed 08/03/2006

<210> 1211
<211> 585
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(562)
<223> FRXA02537

<400> 1211

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tagacgtcga tcttggccac acactgaata agttgcactg atg ctc gcc ctc aaa   115
                                              Met Leu Ala Leu Lys
                                                1               5

agt tca gaa tta gaa ggc ata gcc aca tca ctc acc gcc gtg gcg ggt   163
Ser Ser Glu Leu Glu Gly Ile Ala Thr Ser Leu Thr Ala Val Ala Gly
                10                  15                  20

gcg ctc cac gaa tca aac act gac cgg ttg cag tcc tgg cag cag ctc   211
Ala Leu His Glu Ser Asn Thr Asp Arg Leu Gln Ser Trp Gln Gln Leu
            25                  30                  35

gaa acg atg acc tct gcc agc tcc ctt atc cag ggc ttt atc aag ctt   259
Glu Thr Met Thr Ser Ala Ser Ser Leu Ile Gln Gly Phe Ile Lys Leu
        40                  45                  50

gtc gat tac aac cga ccc aca gtg aat atc gtg gaa caa atg cac aaa   307
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```
Val Asp Tyr Asn Arg Pro Thr Val Asn Ile Val Glu Gln Met His Lys
     55                  60                  65

acc gca tcc acg ctt ttc aac acc gct gat ttc cta cgc act ttg gaa   355
Thr Ala Ser Thr Leu Phe Asn Thr Ala Asp Phe Leu Arg Thr Leu Glu
 70                  75                  80                  85

ggc tat gtt gat gta ctg gaa aaa caa gcc gat aaa tct ata acg ctc   403
Gly Tyr Val Asp Val Leu Glu Lys Gln Ala Asp Lys Ser Ile Thr Leu
                90                  95                 100

acc gtc atg ctt cga tat att gcc agc ttg agt agc ctt tta gac ctc   451
Thr Val Met Leu Arg Tyr Ile Ala Ser Leu Ser Ser Leu Leu Asp Leu
            105                 110                 115

atg tgt gca cgc gag atc aac gcg ttg tgc aca gcg att act cca gaa   499
Met Cys Ala Arg Glu Ile Asn Ala Leu Cys Thr Ala Ile Thr Pro Glu
        120                 125                 130

cca ttg aag cat ctg ggc gat ttt ggc act cta ccg cct cag caa tcc   547
Pro Leu Lys His Leu Gly Asp Phe Gly Thr Leu Pro Pro Gln Gln Ser
    135                 140                 145

acg agt ttc att tgg tgaatgcccc accagaaatc cgt                     585
Thr Ser Phe Ile Trp
150
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Do not add any new matter to the disclosure. Do not add any new matter to the disclosure.

<210> 1212
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 1212

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Met Leu Ala Leu Lys Ser Ser Glu Leu Glu Gly Ile Ala Thr Ser Leu
  1               5                  10                  15

Thr Ala Val Ala Gly Ala Leu His Glu Ser Asn Thr Asp Arg Leu Gln
             20                  25                  30

Ser Trp Gln Gln Leu Glu Thr Met Thr Ser Ala Ser Ser Leu Ile Gln
         35                  40                  45

Gly Phe Ile Lys Leu Val Asp Tyr Asn Arg Pro Thr Val Asn Ile Val
     50                  55                  60

Glu Gln Met His Lys Thr Ala Ser Thr Leu Phe Asn Thr Ala Asp Phe
 65                  70                  75                  80

Leu Arg Thr Leu Glu Gly Tyr Val Asp Val Leu Glu Lys Gln Ala Asp
                 85                  90                  95

Lys Ser Ile Thr Leu Thr Val Met Leu Arg Tyr Ile Ala Ser Leu Ser
            100                 105                 110

Ser Leu Leu Asp Leu Met Cys Ala Arg Glu Ile Asn Ala Leu Cys Thr
        115                 120                 125

Ala Ile Thr Pro Glu Pro Leu Lys His Leu Gly Asp Phe Gly Thr Leu
    130                 135                 140
```

```
Pro Pro Gln Gln Ser Thr Ser Phe Ile Trp
145                 150


<210> 1213
<211> 795
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(772)
<223> RXN02538

<400> 1213
gcgagatcaa cgcgttgtgc acagcgatta ctccagaacc attgaagcat ctgggcgatt 60

ttggcactct accgcctcag caatccacga gtttcatttg gtg aat gcc cca cca   115
                                            Val Asn Ala Pro Pro
                                              1               5

gaa atc cgt gcc tta gcc gaa gcc cat ccc gat atg cag atc cta gaa   163
Glu Ile Arg Ala Leu Ala Glu Ala His Pro Asp Met Gln Ile Leu Glu
                 10                  15                  20

gcc ggc gat ggt tca ttg gta gca tcg ttt ggg gat att gat agg gct   211
Ala Gly Asp Gly Ser Leu Val Ala Ser Phe Gly Asp Ile Asp Arg Ala
             25                  30                  35

acg acc gtg acc acc atc gtg gca ggt gtg ggt tcc tcc aac cca gaa   259
Thr Thr Val Thr Thr Ile Val Ala Gly Val Gly Ser Ser Asn Pro Glu
         40                  45                  50

ggg tgg aat aca tat gtt gac cgt gcc cgc aca gta tct gct tcc acc   307
Gly Trp Asn Thr Tyr Val Asp Arg Ala Arg Thr Val Ser Ala Ser Thr
     55                  60                  65

ggt tcc gca acg gtg ttg tgg ctg gga tat caa gca ccc gct tcg att   355
Gly Ser Ala Thr Val Leu Trp Leu Gly Tyr Gln Ala Pro Ala Ser Ile
 70                  75                  80                  85

cct gct gcg gta tcc ggc gcg gca gcg aat cgc gct gcc gcg gat ctc   403
Pro Ala Ala Val Ser Gly Ala Ala Ala Asn Arg Ala Ala Ala Asp Leu
                 90                  95                 100

cag agg ttt caa gcg gca cta cag tcc cgc aat ccc cac caa aga aaa   451
Gln Arg Phe Gln Ala Ala Leu Gln Ser Arg Asn Pro His Gln Arg Lys
            105                 110                 115

gta gtg atg ggc tac agc tac ggt tcc aca gtg gtg gga aaa gct gcg   499
Val Val Met Gly Tyr Ser Tyr Gly Ser Thr Val Val Gly Lys Ala Ala
        120                 125                 130

tct tcc ggc gag ctc agt gcc gat gcg ttg gta ttg gtt ggc agt ccc   547
Ser Ser Gly Glu Leu Ser Ala Asp Ala Leu Val Leu Val Gly Ser Pro
    135                 140                 145

ggc gcg ggt gtc tcg cac tct tcc cag ctt ggc gca cct gtg tat gcg   595
Gly Ala Gly Val Ser His Ser Ser Gln Leu Gly Ala Pro Val Tyr Ala
150                 155                 160                 165
```

```
gta aca ggg tct gct gat ccc atc ggt ttt gcc ggc acc caa tat gac   643
Val Thr Gly Ser Ala Asp Pro Ile Gly Phe Ala Gly Thr Gln Tyr Asp
                170                 175                 180

ggc atc cac ggc act gat ccc acc gct gcc cta ttc ggt gca aca gtg   691
Gly Ile His Gly Thr Asp Pro Thr Ala Ala Leu Phe Gly Ala Thr Val
            185                 190                 195

tgg gat tcg ccc tca acg cat tcc ggt tat tgg aat gac cag gag ttc   739
Trp Asp Ser Pro Ser Thr His Ser Gly Tyr Trp Asn Asp Gln Glu Phe
        200                 205                 210

ctg ggc aat gtg gcg gag gtg gtt cgc ggc aaa tagaaaagcc gccgcacact 792
Leu Gly Asn Val Ala Glu Val Val Arg Gly Lys
    215                 220

gga                                                               795
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<210> 1214
<211> 224
<212> PRT
<213> Corynebacterium glutamicum

<400> 1214

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Val Asn Ala Pro Pro Glu Ile Arg Ala Leu Ala Glu Ala His Pro Asp
  1               5                  10                  15

Met Gln Ile Leu Glu Ala Gly Asp Gly Ser Leu Val Ala Ser Phe Gly
             20                  25                  30

Asp Ile Asp Arg Ala Thr Thr Val Thr Thr Ile Val Ala Gly Val Gly
         35                  40                  45

Ser Ser Asn Pro Glu Gly Trp Asn Thr Tyr Val Asp Arg Ala Arg Thr
     50                  55                  60

Val Ser Ala Ser Thr Gly Ser Ala Thr Val Leu Trp Leu Gly Tyr Gln
 65                  70                  75                  80

Ala Pro Ala Ser Ile Pro Ala Ala Val Ser Gly Ala Ala Ala Asn Arg
                 85                  90                  95

Ala Ala Ala Asp Leu Gln Arg Phe Gln Ala Ala Leu Gln Ser Arg Asn
            100                 105                 110

Pro His Gln Arg Lys Val Val Met Gly Tyr Ser Tyr Gly Ser Thr Val
        115                 120                 125

Val Gly Lys Ala Ala Ser Ser Gly Glu Leu Ser Ala Asp Ala Leu Val
    130                 135                 140

Leu Val Gly Ser Pro Gly Ala Gly Val Ser His Ser Ser Gln Leu Gly
145                 150                 155                 160

Ala Pro Val Tyr Ala Val Thr Gly Ser Ala Asp Pro Ile Gly Phe Ala
                165                 170                 175

Gly Thr Gln Tyr Asp Gly Ile His Gly Thr Asp Pro Thr Ala Ala Leu
            180                 185                 190
```

```
Phe Gly Ala Thr Val Trp Asp Ser Pro Ser Thr His Ser Gly Tyr Trp
        195                 200                 205

Asn Asp Gln Glu Phe Leu Gly Asn Val Ala Glu Val Val Arg Gly Lys
    210                 215                 220
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<210> 1215
<211> 795
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(772)
<223> FRXA02538

<400> 1215

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ttggcactct accgcctcag caatccacga gtttcatttg gtg aat gcc cca cca   115
                                            Val Asn Ala Pro Pro
                                              1               5

gaa atc cgt gcc tta gcc gaa gcc cat ccc gat atg cag atc cta gaa   163
Glu Ile Arg Ala Leu Ala Glu Ala His Pro Asp Met Gln Ile Leu Glu
                 10                  15                  20

gcc ggc gat ggt tca ttg gta gca tcg ttt ggg gat att gat agg gct   211
Ala Gly Asp Gly Ser Leu Val Ala Ser Phe Gly Asp Ile Asp Arg Ala
             25                  30                  35

acg acc gtg acc acc atc gtg gca ggt gtg ggt tcc tcc aac cca gaa   259
Thr Thr Val Thr Thr Ile Val Ala Gly Val Gly Ser Ser Asn Pro Glu
         40                  45                  50

ggg tgg aat aca tat gtt gac cgt gcc cgc aca gta tct gct tcc acc   307
Gly Trp Asn Thr Tyr Val Asp Arg Ala Arg Thr Val Ser Ala Ser Thr
     55                  60                  65

ggt tcc gca acg gtg ttg tgg ctg gga tat caa gca ccc gct tcg att   355
Gly Ser Ala Thr Val Leu Trp Leu Gly Tyr Gln Ala Pro Ala Ser Ile
 70                  75                  80                  85

cct gct gcg gta tcc ggc gcg gca gcg aat cgc gct gcc gcg gat ctc   403
Pro Ala Ala Val Ser Gly Ala Ala Ala Asn Arg Ala Ala Ala Asp Leu
                 90                  95                 100

cag agg ttt caa gcg gca cta cag tcc cgc aat ccc cac caa aga aaa   451
Gln Arg Phe Gln Ala Ala Leu Gln Ser Arg Asn Pro His Gln Arg Lys
            105                 110                 115

gta gtg atg ggc tac agc tac ggt tcc aca gtg gtg gga aaa gct gcg   499
Val Val Met Gly Tyr Ser Tyr Gly Ser Thr Val Val Gly Lys Ala Ala
        120                 125                 130

tct tcc ggc gag ctc agt gcc gat gcg ttg gta ttg gtt ggc agt ccc   547
Ser Ser Gly Glu Leu Ser Ala Asp Ala Leu Val Leu Val Gly Ser Pro
```

```
    135                 140                 145

ggc gcg ggt gtc tcg cac tct tcc cag ctt ggc gca cct gtg tat gcg   595
Gly Ala Gly Val Ser His Ser Ser Gln Leu Gly Ala Pro Val Tyr Ala
150                 155                 160                 165

gta aca ggg tct gct gat ccc atc ggt ttt gcc ggc acc caa tat gac   643
Val Thr Gly Ser Ala Asp Pro Ile Gly Phe Ala Gly Thr Gln Tyr Asp
                170                 175                 180

ggc atc cac ggc act gat ccc acc gct gcc cta ttc ggt gca aca gtg   691
Gly Ile His Gly Thr Asp Pro Thr Ala Ala Leu Phe Gly Ala Thr Val
            185                 190                 195

tgg gat tcg ccc tca acg cat tcc ggt tat tgg aat gac cag gag ttc   739
Trp Asp Ser Pro Ser Thr His Ser Gly Tyr Trp Asn Asp Gln Glu Phe
        200                 205                 210

ctg ggc aat gtg gcg gag gtg gtt cgc ggc aaa tagaaaagcc gccgcacact 792
Leu Gly Asn Val Ala Glu Val Val Arg Gly Lys
    215                 220

gga                                                               795


<210> 1216
<211> 224
<212> PRT
<213> Corynebacterium glutamicum

<400> 1216
Val Asn Ala Pro Pro Glu Ile Arg Ala Leu Ala Glu Ala His Pro Asp
  1               5                  10                  15

Met Gln Ile Leu Glu Ala Gly Asp Gly Ser Leu Val Ala Ser Phe Gly
             20                  25                  30

Asp Ile Asp Arg Ala Thr Thr Val Thr Thr Ile Val Ala Gly Val Gly
         35                  40                  45

Ser Ser Asn Pro Glu Gly Trp Asn Thr Tyr Val Asp Arg Ala Arg Thr
     50                  55                  60

Val Ser Ala Ser Thr Gly Ser Ala Thr Val Leu Trp Leu Gly Tyr Gln
 65                  70                  75                  80

Ala Pro Ala Ser Ile Pro Ala Ala Val Ser Gly Ala Ala Ala Asn Arg
                 85                  90                  95

Ala Ala Ala Asp Leu Gln Arg Phe Gln Ala Ala Leu Gln Ser Arg Asn
            100                 105                 110

Pro His Gln Arg Lys Val Val Met Gly Tyr Ser Tyr Gly Ser Thr Val
        115                 120                 125

Val Gly Lys Ala Ala Ser Ser Gly Glu Leu Ser Ala Asp Ala Leu Val
    130                 135                 140

Leu Val Gly Ser Pro Gly Ala Gly Val Ser His Ser Ser Gln Leu Gly
145                 150                 155                 160
```

```
Ala Pro Val Tyr Ala Val Thr Gly Ser Ala Asp Pro Ile Gly Phe Ala
                165                 170                 175

Gly Thr Gln Tyr Asp Gly Ile His Gly Thr Asp Pro Thr Ala Ala Leu
            180                 185                 190

Phe Gly Ala Thr Val Trp Asp Ser Pro Ser Thr His Ser Gly Tyr Trp
        195                 200                 205

Asn Asp Gln Glu Phe Leu Gly Asn Val Ala Glu Val Val Arg Gly Lys
    210                 215                 220
```

<210> 1217
<211> 726
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(703)
<223> RXN02555

<400> 1217

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gttttatcgc tatttaatac aggcctaccc ccactacccc cattcagttc agggaatccc 60

cggatttaaa acaattaaaa accctctaga atgagacatt atg ggc gaa caa ttt   115
                                            Met Gly Glu Gln Phe
                                              1               5

cca ggc gat aaa aac atc cga gtc agc gac acc gaa aga tca gca gca   163
Pro Gly Asp Lys Asn Ile Arg Val Ser Asp Thr Glu Arg Ser Ala Ala
                10                  15                  20

cta gca gca ctc ggc cag ttc tac gca gaa ggt cgc ctc tcc cta gaa   211
Leu Ala Ala Leu Gly Gln Phe Tyr Ala Glu Gly Arg Leu Ser Leu Glu
            25                  30                  35

gaa acc gac gac cgc tgc gaa gcc gtc gcc gac gcc aaa acc cgc ggc   259
Glu Thr Asp Asp Arg Cys Glu Ala Val Ala Asp Ala Lys Thr Arg Gly
        40                  45                  50

gac ctc aac gcc atc ttc tac gat ctg ccc aac caa caa atc gca gtc   307
Asp Leu Asn Ala Ile Phe Tyr Asp Leu Pro Asn Gln Gln Ile Ala Val
    55                  60                  65

gtc gac cgc tcc gaa caa acc tac aca gcc acc gaa gtt gcc gaa ctc   355
Val Asp Arg Ser Glu Gln Thr Tyr Thr Ala Thr Glu Val Ala Glu Leu
70                  75                  80                  85

cac cgc aaa ggc gca cgc cca cgc gcc gga atc ctc gga ctc acc aca   403
His Arg Lys Gly Ala Arg Pro Arg Ala Gly Ile Leu Gly Leu Thr Thr
                90                  95                  100

gtt tta gcc atc acc ggt acc gct gct ttc gcc agc acc aca gct ttt   451
Val Leu Ala Ile Thr Gly Thr Ala Ala Phe Ala Ser Thr Thr Ala Phe
            105                 110                 115
```

```
gca aca gta ctt tta gcc ctg att ccg atc gtg ttc atc atg ctg tac   499
Ala Thr Val Leu Leu Ala Leu Ile Pro Ile Val Phe Ile Met Leu Tyr
        120                 125                 130

gtg atg aaa att ggt cct gaa tcc tgg cac gca cca aca cct cgc caa   547
Val Met Lys Ile Gly Pro Glu Ser Trp His Ala Pro Thr Pro Arg Gln
    135                 140                 145

ctt cag cga aag cgc atg atc gaa ctg cgt gaa aag gaa aaa ctc cgc   595
Leu Gln Arg Lys Arg Met Ile Glu Leu Arg Glu Lys Glu Lys Leu Arg
150                 155                 160                 165

gac atg gag ctc aaa gcc cag cgc aag gaa cgc acc cac gca tta acc   643
Asp Met Glu Leu Lys Ala Gln Arg Lys Glu Arg Thr His Ala Leu Thr
                170                 175                 180

aac cgc gcg ttg gat gct gct gaa act gct ttc aac acc aag ccc tgg   691
Asn Arg Ala Leu Asp Ala Ala Glu Thr Ala Phe Asn Thr Lys Pro Trp
            185                 190                 195

aag aag aac aaa tagggctttt gaagtgtgtc gcg                        726
Lys Lys Asn Lys
        200
```

<210> 1218
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 1218

```
Met Gly Glu Gln Phe Pro Gly Asp Lys Asn Ile Arg Val Ser Asp Thr
  1               5                  10                  15

Glu Arg Ser Ala Ala Leu Ala Ala Leu Gly Gln Phe Tyr Ala Glu Gly
             20                  25                  30

Arg Leu Ser Leu Glu Glu Thr Asp Asp Arg Cys Glu Ala Val Ala Asp
         35                  40                  45

Ala Lys Thr Arg Gly Asp Leu Asn Ala Ile Phe Tyr Asp Leu Pro Asn
     50                  55                  60

Gln Gln Ile Ala Val Val Asp Arg Ser Glu Gln Thr Tyr Thr Ala Thr
 65                  70                  75                  80

Glu Val Ala Glu Leu His Arg Lys Gly Ala Arg Pro Arg Ala Gly Ile
                 85                  90                  95

Leu Gly Leu Thr Thr Val Leu Ala Ile Thr Gly Thr Ala Ala Phe Ala
            100                 105                 110

Ser Thr Thr Ala Phe Ala Thr Val Leu Leu Ala Leu Ile Pro Ile Val
        115                 120                 125

Phe Ile Met Leu Tyr Val Met Lys Ile Gly Pro Glu Ser Trp His Ala
    130                 135                 140

Pro Thr Pro Arg Gln Leu Gln Arg Lys Arg Met Ile Glu Leu Arg Glu
145                 150                 155                 160
```

```
Lys Glu Lys Leu Arg Asp Met Glu Leu Lys Ala Gln Arg Lys Glu Arg
                165                 170                 175

Thr His Ala Leu Thr Asn Arg Ala Leu Asp Ala Ala Glu Thr Ala Phe
            180                 185                 190

Asn Thr Lys Pro Trp Lys Lys Asn Lys
        195                 200


<210> 1219
<211> 726
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(703)
<223> FRXA02555

<400> 1219
gttttatcgc tatttaatac aggcctaccc ccactacccc cattcagttc agggaatccc 60

cggatttaaa acaattaaaa accctctaga atgagacatt atg ggc gaa caa ttt   115
                                            Met Gly Glu Gln Phe
                                              1               5

cca ggc gat aaa aac atc cga gtc agc gac acc gaa aga tca gca gca   163
Pro Gly Asp Lys Asn Ile Arg Val Ser Asp Thr Glu Arg Ser Ala Ala
                10                  15                  20

cta gca gca ctc ggc cag ttc tac gca gaa ggt cgc ctc tcc cta gaa   211
Leu Ala Ala Leu Gly Gln Phe Tyr Ala Glu Gly Arg Leu Ser Leu Glu
            25                  30                  35

gaa acc gac gac cgc tgc gaa gcc gtc gcc gac gcc aaa acc cgc ggc   259
Glu Thr Asp Asp Arg Cys Glu Ala Val Ala Asp Ala Lys Thr Arg Gly
        40                  45                  50

gac ctc aac gcc atc ttc tac gat ctg ccc aac caa caa atc gca gtc   307
Asp Leu Asn Ala Ile Phe Tyr Asp Leu Pro Asn Gln Gln Ile Ala Val
    55                  60                  65

gtc gac cgc tcc gaa caa acc tac aca gcc acc gaa gtt gcc gaa ctc   355
Val Asp Arg Ser Glu Gln Thr Tyr Thr Ala Thr Glu Val Ala Glu Leu
70                  75                  80                  85

cac cgc aaa ggc gca cgc cca cgc gcc gga atc ctc gga ctc acc aca   403
His Arg Lys Gly Ala Arg Pro Arg Ala Gly Ile Leu Gly Leu Thr Thr
                90                  95                  100

gtt tta gcc atc acc ggt acc gct gct ttc gcc agc acc aca gct ttt   451
Val Leu Ala Ile Thr Gly Thr Ala Ala Phe Ala Ser Thr Thr Ala Phe
            105                 110                 115

gca aca gta ctt tta gcc ctg att ccg atc gtg ttc atc atg ctg tac   499
Ala Thr Val Leu Leu Ala Leu Ile Pro Ile Val Phe Ile Met Leu Tyr
        120                 125                 130

gtg atg aaa att ggt cct gaa tcc tgg cac gca cca aca cct cgc caa   547
Val Met Lys Ile Gly Pro Glu Ser Trp His Ala Pro Thr Pro Arg Gln
```

```
    135                 140                 145

ctt cag cga aag cgc atg atc gaa ctg cgt gaa aag gaa aaa ctc cgc   595
Leu Gln Arg Lys Arg Met Ile Glu Leu Arg Glu Lys Glu Lys Leu Arg
150                 155                 160                 165

gac atg gag ctc aaa gcc cag cgc aag gaa cgc acc cac gca tta acc   643
Asp Met Glu Leu Lys Ala Gln Arg Lys Glu Arg Thr His Ala Leu Thr
                170                 175                 180

aac cgc gcg ttg gat gct gct gaa act gct ttc aac acc aag ccc tgg   691
Asn Arg Ala Leu Asp Ala Ala Glu Thr Ala Phe Asn Thr Lys Pro Trp
            185                 190                 195

aag aag aac aaa tagggctttt gaagtgtgtc gcg                        726
Lys Lys Asn Lys
        200
```

<210> 1220
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 1220

```
Met Gly Glu Gln Phe Pro Gly Asp Lys Asn Ile Arg Val Ser Asp Thr
  1               5                  10                  15

Glu Arg Ser Ala Ala Leu Ala Ala Leu Gly Gln Phe Tyr Ala Glu Gly
             20                  25                  30

Arg Leu Ser Leu Glu Glu Thr Asp Asp Arg Cys Glu Ala Val Ala Asp
         35                  40                  45

Ala Lys Thr Arg Gly Asp Leu Asn Ala Ile Phe Tyr Asp Leu Pro Asn
     50                  55                  60

Gln Gln Ile Ala Val Val Asp Arg Ser Glu Gln Thr Tyr Thr Ala Thr
 65                  70                  75                  80

Glu Val Ala Glu Leu His Arg Lys Gly Ala Arg Pro Arg Ala Gly Ile
                 85                  90                  95

Leu Gly Leu Thr Thr Val Leu Ala Ile Thr Gly Thr Ala Ala Phe Ala
            100                 105                 110

Ser Thr Thr Ala Phe Ala Thr Val Leu Leu Ala Leu Ile Pro Ile Val
        115                 120                 125

Phe Ile Met Leu Tyr Val Met Lys Ile Gly Pro Glu Ser Trp His Ala
    130                 135                 140

Pro Thr Pro Arg Gln Leu Gln Arg Lys Arg Met Ile Glu Leu Arg Glu
145                 150                 155                 160

Lys Glu Lys Leu Arg Asp Met Glu Leu Lys Ala Gln Arg Lys Glu Arg
                165                 170                 175

Thr His Ala Leu Thr Asn Arg Ala Leu Asp Ala Ala Glu Thr Ala Phe
            180                 185                 190
```

```
Asn Thr Lys Pro Trp Lys Lys Asn Lys
        195                 200


<210> 1221
<211> 1125
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1102)
<223> RXN02564

<400> 1221
acaccacagt gaagcggtga cgtgaatcac ccaagcactt aggcatcaaa cattcaagag 60

cttgttgtcc aaaagtccga ccgagaggga ttcccccaaa atg gcc gaa gta gga   115
                                            Met Ala Glu Val Gly
                                              1               5

gca gaa ccc gca ggg tct gca caa tcc aaa act aaa caa ttt gtt gta   163
Ala Glu Pro Ala Gly Ser Ala Gln Ser Lys Thr Lys Gln Phe Val Val
                 10                  15                  20

ggt acc gca gcg gtg gtc atc act gca atc gct gcg ttt ttc tcc atc   211
Gly Thr Ala Ala Val Val Ile Thr Ala Ile Ala Ala Phe Phe Ser Ile
             25                  30                  35

cag tct gca tcc ggt ggc gag gat att cgt tcc aac atg acg ctg att   259
Gln Ser Ala Ser Gly Gly Glu Asp Ile Arg Ser Asn Met Thr Leu Ile
         40                  45                  50

gct cct gca gct gca ggt gga ggt tgg gat act ttc caa cgt gag cag   307
Ala Pro Ala Ala Ala Gly Gly Gly Trp Asp Thr Phe Gln Arg Glu Gln
     55                  60                  65

cag cag tct atg cgc gtg aat aag atc gtg aac aat att cag gtg gtc   355
Gln Gln Ser Met Arg Val Asn Lys Ile Val Asn Asn Ile Gln Val Val
 70                  75                  80                  85

aac atc cct gga gct ggt gga acc att gca ctt ggc aaa ctg tct acc   403
Asn Ile Pro Gly Ala Gly Gly Thr Ile Ala Leu Gly Lys Leu Ser Thr
                 90                  95                 100

atg act gca ccg aac acc ttg atg gtg ggt gga acg ggg cat atc gca   451
Met Thr Ala Pro Asn Thr Leu Met Val Gly Gly Thr Gly His Ile Ala
            105                 110                 115

gca caa att caa ttc gat acc cct gcg aaa atc cag gat gtc acc cca   499
Ala Gln Ile Gln Phe Asp Thr Pro Ala Lys Ile Gln Asp Val Thr Pro
        120                 125                 130

att gct cgt gtg gtg gaa gag ttc gac atc atc acc gtg cca gcg gat   547
Ile Ala Arg Val Val Glu Glu Phe Asp Ile Ile Thr Val Pro Ala Asp
    135                 140                 145

tct cca tac aac acc ctt gaa gag ctc att gaa ggt tgg aag gca gat   595
Ser Pro Tyr Asn Thr Leu Glu Glu Leu Ile Glu Gly Trp Lys Ala Asp
150                 155                 160                 165
```

```
cca gca gga gtg tcc tgg acc ggt ggt ggt tcc ttt gac cag ctt gtt   643
Pro Ala Gly Val Ser Trp Thr Gly Gly Gly Ser Phe Asp Gln Leu Val
                170                 175                 180

atg aca gaa att gca ctg tct gca ggt ata gat cct aag caa acc acc   691
Met Thr Glu Ile Ala Leu Ser Ala Gly Ile Asp Pro Lys Gln Thr Thr
            185                 190                 195

ttt att cct tct gat ggt ggt ggc gaa gcg att cag gcg cta ctg aac   739
Phe Ile Pro Ser Asp Gly Gly Gly Glu Ala Ile Gln Ala Leu Leu Asn
        200                 205                 210

gga acc gca aag gca tca act ggt ggt ttt gct gat atg tat ccg cag   787
Gly Thr Ala Lys Ala Ser Thr Gly Gly Phe Ala Asp Met Tyr Pro Gln
    215                 220                 225

gta gaa gcc ggt cga ttg aag gtt ttg gga att gct gca gaa gaa cgc   835
Val Glu Ala Gly Arg Leu Lys Val Leu Gly Ile Ala Ala Glu Glu Arg
230                 235                 240                 245

ctt cca ggt tct gac att cca acg cta gtg gaa caa ggc tat gac gtg   883
Leu Pro Gly Ser Asp Ile Pro Thr Leu Val Glu Gln Gly Tyr Asp Val
                250                 255                 260

acc ttg acc aac tgg cgt gcc atg ttc gct cct cct ggt ttg agc gat   931
Thr Leu Thr Asn Trp Arg Ala Met Phe Ala Pro Pro Gly Leu Ser Asp
            265                 270                 275

gat caa att gcg gaa ctt cga gca atc gtt gcg gag tct gtg gag act   979
Asp Gln Ile Ala Glu Leu Arg Ala Ile Val Ala Glu Ser Val Glu Thr
        280                 285                 290

gct gaa tgg cag tcc gcg gtg gaa cga aac tac tgg atg aac gcc tca   1027
Ala Glu Trp Gln Ser Ala Val Glu Arg Asn Tyr Trp Met Asn Ala Ser
    295                 300                 305

ctt gaa ggc gaa gaa ctc gac cag ttt gtt gaa gat gaa att gac cga   1075
Leu Glu Gly Glu Glu Leu Asp Gln Phe Val Glu Asp Glu Ile Asp Arg
310                 315                 320                 325

att gat cag cta ttc aag gag atg ggc tagtgaacgt cactgaacaa        1122
Ile Asp Gln Leu Phe Lys Glu Met Gly
                330

tcc                                                              1125
```

<210> 1222
<211> 334
<212> PRT
<213> Corynebacterium glutamicum

<400> 1222

```
Met Ala Glu Val Gly Ala Glu Pro Ala Gly Ser Ala Gln Ser Lys Thr
  1               5                  10                  15

Lys Gln Phe Val Val Gly Thr Ala Ala Val Val Ile Thr Ala Ile Ala
             20                  25                  30

Ala Phe Phe Ser Ile Gln Ser Ala Ser Gly Gly Glu Asp Ile Arg Ser
         35                  40                  45
```

```
Asn Met Thr Leu Ile Ala Pro Ala Ala Ala Gly Gly Gly Trp Asp Thr
     50                  55                  60

Phe Gln Arg Glu Gln Gln Gln Ser Met Arg Val Asn Lys Ile Val Asn
 65                  70                  75                  80

Asn Ile Gln Val Val Asn Ile Pro Gly Ala Gly Gly Thr Ile Ala Leu
                85                  90                  95

Gly Lys Leu Ser Thr Met Thr Ala Pro Asn Thr Leu Met Val Gly Gly
            100                 105                 110

Thr Gly His Ile Ala Ala Gln Ile Gln Phe Asp Thr Pro Ala Lys Ile
        115                 120                 125

Gln Asp Val Thr Pro Ile Ala Arg Val Val Glu Glu Phe Asp Ile Ile
    130                 135                 140

Thr Val Pro Ala Asp Ser Pro Tyr Asn Thr Leu Glu Glu Leu Ile Glu
145                 150                 155                 160

Gly Trp Lys Ala Asp Pro Ala Gly Val Ser Trp Thr Gly Gly Gly Ser
                165                 170                 175

Phe Asp Gln Leu Val Met Thr Glu Ile Ala Leu Ser Ala Gly Ile Asp
            180                 185                 190

Pro Lys Gln Thr Thr Phe Ile Pro Ser Asp Gly Gly Gly Glu Ala Ile
        195                 200                 205

Gln Ala Leu Leu Asn Gly Thr Ala Lys Ala Ser Thr Gly Gly Phe Ala
    210                 215                 220

Asp Met Tyr Pro Gln Val Glu Ala Gly Arg Leu Lys Val Leu Gly Ile
225                 230                 235                 240

Ala Ala Glu Glu Arg Leu Pro Gly Ser Asp Ile Pro Thr Leu Val Glu
                245                 250                 255

Gln Gly Tyr Asp Val Thr Leu Thr Asn Trp Arg Ala Met Phe Ala Pro
            260                 265                 270

Pro Gly Leu Ser Asp Asp Gln Ile Ala Glu Leu Arg Ala Ile Val Ala
        275                 280                 285

Glu Ser Val Glu Thr Ala Glu Trp Gln Ser Ala Val Glu Arg Asn Tyr
    290                 295                 300

Trp Met Asn Ala Ser Leu Glu Gly Glu Glu Leu Asp Gln Phe Val Glu
305                 310                 315                 320

Asp Glu Ile Asp Arg Ile Asp Gln Leu Phe Lys Glu Met Gly
                325                 330
```

<210> 1223
<211> 775
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(775)
<223> FRXA02564

<400> 1223
acaccacagt gaagcggtga cgtgaatcac ccaagcactt aggcatcaaa cattcaagag 60

cttgttgtcc aaaagtccga ccgagaggga ttcccccaaa atg gcc gaa gta gga 115
Met Ala Glu Val Gly
1 5

gca gaa ccc gca ggg tct gca caa tcc aaa act aaa caa ttt gtt gta 163
Ala Glu Pro Ala Gly Ser Ala Gln Ser Lys Thr Lys Gln Phe Val Val
10 15 20

ggt acc gca gcg gtg gtc atc act gca atc gct gcg ttt ttc tcc atc 211
Gly Thr Ala Ala Val Val Ile Thr Ala Ile Ala Ala Phe Phe Ser Ile
25 30 35

cag tct gca tcc ggt ggc gag gat att cgt tcc aac atg acg ctg att 259
Gln Ser Ala Ser Gly Gly Glu Asp Ile Arg Ser Asn Met Thr Leu Ile
40 45 50

gct cct gca gct gca ggt gga ggt tgg gat act ttc caa cgt gag cag 307
Ala Pro Ala Ala Ala Gly Gly Gly Trp Asp Thr Phe Gln Arg Glu Gln
55 60 65

cag cag tct atg cgc gtg aat aag atc gtg aac aat att cag gtg gtc 355
Gln Gln Ser Met Arg Val Asn Lys Ile Val Asn Asn Ile Gln Val Val
70 75 80 85

aac atc cct gga gct ggt gga acc att gca ctt ggc aaa ctg tct acc 403
Asn Ile Pro Gly Ala Gly Gly Thr Ile Ala Leu Gly Lys Leu Ser Thr
90 95 100

atg act gca ccg aac acc ttg atg gtg ggt gga acg ggg cat atc gca 451
Met Thr Ala Pro Asn Thr Leu Met Val Gly Gly Thr Gly His Ile Ala
105 110 115

gca caa att caa ttc gat acc cct gcg aaa atc cag gat gtc acc cca 499
Ala Gln Ile Gln Phe Asp Thr Pro Ala Lys Ile Gln Asp Val Thr Pro
120 125 130

att gct cgt gtg gtg gaa gag ttc gac atc atc acc gtg cca gcg gat 547
Ile Ala Arg Val Val Glu Glu Phe Asp Ile Ile Thr Val Pro Ala Asp
135 140 145

tct cca tac aac acc ctt gaa gag ctc att gaa ggt tgg aag gca gat 595
Ser Pro Tyr Asn Thr Leu Glu Glu Leu Ile Glu Gly Trp Lys Ala Asp
150 155 160 165

cca gca gga gtg tcc tgg acc ggt ggt ggt tcc ttt gac cag ctt gtt 643
Pro Ala Gly Val Ser Trp Thr Gly Gly Gly Ser Phe Asp Gln Leu Val
170 175 180

atg aca gaa att gca ctg tct gca ggt ata gat cct aag caa acc acc 691
Met Thr Glu Ile Ala Leu Ser Ala Gly Ile Asp Pro Lys Gln Thr Thr
185 190 195

ttt att cct tct gat ggt ggt ggc gaa gcg att cag gcg cta ctg aac 739

```
Phe Ile Pro Ser Asp Gly Gly Gly Glu Ala Ile Gln Ala Leu Leu Asn
        200                 205                 210

gga acc gca aag gca tca act ggt ggt ttt gct gat                  775
Gly Thr Ala Lys Ala Ser Thr Gly Gly Phe Ala Asp
    215                 220                 225


<210> 1224
<211> 225
<212> PRT
<213> Corynebacterium glutamicum

<400> 1224
Met Ala Glu Val Gly Ala Glu Pro Ala Gly Ser Ala Gln Ser Lys Thr
  1               5                  10                  15

Lys Gln Phe Val Val Gly Thr Ala Ala Val Val Ile Thr Ala Ile Ala
             20                  25                  30

Ala Phe Phe Ser Ile Gln Ser Ala Ser Gly Gly Glu Asp Ile Arg Ser
         35                  40                  45

Asn Met Thr Leu Ile Ala Pro Ala Ala Ala Gly Gly Gly Trp Asp Thr
     50                  55                  60

Phe Gln Arg Glu Gln Gln Gln Ser Met Arg Val Asn Lys Ile Val Asn
 65                  70                  75                  80

Asn Ile Gln Val Val Asn Ile Pro Gly Ala Gly Gly Thr Ile Ala Leu
                 85                  90                  95

Gly Lys Leu Ser Thr Met Thr Ala Pro Asn Thr Leu Met Val Gly Gly
            100                 105                 110

Thr Gly His Ile Ala Ala Gln Ile Gln Phe Asp Thr Pro Ala Lys Ile
        115                 120                 125

Gln Asp Val Thr Pro Ile Ala Arg Val Val Glu Glu Phe Asp Ile Ile
    130                 135                 140

Thr Val Pro Ala Asp Ser Pro Tyr Asn Thr Leu Glu Glu Leu Ile Glu
145                 150                 155                 160

Gly Trp Lys Ala Asp Pro Ala Gly Val Ser Trp Thr Gly Gly Gly Ser
                165                 170                 175

Phe Asp Gln Leu Val Met Thr Glu Ile Ala Leu Ser Ala Gly Ile Asp
            180                 185                 190

Pro Lys Gln Thr Thr Phe Ile Pro Ser Asp Gly Gly Gly Glu Ala Ile
        195                 200                 205

Gln Ala Leu Leu Asn Gly Thr Ala Lys Ala Ser Thr Gly Gly Phe Ala
    210                 215                 220

Asp
225


<210> 1225
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<211> 1753
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1753)
<223> RXN02568

<400> 1225
ccagctacga tatggaattt caccaaatgc gaactaccct aaataccaaa gacagacagt 60

gacagcccct tcgagaatgc agcaagagac gacacctcct atg gac ggc acc tcg 115
Met Asp Gly Thr Ser
1 5

cca cag aac aaa att tcc acc act ccc cca gcg cca gga aat gct att 163
Pro Gln Asn Lys Ile Ser Thr Thr Pro Pro Ala Pro Gly Asn Ala Ile
10 15 20

cct gca cct gga ggc gcc att cct aca cca gcg aaa act gag cag gac 211
Pro Ala Pro Gly Gly Ala Ile Pro Thr Pro Ala Lys Thr Glu Gln Asp
25 30 35

gca gta cct cca act gtg gcg gcg aaa cta ccc gta cct gga agt tct 259
Ala Val Pro Pro Thr Val Ala Ala Lys Leu Pro Val Pro Gly Ser Ser
40 45 50

att cca gca ccc ggt aga gca ttg cca act cca gtg gct ccg gga ggt 307
Ile Pro Ala Pro Gly Arg Ala Leu Pro Thr Pro Val Ala Pro Gly Gly
55 60 65

tcc gtc cca gct ccg aga gcg tcc gca cct gcg gtt cct aac gtt cct 355
Ser Val Pro Ala Pro Arg Ala Ser Ala Pro Ala Val Pro Asn Val Pro
70 75 80 85

gca gct ccc ggc gct gct gtt cca gct ccg gga atc tcg atc ccg gca 403
Ala Ala Pro Gly Ala Ala Val Pro Ala Pro Gly Ile Ser Ile Pro Ala
90 95 100

gca cct agt gcc cca ggc agt gca att cca aca cca ggc aca gca atc 451
Ala Pro Ser Ala Pro Gly Ser Ala Ile Pro Thr Pro Gly Thr Ala Ile
105 110 115

cct gtg cct gga agt gca act cct gtc cca gca cct ggg gtt agt gca 499
Pro Val Pro Gly Ser Ala Thr Pro Val Pro Ala Pro Gly Val Ser Ala
120 125 130

cct ggc gca agc gtt cca agc att cca gta cca gga tct gtc acc cca 547
Pro Gly Ala Ser Val Pro Ser Ile Pro Val Pro Gly Ser Val Thr Pro
135 140 145

cct gca cca gga att tcc gca cct ggc ggt gca ctt ccg act cct ggc 595
Pro Ala Pro Gly Ile Ser Ala Pro Gly Gly Ala Leu Pro Thr Pro Gly
150 155 160 165

agt gcg ccc cca aca cct ggc ggt gcc ctt ccg act cca ggt gag gca 643
Ser Ala Pro Pro Thr Pro Gly Gly Ala Leu Pro Thr Pro Gly Glu Ala
170 175 180

ctt ccc gtt ccc gga gca cct ggt gca ccc gga gca tcc gga atc cca 691

```
Leu Pro Val Pro Gly Ala Pro Gly Ala Pro Gly Ala Ser Gly Ile Pro
            185                 190                 195

agt cct ggc ctt cca acc cca ggt gtc cca act ccc gga gct tcc tta   739
Ser Pro Gly Leu Pro Thr Pro Gly Val Pro Thr Pro Gly Ala Ser Leu
        200                 205                 210

cca gtc cca gga gca cca gac gca cct gga acc cca agc att ccc gca   787
Pro Val Pro Gly Ala Pro Asp Ala Pro Gly Thr Pro Ser Ile Pro Ala
    215                 220                 225

gct ccc ggc att caa gca cca gga att cca gca gca cca gga gcc cct   835
Ala Pro Gly Ile Gln Ala Pro Gly Ile Pro Ala Ala Pro Gly Ala Pro
230                 235                 240                 245

gcc caa gct gct gct cac gca aag cca gta ttc caa gat gca gag aaa   883
Ala Gln Ala Ala Ala His Ala Lys Pro Val Phe Gln Asp Ala Glu Lys
                250                 255                 260

cga cct cgc aca gat gaa gct gga aat gcg aag aag gaa ctg ccg ctg   931
Arg Pro Arg Thr Asp Glu Ala Gly Asn Ala Lys Lys Glu Leu Pro Leu
            265                 270                 275

aga gtt cgg ttg gcg cag cca att aca cgt aag cag tgg gca atg act   979
Arg Val Arg Leu Ala Gln Pro Ile Thr Arg Lys Gln Trp Ala Met Thr
        280                 285                 290

ctt ggt gtc ctg gtt ctc gga gca att gtc gtg gct gca atc gcg gtg   1027
Leu Gly Val Leu Val Leu Gly Ala Ile Val Val Ala Ala Ile Ala Val
    295                 300                 305

gtc ctt gcc aaa tgg gcg ttt acc acg gag tgg ttg cag gac ttc gtc   1075
Val Leu Ala Lys Trp Ala Phe Thr Thr Glu Trp Leu Gln Asp Phe Val
310                 315                 320                 325

gag aag tat ccg ggt aaa tat gac aac ccc gaa ggt gcg cca gta gga   1123
Glu Lys Tyr Pro Gly Lys Tyr Asp Asn Pro Glu Gly Ala Pro Val Gly
                330                 335                 340

att cca acg tgg ctg agt tgg cag cac ttc ttc aac atg ttc ttc atg   1171
Ile Pro Thr Trp Leu Ser Trp Gln His Phe Phe Asn Met Phe Phe Met
            345                 350                 355

gtg ttg att atc aag acg ggc att gag atc aat aga acc cgc agg cca   1219
Val Leu Ile Ile Lys Thr Gly Ile Glu Ile Asn Arg Thr Arg Arg Pro
        360                 365                 370

aag ggt tat tgg acg ccg aaa aag ggt ggc aag aag atc tcc ttg acg   1267
Lys Gly Tyr Trp Thr Pro Lys Lys Gly Gly Lys Lys Ile Ser Leu Thr
    375                 380                 385

ttg tgg atc cac ctg gtt ttg gat ttg ttg tgg atc atc aac ggt gcg   1315
Leu Trp Ile His Leu Val Leu Asp Leu Leu Trp Ile Ile Asn Gly Ala
390                 395                 400                 405

gtg ttc atc att ttg ttg ttc gcg acg ggt cag tgg atg cgc att gtt   1363
Val Phe Ile Ile Leu Leu Phe Ala Thr Gly Gln Trp Met Arg Ile Val
                410                 415                 420

cca acc agt tgg gat gtg ttc ccg aac gcg ctg agt gct ggt ttg cag   1411
Pro Thr Ser Trp Asp Val Phe Pro Asn Ala Leu Ser Ala Gly Leu Gln
```

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            425                 430                 435

tat gtg tcg ttg gat tgg ccg act gag aat ggt tgg gcg aat tac aac   1459
Tyr Val Ser Leu Asp Trp Pro Thr Glu Asn Gly Trp Ala Asn Tyr Asn
        440                 445                 450

agt ttg cag gag ctg acg tac ttc ttc act gtc ttt att gcg gca ccg   1507
Ser Leu Gln Glu Leu Thr Tyr Phe Phe Thr Val Phe Ile Ala Ala Pro
    455                 460                 465

ttg tcg att gtg tct ggt ttc cgg atg tcg agt tac tgg cct aag aac   1555
Leu Ser Ile Val Ser Gly Phe Arg Met Ser Ser Tyr Trp Pro Lys Asn
470                 475                 480                 485

aat gcg acg atg aat aag ttg atc ccc atc ggg ttt gct cgt gcg ctg   1603
Asn Ala Thr Met Asn Lys Leu Ile Pro Ile Gly Phe Ala Arg Ala Leu
                490                 495                 500

cac atg cca gtg atg gtg tat tac atc gtg ttc att tgt atc cac gtg   1651
His Met Pro Val Met Val Tyr Tyr Ile Val Phe Ile Cys Ile His Val
            505                 510                 515

ttc ttg gtg ttg gcg acc ggc gcg ttg cgc aat ttc aac cat atg tat   1699
Phe Leu Val Leu Ala Thr Gly Ala Leu Arg Asn Phe Asn His Met Tyr
        520                 525                 530

gca ggt caa gac gtt gtg aac tgg gtt ggt ttt ggt tgg ttc gtg gcg   1747
Ala Gly Gln Asp Val Val Asn Trp Val Gly Phe Gly Trp Phe Val Ala
    535                 540                 545

tcg ttg                                                           1753
Ser Leu
550
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<210> 1226
<211> 551
<212> PRT
<213> Corynebacterium glutamicum

<400> 1226

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Met Asp Gly Thr Ser Pro Gln Asn Lys Ile Ser Thr Thr Pro Pro Ala
  1               5                  10                  15

Pro Gly Asn Ala Ile Pro Ala Pro Gly Gly Ala Ile Pro Thr Pro Ala
             20                  25                  30

Lys Thr Glu Gln Asp Ala Val Pro Pro Thr Val Ala Ala Lys Leu Pro
         35                  40                  45

Val Pro Gly Ser Ser Ile Pro Ala Pro Gly Arg Ala Leu Pro Thr Pro
     50                  55                  60

Val Ala Pro Gly Gly Ser Val Pro Ala Pro Arg Ala Ser Ala Pro Ala
 65                  70                  75                  80

Val Pro Asn Val Pro Ala Ala Pro Gly Ala Ala Val Pro Ala Pro Gly
                 85                  90                  95

Ile Ser Ile Pro Ala Ala Pro Ser Ala Pro Gly Ser Ala Ile Pro Thr
            100                 105                 110
```

```
Pro Gly Thr Ala Ile Pro Val Pro Gly Ser Ala Thr Pro Val Pro Ala
        115                 120                 125

Pro Gly Val Ser Ala Pro Gly Ala Ser Val Pro Ser Ile Pro Val Pro
    130                 135                 140

Gly Ser Val Thr Pro Pro Ala Pro Gly Ile Ser Ala Pro Gly Gly Ala
145                 150                 155                 160

Leu Pro Thr Pro Gly Ser Ala Pro Pro Thr Pro Gly Gly Ala Leu Pro
                165                 170                 175

Thr Pro Gly Glu Ala Leu Pro Val Pro Gly Ala Pro Gly Ala Pro Gly
            180                 185                 190

Ala Ser Gly Ile Pro Ser Pro Gly Leu Pro Thr Pro Gly Val Pro Thr
        195                 200                 205

Pro Gly Ala Ser Leu Pro Val Pro Gly Ala Pro Asp Ala Pro Gly Thr
    210                 215                 220

Pro Ser Ile Pro Ala Ala Pro Gly Ile Gln Ala Pro Gly Ile Pro Ala
225                 230                 235                 240

Ala Pro Gly Ala Pro Ala Gln Ala Ala Ala His Ala Lys Pro Val Phe
                245                 250                 255

Gln Asp Ala Glu Lys Arg Pro Arg Thr Asp Glu Ala Gly Asn Ala Lys
            260                 265                 270

Lys Glu Leu Pro Leu Arg Val Arg Leu Ala Gln Pro Ile Thr Arg Lys
        275                 280                 285

Gln Trp Ala Met Thr Leu Gly Val Leu Val Leu Gly Ala Ile Val Val
    290                 295                 300

Ala Ala Ile Ala Val Val Leu Ala Lys Trp Ala Phe Thr Thr Glu Trp
305                 310                 315                 320

Leu Gln Asp Phe Val Glu Lys Tyr Pro Gly Lys Tyr Asp Asn Pro Glu
                325                 330                 335

Gly Ala Pro Val Gly Ile Pro Thr Trp Leu Ser Trp Gln His Phe Phe
            340                 345                 350

Asn Met Phe Phe Met Val Leu Ile Ile Lys Thr Gly Ile Glu Ile Asn
        355                 360                 365

Arg Thr Arg Arg Pro Lys Gly Tyr Trp Thr Pro Lys Lys Gly Gly Lys
    370                 375                 380

Lys Ile Ser Leu Thr Leu Trp Ile His Leu Val Leu Asp Leu Leu Trp
385                 390                 395                 400

Ile Ile Asn Gly Ala Val Phe Ile Ile Leu Leu Phe Ala Thr Gly Gln
                405                 410                 415

Trp Met Arg Ile Val Pro Thr Ser Trp Asp Val Phe Pro Asn Ala Leu
            420                 425                 430
```

```
Ser Ala Gly Leu Gln Tyr Val Ser Leu Asp Trp Pro Thr Glu Asn Gly
        435                 440                 445

Trp Ala Asn Tyr Asn Ser Leu Gln Glu Leu Thr Tyr Phe Phe Thr Val
    450                 455                 460

Phe Ile Ala Ala Pro Leu Ser Ile Val Ser Gly Phe Arg Met Ser Ser
465                 470                 475                 480

Tyr Trp Pro Lys Asn Asn Ala Thr Met Asn Lys Leu Ile Pro Ile Gly
                485                 490                 495

Phe Ala Arg Ala Leu His Met Pro Val Met Val Tyr Tyr Ile Val Phe
            500                 505                 510

Ile Cys Ile His Val Phe Leu Val Leu Ala Thr Gly Ala Leu Arg Asn
        515                 520                 525

Phe Asn His Met Tyr Ala Gly Gln Asp Val Val Asn Trp Val Gly Phe
    530                 535                 540

Gly Trp Phe Val Ala Ser Leu
545                 550


<210> 1227
<211> 1359
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1359)
<223> FRXA02568

<400> 1227
atc ccg gca gca cct agt gcc cca ggc agt gca att cca aca cca ggc   48
Ile Pro Ala Ala Pro Ser Ala Pro Gly Ser Ala Ile Pro Thr Pro Gly
  1               5                  10                  15

aca gca atc cct gtg cct gga agt gca act cct gtc cca gca cct ggg   96
Thr Ala Ile Pro Val Pro Gly Ser Ala Thr Pro Val Pro Ala Pro Gly
             20                  25                  30

gtt agt gca cct ggc gca agc gtt cca agc att cca gta cca gga tct   144
Val Ser Ala Pro Gly Ala Ser Val Pro Ser Ile Pro Val Pro Gly Ser
         35                  40                  45

gtc acc cca cct gca cca gga att tcc gca cct ggc ggt gca ctt ccg   192
Val Thr Pro Pro Ala Pro Gly Ile Ser Ala Pro Gly Gly Ala Leu Pro
     50                  55                  60

act cct ggc agt gcg ccc cca aca cct ggc ggt gcc ctt ccg act cca   240
Thr Pro Gly Ser Ala Pro Pro Thr Pro Gly Gly Ala Leu Pro Thr Pro
 65                  70                  75                  80

ggt gag gca ctt ccc gtt ccc gga gca cct ggt gca ccc gga gca tcc   288
Gly Glu Ala Leu Pro Val Pro Gly Ala Pro Gly Ala Pro Gly Ala Ser
                85                  90                  95

gga atc cca agt cct ggc ctt cca acc cca ggt gtc cca act ccc gga   336
```

```
Gly Ile Pro Ser Pro Gly Leu Pro Thr Pro Gly Val Pro Thr Pro Gly
            100                 105                 110

gct tcc tta cca gtc cca gga gca cca gac gca cct gga acc cca agc   384
Ala Ser Leu Pro Val Pro Gly Ala Pro Asp Ala Pro Gly Thr Pro Ser
        115                 120                 125

att ccc gca gct ccc ggc att caa gca cca gga att cca gca gca cca   432
Ile Pro Ala Ala Pro Gly Ile Gln Ala Pro Gly Ile Pro Ala Ala Pro
    130                 135                 140

gga gcc cct gcc caa gct gct gct cac gca aag cca gta ttc caa gat   480
Gly Ala Pro Ala Gln Ala Ala Ala His Ala Lys Pro Val Phe Gln Asp
145                 150                 155                 160

gca gag aaa cga cct cgc aca gat gaa gct gga aat gcg aag aag gaa   528
Ala Glu Lys Arg Pro Arg Thr Asp Glu Ala Gly Asn Ala Lys Lys Glu
                165                 170                 175

ctg ccg ctg aga gtt cgg ttg gcg cag cca att aca cgt aag cag tgg   576
Leu Pro Leu Arg Val Arg Leu Ala Gln Pro Ile Thr Arg Lys Gln Trp
            180                 185                 190

gca atg act ctt ggt gtc ctg gtt ctc gga gca att gtc gtg gct gca   624
Ala Met Thr Leu Gly Val Leu Val Leu Gly Ala Ile Val Val Ala Ala
        195                 200                 205

atc gcg gtg gtc ctt gcc aaa tgg gcg ttt acc acg gag tgg ttg cag   672
Ile Ala Val Val Leu Ala Lys Trp Ala Phe Thr Thr Glu Trp Leu Gln
    210                 215                 220

gac ttc gtc gag aag tat ccg ggt aaa tat gac aac ccc gaa ggt gcg   720
Asp Phe Val Glu Lys Tyr Pro Gly Lys Tyr Asp Asn Pro Glu Gly Ala
225                 230                 235                 240

cca gta gga att cca acg tgg ctg agt tgg cag cac ttc ttc aac atg   768
Pro Val Gly Ile Pro Thr Trp Leu Ser Trp Gln His Phe Phe Asn Met
                245                 250                 255

ttc ttc atg gtg ttg att atc aag acg ggc att gag atc aat aga acc   816
Phe Phe Met Val Leu Ile Ile Lys Thr Gly Ile Glu Ile Asn Arg Thr
            260                 265                 270

cgc agg cca aag ggt tat tgg acg ccg aaa aag ggt ggc aag aag atc   864
Arg Arg Pro Lys Gly Tyr Trp Thr Pro Lys Lys Gly Gly Lys Lys Ile
        275                 280                 285

tcc ttg acg ttg tgg atc cac ctg gtt ttg gat ttg ttg tgg atc atc   912
Ser Leu Thr Leu Trp Ile His Leu Val Leu Asp Leu Leu Trp Ile Ile
    290                 295                 300

aac ggt gcg gtg ttc atc att ttg ttg ttc gcg acg ggt cag tgg atg   960
Asn Gly Ala Val Phe Ile Ile Leu Leu Phe Ala Thr Gly Gln Trp Met
305                 310                 315                 320

cgc att gtt cca acc agt tgg gat gtg ttc ccg aac gcg ctg agt gct  1008
Arg Ile Val Pro Thr Ser Trp Asp Val Phe Pro Asn Ala Leu Ser Ala
                325                 330                 335

ggt ttg cag tat gtg tcg ttg gat tgg ccg act gag aat ggt tgg gcg  1056
Gly Leu Gln Tyr Val Ser Leu Asp Trp Pro Thr Glu Asn Gly Trp Ala
```

```
            340                 345                 350

aat tac aac agt ttg cag gag ctg acg tac ttc ttc act gtc ttt att   1104
Asn Tyr Asn Ser Leu Gln Glu Leu Thr Tyr Phe Phe Thr Val Phe Ile
        355                 360                 365

gcg gca ccg ttg tcg att gtg tct ggt ttc cgg atg tcg agt tac tgg   1152
Ala Ala Pro Leu Ser Ile Val Ser Gly Phe Arg Met Ser Ser Tyr Trp
    370                 375                 380

cct aag aac aat gcg acg atg aat aag ttg atc ccc atc ggg ttt gct   1200
Pro Lys Asn Asn Ala Thr Met Asn Lys Leu Ile Pro Ile Gly Phe Ala
385                 390                 395                 400

cgt gcg ctg cac atg cca gtg atg gtg tat tac atc gtg ttc att tgt   1248
Arg Ala Leu His Met Pro Val Met Val Tyr Tyr Ile Val Phe Ile Cys
                405                 410                 415

atc cac gtg ttc ttg gtg ttg gcg acc ggc gcg ttg cgc aat ttc aac   1296
Ile His Val Phe Leu Val Leu Ala Thr Gly Ala Leu Arg Asn Phe Asn
            420                 425                 430

cat atg tat gca ggt caa gac gtt gtg aac tgg gtt ggt ttt ggt tgg   1344
His Met Tyr Ala Gly Gln Asp Val Val Asn Trp Val Gly Phe Gly Trp
        435                 440                 445

ttc gtg gcg tcg ttg                                              1359
Phe Val Ala Ser Leu
    450
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<210> 1228
<211> 453
<212> PRT
<213> Corynebacterium glutamicum

<400> 1228

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Ile Pro Ala Ala Pro Ser Ala Pro Gly Ser Ala Ile Pro Thr Pro Gly
  1               5                  10                  15

Thr Ala Ile Pro Val Pro Gly Ser Ala Thr Pro Val Pro Ala Pro Gly
             20                  25                  30

Val Ser Ala Pro Gly Ala Ser Val Pro Ser Ile Pro Val Pro Gly Ser
         35                  40                  45

Val Thr Pro Pro Ala Pro Gly Ile Ser Ala Pro Gly Gly Ala Leu Pro
     50                  55                  60

Thr Pro Gly Ser Ala Pro Pro Thr Pro Gly Gly Ala Leu Pro Thr Pro
 65                  70                  75                  80

Gly Glu Ala Leu Pro Val Pro Gly Ala Pro Gly Ala Pro Gly Ala Ser
                 85                  90                  95

Gly Ile Pro Ser Pro Gly Leu Pro Thr Pro Gly Val Pro Thr Pro Gly
            100                 105                 110

Ala Ser Leu Pro Val Pro Gly Ala Pro Asp Ala Pro Gly Thr Pro Ser
        115                 120                 125
```

```
Ile Pro Ala Ala Pro Gly Ile Gln Ala Pro Gly Ile Pro Ala Ala Pro
    130                 135                 140

Gly Ala Pro Ala Gln Ala Ala Ala His Ala Lys Pro Val Phe Gln Asp
145                 150                 155                 160

Ala Glu Lys Arg Pro Arg Thr Asp Glu Ala Gly Asn Ala Lys Lys Glu
                165                 170                 175

Leu Pro Leu Arg Val Arg Leu Ala Gln Pro Ile Thr Arg Lys Gln Trp
            180                 185                 190

Ala Met Thr Leu Gly Val Leu Val Leu Gly Ala Ile Val Val Ala Ala
        195                 200                 205

Ile Ala Val Val Leu Ala Lys Trp Ala Phe Thr Thr Glu Trp Leu Gln
    210                 215                 220

Asp Phe Val Glu Lys Tyr Pro Gly Lys Tyr Asp Asn Pro Glu Gly Ala
225                 230                 235                 240

Pro Val Gly Ile Pro Thr Trp Leu Ser Trp Gln His Phe Phe Asn Met
                245                 250                 255

Phe Phe Met Val Leu Ile Ile Lys Thr Gly Ile Glu Ile Asn Arg Thr
            260                 265                 270

Arg Arg Pro Lys Gly Tyr Trp Thr Pro Lys Lys Gly Gly Lys Lys Ile
        275                 280                 285

Ser Leu Thr Leu Trp Ile His Leu Val Leu Asp Leu Leu Trp Ile Ile
    290                 295                 300

Asn Gly Ala Val Phe Ile Ile Leu Leu Phe Ala Thr Gly Gln Trp Met
305                 310                 315                 320

Arg Ile Val Pro Thr Ser Trp Asp Val Phe Pro Asn Ala Leu Ser Ala
                325                 330                 335

Gly Leu Gln Tyr Val Ser Leu Asp Trp Pro Thr Glu Asn Gly Trp Ala
            340                 345                 350

Asn Tyr Asn Ser Leu Gln Glu Leu Thr Tyr Phe Phe Thr Val Phe Ile
        355                 360                 365

Ala Ala Pro Leu Ser Ile Val Ser Gly Phe Arg Met Ser Ser Tyr Trp
    370                 375                 380

Pro Lys Asn Asn Ala Thr Met Asn Lys Leu Ile Pro Ile Gly Phe Ala
385                 390                 395                 400

Arg Ala Leu His Met Pro Val Met Val Tyr Tyr Ile Val Phe Ile Cys
                405                 410                 415

Ile His Val Phe Leu Val Leu Ala Thr Gly Ala Leu Arg Asn Phe Asn
            420                 425                 430

His Met Tyr Ala Gly Gln Asp Val Val Asn Trp Val Gly Phe Gly Trp
        435                 440                 445

Phe Val Ala Ser Leu
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450

<210> 1229
<211> 720
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(697)
<223> RXN02593

<400> 1229
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catagggtta ttcagtctag ctgcttttaa acaagccata atg gaa gcc atg gcc 115
Met Glu Ala Met Ala
1 5

aca acg atc acc gtt ttc tct ccc acc cac tcc ccc gca caa atc cgc 163
Thr Thr Ile Thr Val Phe Ser Pro Thr His Ser Pro Ala Gln Ile Arg
10 15 20

gaa acc atc ctc agc gcc gcg aaa gaa gac gac gtg gac ttc ctc gga 211
Glu Thr Ile Leu Ser Ala Ala Lys Glu Asp Asp Val Asp Phe Leu Gly
25 30 35

gtc ccc ttt acc cac ccc aga aac gtc acc atc gaa gtc gac gac gaa 259
Val Pro Phe Thr His Pro Arg Asn Val Thr Ile Glu Val Asp Asp Glu
40 45 50

ctg atc aac gac tgc tta ggc tgg ctc gac gac gtg gca ctc gcc tcc 307
Leu Ile Asn Asp Cys Leu Gly Trp Leu Asp Asp Val Ala Leu Ala Ser
55 60 65

ggc ctg ggc atc caa tac aac gac gaa gtg ctc cgc tac ggc gac gaa 355
Gly Leu Gly Ile Gln Tyr Asn Asp Glu Val Leu Arg Tyr Gly Asp Glu
70 75 80 85

gac att tcc ttt acc gtc caa acc aaa aat gac gat gac gcc cgc atc 403
Asp Ile Ser Phe Thr Val Gln Thr Lys Asn Asp Asp Asp Ala Arg Ile
90 95 100

ggc gcc tcc cgc ctt gga ctc gag cac cag ttg aac gtc att gcc ggg 451
Gly Ala Ser Arg Leu Gly Leu Glu His Gln Leu Asn Val Ile Ala Gly
105 110 115

ggc tct gga gat tcc ggg gat tcc ggg gat tat ttg aag att gca cac 499
Gly Ser Gly Asp Ser Gly Asp Ser Gly Asp Tyr Leu Lys Ile Ala His
120 125 130

ttc gac cta gac aac ccc gcc gac gag tcc tcc tac atc ttc gcg cgc 547
Phe Asp Leu Asp Asn Pro Ala Asp Glu Ser Ser Tyr Ile Phe Ala Arg
135 140 145

agc ctc gca gaa gta gac ggc tgg acc cta gaa ttc ggc gtc gca gga 595
Ser Leu Ala Glu Val Asp Gly Trp Thr Leu Glu Phe Gly Val Ala Gly
150 155 160 165

gta aaa aac acc acc att gtt tcc tcc atc gac gat gcc atc acc acc 643

```
Val Lys Asn Thr Thr Ile Val Ser Ser Ile Asp Asp Ala Ile Thr Thr
                170                 175                 180

att ttg cga tgg atg aac ggc gaa gac atc cgc gac ctc aac tgg acc   691
Ile Leu Arg Trp Met Asn Gly Glu Asp Ile Arg Asp Leu Asn Trp Thr
            185                 190                 195

cgc gca taaatggcct catttccgga gct                                 720
Arg Ala
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<210> 1230
<211> 199
<212> PRT
<213> Corynebacterium glutamicum

<400> 1230

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Met Glu Ala Met Ala Thr Thr Ile Thr Val Phe Ser Pro Thr His Ser
  1               5                  10                  15

Pro Ala Gln Ile Arg Glu Thr Ile Leu Ser Ala Ala Lys Glu Asp Asp
             20                  25                  30

Val Asp Phe Leu Gly Val Pro Phe Thr His Pro Arg Asn Val Thr Ile
         35                  40                  45

Glu Val Asp Asp Glu Leu Ile Asn Asp Cys Leu Gly Trp Leu Asp Asp
     50                  55                  60

Val Ala Leu Ala Ser Gly Leu Gly Ile Gln Tyr Asn Asp Glu Val Leu
 65                  70                  75                  80

Arg Tyr Gly Asp Glu Asp Ile Ser Phe Thr Val Gln Thr Lys Asn Asp
                 85                  90                  95

Asp Asp Ala Arg Ile Gly Ala Ser Arg Leu Gly Leu Glu His Gln Leu
            100                 105                 110

Asn Val Ile Ala Gly Gly Ser Gly Asp Ser Gly Asp Ser Gly Asp Tyr
        115                 120                 125

Leu Lys Ile Ala His Phe Asp Leu Asp Asn Pro Ala Asp Glu Ser Ser
    130                 135                 140

Tyr Ile Phe Ala Arg Ser Leu Ala Glu Val Asp Gly Trp Thr Leu Glu
145                 150                 155                 160

Phe Gly Val Ala Gly Val Lys Asn Thr Thr Ile Val Ser Ser Ile Asp
                165                 170                 175

Asp Ala Ile Thr Thr Ile Leu Arg Trp Met Asn Gly Glu Asp Ile Arg
            180                 185                 190

Asp Leu Asn Trp Thr Arg Ala
        195
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<210> 1231
<211> 336
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(313)
<223> FRXA02593

<400> 1231
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tgccgggggc tctggagatt ccggggattc cggggattat ttg aag att gca cac 115
Leu Lys Ile Ala His
1 5

ttc gac cta gac aac ccc gcc gac gag tcc tcc tac atc ttc gcg cgc 163
Phe Asp Leu Asp Asn Pro Ala Asp Glu Ser Ser Tyr Ile Phe Ala Arg
10 15 20

agc ctc gca gaa gta gac ggc tgg acc cta gaa ttc ggc gtc gca gga 211
Ser Leu Ala Glu Val Asp Gly Trp Thr Leu Glu Phe Gly Val Ala Gly
25 30 35

gta aaa aac acc acc att gtt tcc tcc atc gac gat gcc atc acc acc 259
Val Lys Asn Thr Thr Ile Val Ser Ser Ile Asp Asp Ala Ile Thr Thr
40 45 50

att ttg cga tgg atg aac ggc gaa gac atc cgc gac ctc aac tgg acc 307
Ile Leu Arg Trp Met Asn Gly Glu Asp Ile Arg Asp Leu Asn Trp Thr
55 60 65

cgc gca taaatggcct catttccgga gct 336
Arg Ala
70

<210> 1232
<211> 71
<212> PRT
<213> Corynebacterium glutamicum

<400> 1232
Leu Lys Ile Ala His Phe Asp Leu Asp Asn Pro Ala Asp Glu Ser Ser
1 5 10 15

Tyr Ile Phe Ala Arg Ser Leu Ala Glu Val Asp Gly Trp Thr Leu Glu
20 25 30

Phe Gly Val Ala Gly Val Lys Asn Thr Thr Ile Val Ser Ser Ile Asp
35 40 45

Asp Ala Ile Thr Thr Ile Leu Arg Trp Met Asn Gly Glu Asp Ile Arg
50 55 60

Asp Leu Asn Trp Thr Arg Ala
65 70

<210> 1233
<211> 447
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(424)
<223> FRXA02594

<400> 1233
gcgttcactt ccgccacctt gaggatgagt ggtatcacgc cagcacaaca aaaggatctt 60

catagggtta ttcagtctag ctgcttttaa acaagccata atg gaa gcc atg gcc 115
Met Glu Ala Met Ala
1 5

aca acg atc acc gtt ttc tct ccc acc cac tcc ccc gca caa atc cgc 163
Thr Thr Ile Thr Val Phe Ser Pro Thr His Ser Pro Ala Gln Ile Arg
10 15 20

gaa acc atc ctc agc gcc gcg aaa gaa gac gac gtg gac ttc ctc gga 211
Glu Thr Ile Leu Ser Ala Ala Lys Glu Asp Asp Val Asp Phe Leu Gly
25 30 35

gtc ccc ttt acc cac ccc aga aac gtc acc atc gaa gtc gac gac gaa 259
Val Pro Phe Thr His Pro Arg Asn Val Thr Ile Glu Val Asp Asp Glu
40 45 50

ctg atc aac gac tgc tta ggc tgg ctc gac gac gtg gca ctc gcc tcc 307
Leu Ile Asn Asp Cys Leu Gly Trp Leu Asp Asp Val Ala Leu Ala Ser
55 60 65

ggc ctg ggc atc caa tac aac gac gaa gtg ctc cgc tac ggc gac gaa 355
Gly Leu Gly Ile Gln Tyr Asn Asp Glu Val Leu Arg Tyr Gly Asp Glu
70 75 80 85

gac att tcc ttt acc gtc caa acc aaa aat gac gat gac gcc cgc atc 403
Asp Ile Ser Phe Thr Val Gln Thr Lys Asn Asp Asp Asp Ala Arg Ile
90 95 100

ggc gcc tcc cgc ctt gga ctc tagcaccagt tgaacgtcat tgc 447
Gly Ala Ser Arg Leu Gly Leu
105

<210> 1234
<211> 108
<212> PRT
<213> Corynebacterium glutamicum

<400> 1234
Met Glu Ala Met Ala Thr Thr Ile Thr Val Phe Ser Pro Thr His Ser
1 5 10 15

Pro Ala Gln Ile Arg Glu Thr Ile Leu Ser Ala Ala Lys Glu Asp Asp
20 25 30

Val Asp Phe Leu Gly Val Pro Phe Thr His Pro Arg Asn Val Thr Ile
35 40 45

Glu Val Asp Asp Glu Leu Ile Asn Asp Cys Leu Gly Trp Leu Asp Asp
50 55 60

Val Ala Leu Ala Ser Gly Leu Gly Ile Gln Tyr Asn Asp Glu Val Leu

```
 65                  70                  75                  80

Arg Tyr Gly Asp Glu Asp Ile Ser Phe Thr Val Gln Thr Lys Asn Asp
                85                  90                  95

Asp Asp Ala Arg Ile Gly Ala Ser Arg Leu Gly Leu
            100                 105


<210> 1235
<211> 1494
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1471)
<223> RXN02606

<400> 1235
agggcgcgga tcacttcgga tctgtggata acttttaagg cccttgtttt ccccttgaag 60

cttcggttgt gtggaaaaca gaaaaggagg ggaaaacaaa atg caa gaa atc cac   115
                                              Met Gln Glu Ile His
                                                1               5

acc atc atg aaa cac atg gac gcg ctc atc gcc gac ccg tcc gcc gcc   163
Thr Ile Met Lys His Met Asp Ala Leu Ile Ala Asp Pro Ser Ala Ala
            10                  15                  20

gca ttc aaa gca aca ctc ccc ttc gcc gaa ctc ctc gaa aag ctc cac   211
Ala Phe Lys Ala Thr Leu Pro Phe Ala Glu Leu Leu Glu Lys Leu His
        25                  30                  35

aac aaa aaa gcg ctt ttc gac gcc gcc ctc gcc aaa tcc gcc gag cgc   259
Asn Lys Lys Ala Leu Phe Asp Ala Ala Leu Ala Lys Ser Ala Glu Arg
    40                  45                  50

gcc gat gcc gga cgc atc atc gga aaa acc tcc cac atc gat gcc ctc   307
Ala Asp Ala Gly Arg Ile Ile Gly Lys Thr Ser His Ile Asp Ala Leu
55                  60                  65

gcg tac ctt ctc gac atc tcc aaa tcc gaa gca ttc cga cgc aca aaa   355
Ala Tyr Leu Leu Asp Ile Ser Lys Ser Glu Ala Phe Arg Arg Thr Lys
70                  75                  80                  85

cgc gcc gaa gaa cac tac ggc aac cca agc ccg gaa ccc agt tca gaa   403
Arg Ala Glu Glu His Tyr Gly Asn Pro Ser Pro Glu Pro Ser Ser Glu
                90                  95                  100

gaa ctc gcg aaa gaa acc ccc gaa gag aag cta gcc aga gaa gaa aaa   451
Glu Leu Ala Lys Glu Thr Pro Glu Glu Lys Leu Ala Arg Glu Glu Lys
            105                 110                 115

gag aaa caa gac cta gcc gaa caa gca gaa gcc aac cgc atc gcc cgc   499
Glu Lys Gln Asp Leu Ala Glu Gln Ala Glu Ala Asn Arg Ile Ala Arg
        120                 125                 130

gaa cac ggc atc tcc gcc gaa aaa caa gac acc atc cgc tac gaa cta   547
Glu His Gly Ile Ser Ala Glu Lys Gln Asp Thr Ile Arg Tyr Glu Leu
    135                 140                 145
```

```
gaa aaa ctc aac gac aac aca tcc cta tcc cga gcc tca ctc cgc aaa   595
Glu Lys Leu Asn Asp Asn Thr Ser Leu Ser Arg Ala Ser Leu Arg Lys
150                 155                 160                 165

cta gca atg cag gaa gcc acc agc cga acc ccc gaa gac cta cgc aac   643
Leu Ala Met Gln Glu Ala Thr Ser Arg Thr Pro Glu Asp Leu Arg Asn
                170                 175                 180

tgg acc cgc aac aaa gtt atc cgc ata aac ccc acc gcc aaa gac cca   691
Trp Thr Arg Asn Lys Val Ile Arg Ile Asn Pro Thr Ala Lys Asp Pro
            185                 190                 195

ctc gcc gca gta aag aaa cgc tcc tta agc atc gga cgc caa gac cac   739
Leu Ala Ala Val Lys Lys Arg Ser Leu Ser Ile Gly Arg Gln Asp His
        200                 205                 210

gac ggc gga gcc aaa gca tcc ctc tat tta gat gcc aaa ggt cta gcc   787
Asp Gly Gly Ala Lys Ala Ser Leu Tyr Leu Asp Ala Lys Gly Leu Ala
    215                 220                 225

ctg ctc aaa tca ctg atg tct aaa gcc aag ccg ggg cat ttg ctt gaa   835
Leu Leu Lys Ser Leu Met Ser Lys Ala Lys Pro Gly His Leu Leu Glu
230                 235                 240                 245

gac tct ttg gcg gag gat aaa cgt acg aaa ccg caa cgc caa tac gat   883
Asp Ser Leu Ala Glu Asp Lys Arg Thr Lys Pro Gln Arg Gln Tyr Asp
                250                 255                 260

gcc ttc gcc gac atc ctc cac cgc gca cac agc gat ctc ctc ccc gca   931
Ala Phe Ala Asp Ile Leu His Arg Ala His Ser Asp Leu Leu Pro Ala
            265                 270                 275

cga tcc gga gtg ggc acc atc ctc gtc tcc ctc tcc gcc aaa gac gta   979
Arg Ser Gly Val Gly Thr Ile Leu Val Ser Leu Ser Ala Lys Asp Val
        280                 285                 290

aca aac ctc aaa gca tcg ggc ccc gac cac cgc tac ccc acc agc acc   1027
Thr Asn Leu Lys Ala Ser Gly Pro Asp His Arg Tyr Pro Thr Ser Thr
    295                 300                 305

ggc ata aaa ctc aca ccg ctt gag atc ctg cga ctc ggt gca gcc aaa   1075
Gly Ile Lys Leu Thr Pro Leu Glu Ile Leu Arg Leu Gly Ala Ala Lys
310                 315                 320                 325

tat gac ttc gtg acc gtc ctc gac tcc gaa tcc ggc cgt ccg ctg cac   1123
Tyr Asp Phe Val Thr Val Leu Asp Ser Glu Ser Gly Arg Pro Leu His
                330                 335                 340

ctg gca cgc act caa cgc acc gcc agc ctg tat caa cgc cta gcc ctc   1171
Leu Ala Arg Thr Gln Arg Thr Ala Ser Leu Tyr Gln Arg Leu Ala Leu
            345                 350                 355

ttc gcc tcc gaa ctc gtc tgc acc cgc gaa ggc tgc gac tcc ccc ttc   1219
Phe Ala Ser Glu Leu Val Cys Thr Arg Glu Gly Cys Asp Ser Pro Phe
        360                 365                 370

gaa gac aac gaa ata cac cac atc aga tcc tgg cta gac ggc ggc ccc   1267
Glu Asp Asn Glu Ile His His Ile Arg Ser Trp Leu Asp Gly Gly Pro
    375                 380                 385
```

```
aca gac ata gaa aac atc acc aac atc tgc ccc cac gac cac gga aac   1315
Thr Asp Ile Glu Asn Ile Thr Asn Ile Cys Pro His Asp His Gly Asn
390                 395                 400                 405

aac aac gac caa cgc gac ggc aaa gac aac atg ggg cac atg aac ata   1363
Asn Asn Asp Gln Arg Asp Gly Lys Asp Asn Met Gly His Met Asn Ile
                410                 415                 420

gat ccc aca acc ggg cgc gtc gga tat caa ccc gcc gac cgc cga aaa   1411
Asp Pro Thr Thr Gly Arg Val Gly Tyr Gln Pro Ala Asp Arg Arg Lys
            425                 430                 435

ccc atg cgg ttt aac aac acc gca gcc gca gca gaa tca gga gga gca   1459
Pro Met Arg Phe Asn Asn Thr Ala Ala Ala Ala Glu Ser Gly Gly Ala
        440                 445                 450

cag gcc agg acc taagttttta gcgcgccaaa aag                        1494
Gln Ala Arg Thr
    455
```

<210> 1236
<211> 457
<212> PRT
<213> Corynebacterium glutamicum

<400> 1236

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Met Gln Glu Ile His Thr Ile Met Lys His Met Asp Ala Leu Ile Ala
  1               5                  10                  15

Asp Pro Ser Ala Ala Ala Phe Lys Ala Thr Leu Pro Phe Ala Glu Leu
             20                  25                  30

Leu Glu Lys Leu His Asn Lys Lys Ala Leu Phe Asp Ala Ala Leu Ala
         35                  40                  45

Lys Ser Ala Glu Arg Ala Asp Ala Gly Arg Ile Ile Gly Lys Thr Ser
     50                  55                  60

His Ile Asp Ala Leu Ala Tyr Leu Leu Asp Ile Ser Lys Ser Glu Ala
 65                  70                  75                  80

Phe Arg Arg Thr Lys Arg Ala Glu Glu His Tyr Gly Asn Pro Ser Pro
                 85                  90                  95

Glu Pro Ser Ser Glu Glu Leu Ala Lys Glu Thr Pro Glu Glu Lys Leu
            100                 105                 110

Ala Arg Glu Glu Lys Glu Lys Gln Asp Leu Ala Glu Gln Ala Glu Ala
        115                 120                 125

Asn Arg Ile Ala Arg Glu His Gly Ile Ser Ala Glu Lys Gln Asp Thr
    130                 135                 140

Ile Arg Tyr Glu Leu Glu Lys Leu Asn Asp Asn Thr Ser Leu Ser Arg
145                 150                 155                 160

Ala Ser Leu Arg Lys Leu Ala Met Gln Glu Ala Thr Ser Arg Thr Pro
                165                 170                 175

Glu Asp Leu Arg Asn Trp Thr Arg Asn Lys Val Ile Arg Ile Asn Pro
```

```
            180                 185                 190

Thr Ala Lys Asp Pro Leu Ala Ala Val Lys Lys Arg Ser Leu Ser Ile
        195                 200                 205

Gly Arg Gln Asp His Asp Gly Gly Ala Lys Ala Ser Leu Tyr Leu Asp
    210                 215                 220

Ala Lys Gly Leu Ala Leu Leu Lys Ser Leu Met Ser Lys Ala Lys Pro
225                 230                 235                 240

Gly His Leu Leu Glu Asp Ser Leu Ala Glu Asp Lys Arg Thr Lys Pro
                245                 250                 255

Gln Arg Gln Tyr Asp Ala Phe Ala Asp Ile Leu His Arg Ala His Ser
            260                 265                 270

Asp Leu Leu Pro Ala Arg Ser Gly Val Gly Thr Ile Leu Val Ser Leu
        275                 280                 285

Ser Ala Lys Asp Val Thr Asn Leu Lys Ala Ser Gly Pro Asp His Arg
    290                 295                 300

Tyr Pro Thr Ser Thr Gly Ile Lys Leu Thr Pro Leu Glu Ile Leu Arg
305                 310                 315                 320

Leu Gly Ala Ala Lys Tyr Asp Phe Val Thr Val Leu Asp Ser Glu Ser
                325                 330                 335

Gly Arg Pro Leu His Leu Ala Arg Thr Gln Arg Thr Ala Ser Leu Tyr
            340                 345                 350

Gln Arg Leu Ala Leu Phe Ala Ser Glu Leu Val Cys Thr Arg Glu Gly
        355                 360                 365

Cys Asp Ser Pro Phe Glu Asp Asn Glu Ile His His Ile Arg Ser Trp
    370                 375                 380

Leu Asp Gly Gly Pro Thr Asp Ile Glu Asn Ile Thr Asn Ile Cys Pro
385                 390                 395                 400

His Asp His Gly Asn Asn Asn Asp Gln Arg Asp Gly Lys Asp Asn Met
                405                 410                 415

Gly His Met Asn Ile Asp Pro Thr Thr Gly Arg Val Gly Tyr Gln Pro
            420                 425                 430

Ala Asp Arg Arg Lys Pro Met Arg Phe Asn Asn Thr Ala Ala Ala Ala
        435                 440                 445

Glu Ser Gly Gly Ala Gln Ala Arg Thr
    450                 455
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<210> 1237
<211> 1494
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(1471)
<223> FRXA02606

<400> 1237
agggcgcgga tcacttcgga tctgtggata acttttaagg cccttgtttt ccccttgaag 60

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cttcggttgt gtggaaaaca gaaaaggagg ggaaaacaaa atg caa gaa atc cac   115
                                             Met Gln Glu Ile His
                                               1               5

acc atc atg aaa cac atg gac gcg ctc atc gcc gac ccg tcc gcc gcc   163
Thr Ile Met Lys His Met Asp Ala Leu Ile Ala Asp Pro Ser Ala Ala
               10                  15                  20

gca ttc aaa gca aca ctc ccc ttc gcc gaa ctc ctc gaa aag ctc cac   211
Ala Phe Lys Ala Thr Leu Pro Phe Ala Glu Leu Leu Glu Lys Leu His
            25                  30                  35

aac aaa aaa gcg ctt ttc gac gcc gcc ctc gcc aaa tcc gcc gag cgc   259
Asn Lys Lys Ala Leu Phe Asp Ala Ala Leu Ala Lys Ser Ala Glu Arg
         40                  45                  50

gcc gat gcc gga cgc atc atc gga aaa acc tcc cac atc gat gcc ctc   307
Ala Asp Ala Gly Arg Ile Ile Gly Lys Thr Ser His Ile Asp Ala Leu
     55                  60                  65

gcg tac ctt ctc gac atc tcc aaa tcc gaa gca ttc cga cgc aca aaa   355
Ala Tyr Leu Leu Asp Ile Ser Lys Ser Glu Ala Phe Arg Arg Thr Lys
 70                  75                  80                  85

cgc gcc gaa gaa cac tac ggc aac cca agc ccg gaa ccc agt tca gaa   403
Arg Ala Glu Glu His Tyr Gly Asn Pro Ser Pro Glu Pro Ser Ser Glu
               90                  95                 100

gaa ctc gcg aaa gaa acc ccc gaa gag aag cta gcc aga gaa gaa aaa   451
Glu Leu Ala Lys Glu Thr Pro Glu Glu Lys Leu Ala Arg Glu Glu Lys
            105                 110                 115

gag aaa caa gac cta gcc gaa caa gca gaa gcc aac cgc atc gcc cgc   499
Glu Lys Gln Asp Leu Ala Glu Gln Ala Glu Ala Asn Arg Ile Ala Arg
        120                 125                 130

gaa cac ggc atc tcc gcc gaa aaa caa gac acc atc cgc tac gaa cta   547
Glu His Gly Ile Ser Ala Glu Lys Gln Asp Thr Ile Arg Tyr Glu Leu
    135                 140                 145

gaa aaa ctc aac gac aac aca tcc cta tcc cga gcc tca ctc cgc aaa   595
Glu Lys Leu Asn Asp Asn Thr Ser Leu Ser Arg Ala Ser Leu Arg Lys
150                 155                 160                 165

cta gca atg cag gaa gcc acc agc cga acc ccc gaa gac cta cgc aac   643
Leu Ala Met Gln Glu Ala Thr Ser Arg Thr Pro Glu Asp Leu Arg Asn
               170                 175                 180

tgg acc cgc aac aaa gtt atc cgc ata aac ccc acc gcc aaa gac cca   691
Trp Thr Arg Asn Lys Val Ile Arg Ile Asn Pro Thr Ala Lys Asp Pro
            185                 190                 195

ctc gcc gca gta aag aaa cgc tcc tta agc atc gga cgc caa gac cac   739
Leu Ala Ala Val Lys Lys Arg Ser Leu Ser Ile Gly Arg Gln Asp His
        200                 205                 210
```

```
gac ggc gga gcc aaa gca tcc ctc tat tta gat gcc aaa ggt cta gcc   787
Asp Gly Gly Ala Lys Ala Ser Leu Tyr Leu Asp Ala Lys Gly Leu Ala
    215                 220                 225

ctg ctc aaa tca ctg atg tct aaa gcc aag ccg ggg cat ttg ctt gaa   835
Leu Leu Lys Ser Leu Met Ser Lys Ala Lys Pro Gly His Leu Leu Glu
230                 235                 240                 245

gac tct ttg gcg gag gat aaa cgt acg aaa ccg caa cgc caa tac gat   883
Asp Ser Leu Ala Glu Asp Lys Arg Thr Lys Pro Gln Arg Gln Tyr Asp
                250                 255                 260

gcc ttc gcc gac atc ctc cac cgc gca cac agc gat ctc ctc ccc gca   931
Ala Phe Ala Asp Ile Leu His Arg Ala His Ser Asp Leu Leu Pro Ala
            265                 270                 275

cga tcc gga gtg ggc acc atc ctc gtc tcc ctc tcc gcc aaa gac gta   979
Arg Ser Gly Val Gly Thr Ile Leu Val Ser Leu Ser Ala Lys Asp Val
        280                 285                 290

aca aac ctc aaa gca tcg ggc ccc gac cac cgc tac ccc acc agc acc   1027
Thr Asn Leu Lys Ala Ser Gly Pro Asp His Arg Tyr Pro Thr Ser Thr
    295                 300                 305

ggc ata aaa ctc aca ccg ctt gag atc ctg cga ctc ggt gca gcc aaa   1075
Gly Ile Lys Leu Thr Pro Leu Glu Ile Leu Arg Leu Gly Ala Ala Lys
310                 315                 320                 325

tat gac ttc gtg acc gtc ctc gac tcc gaa tcc ggc cgt ccg ctg cac   1123
Tyr Asp Phe Val Thr Val Leu Asp Ser Glu Ser Gly Arg Pro Leu His
                330                 335                 340

ctg gca cgc act caa cgc acc gcc agc ctg tat caa cgc cta gcc ctc   1171
Leu Ala Arg Thr Gln Arg Thr Ala Ser Leu Tyr Gln Arg Leu Ala Leu
            345                 350                 355

ttc gcc tcc gaa ctc gtc tgc acc cgc gaa ggc tgc gac tcc ccc ttc   1219
Phe Ala Ser Glu Leu Val Cys Thr Arg Glu Gly Cys Asp Ser Pro Phe
        360                 365                 370

gaa gac aac gaa ata cac cac atc aga tcc tgg cta gac ggc ggc ccc   1267
Glu Asp Asn Glu Ile His His Ile Arg Ser Trp Leu Asp Gly Gly Pro
    375                 380                 385

aca gac ata gaa aac atc acc aac atc tgc ccc cac gac cac gga aac   1315
Thr Asp Ile Glu Asn Ile Thr Asn Ile Cys Pro His Asp His Gly Asn
390                 395                 400                 405

aac aac gac caa cgc gac ggc aaa gac aac atg ggg cac atg aac ata   1363
Asn Asn Asp Gln Arg Asp Gly Lys Asp Asn Met Gly His Met Asn Ile
                410                 415                 420

gat ccc aca acc ggg cgc gtc gga tat caa ccc gcc gac cgc cga aaa   1411
Asp Pro Thr Thr Gly Arg Val Gly Tyr Gln Pro Ala Asp Arg Arg Lys
            425                 430                 435

ccc atg cgg ttt aac aac acc gca gcc gca gca gaa tca gga gga gca   1459
Pro Met Arg Phe Asn Asn Thr Ala Ala Ala Ala Glu Ser Gly Gly Ala
        440                 445                 450
```

```
cag gcc agg acc taagttttta gcgcgccaaa aag                              1494
Gln Ala Arg Thr
    455


<210> 1238
<211> 457
<212> PRT
<213> Corynebacterium glutamicum

<400> 1238
Met Gln Glu Ile His Thr Ile Met Lys His Met Asp Ala Leu Ile Ala
  1               5                  10                  15

Asp Pro Ser Ala Ala Ala Phe Lys Ala Thr Leu Pro Phe Ala Glu Leu
             20                  25                  30

Leu Glu Lys Leu His Asn Lys Lys Ala Leu Phe Asp Ala Ala Leu Ala
         35                  40                  45

Lys Ser Ala Glu Arg Ala Asp Ala Gly Arg Ile Ile Gly Lys Thr Ser
     50                  55                  60

His Ile Asp Ala Leu Ala Tyr Leu Leu Asp Ile Ser Lys Ser Glu Ala
 65                  70                  75                  80

Phe Arg Arg Thr Lys Arg Ala Glu Glu His Tyr Gly Asn Pro Ser Pro
                 85                  90                  95

Glu Pro Ser Ser Glu Glu Leu Ala Lys Glu Thr Pro Glu Glu Lys Leu
            100                 105                 110

Ala Arg Glu Glu Lys Glu Lys Gln Asp Leu Ala Glu Gln Ala Glu Ala
        115                 120                 125

Asn Arg Ile Ala Arg Glu His Gly Ile Ser Ala Glu Lys Gln Asp Thr
    130                 135                 140

Ile Arg Tyr Glu Leu Glu Lys Leu Asn Asp Asn Thr Ser Leu Ser Arg
145                 150                 155                 160

Ala Ser Leu Arg Lys Leu Ala Met Gln Glu Ala Thr Ser Arg Thr Pro
                165                 170                 175

Glu Asp Leu Arg Asn Trp Thr Arg Asn Lys Val Ile Arg Ile Asn Pro
            180                 185                 190

Thr Ala Lys Asp Pro Leu Ala Ala Val Lys Lys Arg Ser Leu Ser Ile
        195                 200                 205

Gly Arg Gln Asp His Asp Gly Gly Ala Lys Ala Ser Leu Tyr Leu Asp
    210                 215                 220

Ala Lys Gly Leu Ala Leu Leu Lys Ser Leu Met Ser Lys Ala Lys Pro
225                 230                 235                 240

Gly His Leu Leu Glu Asp Ser Leu Ala Glu Asp Lys Arg Thr Lys Pro
                245                 250                 255

Gln Arg Gln Tyr Asp Ala Phe Ala Asp Ile Leu His Arg Ala His Ser
            260                 265                 270
```

```
Asp Leu Leu Pro Ala Arg Ser Gly Val Gly Thr Ile Leu Val Ser Leu
        275                 280                 285

Ser Ala Lys Asp Val Thr Asn Leu Lys Ala Ser Gly Pro Asp His Arg
    290                 295                 300

Tyr Pro Thr Ser Thr Gly Ile Lys Leu Thr Pro Leu Glu Ile Leu Arg
305       .         310                 315                 320

Leu Gly Ala Ala Lys Tyr Asp Phe Val Thr Val Leu Asp Ser Glu Ser
                325                 330                 335

Gly Arg Pro Leu His Leu Ala Arg Thr Gln Arg Thr Ala Ser Leu Tyr
            340                 345                 350

Gln Arg Leu Ala Leu Phe Ala Ser Glu Leu Val Cys Thr Arg Glu Gly
        355                 360                 365

Cys Asp Ser Pro Phe Glu Asp Asn Glu Ile His His Ile Arg Ser Trp
    370                 375                 380

Leu Asp Gly Gly Pro Thr Asp Ile Glu Asn Ile Thr Asn Ile Cys Pro
385                 390                 395                 400

His Asp His Gly Asn Asn Asn Asp Gln Arg Asp Gly Lys Asp Asn Met
                405                 410                 415

Gly His Met Asn Ile Asp Pro Thr Thr Gly Arg Val Gly Tyr Gln Pro
            420                 425                 430

Ala Asp Arg Arg Lys Pro Met Arg Phe Asn Asn Thr Ala Ala Ala Ala
        435                 440                 445

Glu Ser Gly Gly Ala Gln Ala Arg Thr
    450                 455


<210> 1239
<211> 1050
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1027)
<223> RXN02610

<400> 1239
ccagctcatc gtgcagggac gcaccagcgt gaaggaagat caagcagcgg aaatttctac 60

gctgctgaag gaatctgcgg atcggacgta ttgttaaccg atg agg aaa acc atc   115
                                            Met Arg Lys Thr Ile
                                              1               5

acc gtt att gct gta ttg atc gtc ctc gcc tta atc ggc gtg ggc atc   163
Thr Val Ile Ala Val Leu Ile Val Leu Ala Leu Ile Gly Val Gly Ile
                 10                  15                  20

gtg cag tat gtg aac aca tcc gat gac tca gat ttc att ggc cag cct   211
Val Gln Tyr Val Asn Thr Ser Asp Asp Ser Asp Phe Ile Gly Gln Pro
```

```
                25                  30                  35

ggc gag cca acc ggt acc gaa acc acg gaa cca ccg gtt caa cct gat   259
Gly Glu Pro Thr Gly Thr Glu Thr Thr Glu Pro Pro Val Gln Pro Asp
         40                  45                  50

tgg tgc cct gcg gta gaa gtc att gcc gcg ccg ggt acg tgg gag tcg   307
Trp Cys Pro Ala Val Glu Val Ile Ala Ala Pro Gly Thr Trp Glu Ser
     55                  60                  65

gct gct aat gat gat ccg atc aac ccg acc gct aat ccg ctg tca ttc   355
Ala Ala Asn Asp Asp Pro Ile Asn Pro Thr Ala Asn Pro Leu Ser Phe
 70                  75                  80                  85

atg ttg agc atc act cag cca ctg cag gag cgt tat tct gcg gat gac   403
Met Leu Ser Ile Thr Gln Pro Leu Gln Glu Arg Tyr Ser Ala Asp Asp
                90                  95                 100

gtc aag gtg tgg acg ctg ccg tac act gcg cag ttc cgc aac atc aac   451
Val Lys Val Trp Thr Leu Pro Tyr Thr Ala Gln Phe Arg Asn Ile Asn
            105                 110                 115

tcg caa aat gag atg tcc tat gat gat tcg cgc aat gaa ggc acc gcg   499
Ser Gln Asn Glu Met Ser Tyr Asp Asp Ser Arg Asn Glu Gly Thr Ala
        120                 125                 130

aag atg aat gag gaa ctg atc aac act cac aat gag tgc cct gcc acg   547
Lys Met Asn Glu Glu Leu Ile Asn Thr His Asn Glu Cys Pro Ala Thr
    135                 140                 145

gag ttc atc atc gtt ggt ttc tcc cag ggt gcg gtc att gcg ggc gat   595
Glu Phe Ile Ile Val Gly Phe Ser Gln Gly Ala Val Ile Ala Gly Asp
150                 155                 160                 165

gtg gct gct cag atc ggt tca gag caa ggt gtt att cca gct gac agc   643
Val Ala Ala Gln Ile Gly Ser Glu Gln Gly Val Ile Pro Ala Asp Ser
                170                 175                 180

gtc agg ggt gtc gcc ctg atc gct gac ggt cgc cgg gag cct ggt gtg   691
Val Arg Gly Val Ala Leu Ile Ala Asp Gly Arg Arg Glu Pro Gly Val
            185                 190                 195

ggc cag ttc cca ggc acg ttt gtg gat ggc atc ggc gcg gag gtt act   739
Gly Gln Phe Pro Gly Thr Phe Val Asp Gly Ile Gly Ala Glu Val Thr
        200                 205                 210

ctg cag cct ttg aac ttg ctg gtg cag ccg att gtt ccg ggc gca acc   787
Leu Gln Pro Leu Asn Leu Leu Val Gln Pro Ile Val Pro Gly Ala Thr
    215                 220                 225

atg cgt ggc ggg cgc gcg ggc ggt ttc ggt gtg ctc aac gac cgg gtg   835
Met Arg Gly Gly Arg Ala Gly Gly Phe Gly Val Leu Asn Asp Arg Val
230                 235                 240                 245

cag gat att tgt gct cca aat gat gcg atc tgt gat gct ccg gtg aat   883
Gln Asp Ile Cys Ala Pro Asn Asp Ala Ile Cys Asp Ala Pro Val Asn
                250                 255                 260

gtc ggc aac gcc ctt gat cgt gcg ttg gcc atg gtc tcc gcc aac ggt   931
Val Gly Asn Ala Leu Asp Arg Ala Leu Ala Met Val Ser Ala Asn Gly
            265                 270                 275
```

```
gtg cac gcg ctc tac gcc acc aat ccg gat gtt ttc cca ggc aca acc   979
Val His Ala Leu Tyr Ala Thr Asn Pro Asp Val Phe Pro Gly Thr Thr
        280                 285                 290

acc aat gcg tgg gtt gtg gat tgg gcg acc aac ctc atc gac aac gga   1027
Thr Asn Ala Trp Val Val Asp Trp Ala Thr Asn Leu Ile Asp Asn Gly
    295                 300                 305

taaagctttt tcgcttttcg acg                                        1050


<210> 1240
<211> 309
<212> PRT
<213> Corynebacterium glutamicum

<400> 1240
Met Arg Lys Thr Ile Thr Val Ile Ala Val Leu Ile Val Leu Ala Leu
  1               5                  10                  15

Ile Gly Val Gly Ile Val Gln Tyr Val Asn Thr Ser Asp Asp Ser Asp
             20                  25                  30

Phe Ile Gly Gln Pro Gly Glu Pro Thr Gly Thr Glu Thr Thr Glu Pro
         35                  40                  45

Pro Val Gln Pro Asp Trp Cys Pro Ala Val Glu Val Ile Ala Ala Pro
     50                  55                  60

Gly Thr Trp Glu Ser Ala Ala Asn Asp Asp Pro Ile Asn Pro Thr Ala
 65                  70                  75                  80

Asn Pro Leu Ser Phe Met Leu Ser Ile Thr Gln Pro Leu Gln Glu Arg
                 85                  90                  95

Tyr Ser Ala Asp Asp Val Lys Val Trp Thr Leu Pro Tyr Thr Ala Gln
            100                 105                 110

Phe Arg Asn Ile Asn Ser Gln Asn Glu Met Ser Tyr Asp Asp Ser Arg
        115                 120                 125

Asn Glu Gly Thr Ala Lys Met Asn Glu Glu Leu Ile Asn Thr His Asn
    130                 135                 140

Glu Cys Pro Ala Thr Glu Phe Ile Ile Val Gly Phe Ser Gln Gly Ala
145                 150                 155                 160

Val Ile Ala Gly Asp Val Ala Ala Gln Ile Gly Ser Glu Gln Gly Val
                165                 170                 175

Ile Pro Ala Asp Ser Val Arg Gly Val Ala Leu Ile Ala Asp Gly Arg
            180                 185                 190

Arg Glu Pro Gly Val Gly Gln Phe Pro Gly Thr Phe Val Asp Gly Ile
        195                 200                 205

Gly Ala Glu Val Thr Leu Gln Pro Leu Asn Leu Leu Val Gln Pro Ile
    210                 215                 220

Val Pro Gly Ala Thr Met Arg Gly Gly Arg Ala Gly Gly Phe Gly Val
```

```
225                 230                 235                 240

Leu Asn Asp Arg Val Gln Asp Ile Cys Ala Pro Asn Asp Ala Ile Cys
                245                 250                 255

Asp Ala Pro Val Asn Val Gly Asn Ala Leu Asp Arg Ala Leu Ala Met
            260                 265                 270

Val Ser Ala Asn Gly Val His Ala Leu Tyr Ala Thr Asn Pro Asp Val
        275                 280                 285

Phe Pro Gly Thr Thr Thr Asn Ala Trp Val Val Asp Trp Ala Thr Asn
    290                 295                 300

Leu Ile Asp Asn Gly
305
```

<210> 1241
<211> 1050
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1027)
<223> FRXA02610

<400> 1241

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ccagctcatc gtgcagggac gcaccagcgt gaaggaagat caagcagcgg aaatttctac 60

gctgctgaag gaatctgcgg atcggacgta ttgttaaccg atg agg aaa acc atc   115
                                            Met Arg Lys Thr Ile
                                              1               5

acc gtt att gct gta ttg atc gtc ctc gcc tta atc ggc gtg ggc atc   163
Thr Val Ile Ala Val Leu Ile Val Leu Ala Leu Ile Gly Val Gly Ile
                 10                  15                  20

gtg cag tat gtg aac aca tcc gat gac tca gat ttc att ggc cag cct   211
Val Gln Tyr Val Asn Thr Ser Asp Asp Ser Asp Phe Ile Gly Gln Pro
             25                  30                  35

ggc gag cca acc ggt acc gaa acc acg gaa cca ccg gtt caa cct gat   259
Gly Glu Pro Thr Gly Thr Glu Thr Thr Glu Pro Pro Val Gln Pro Asp
         40                  45                  50

tgg tgc cct gcg gta gaa gtc att gcc gcg ccg ggt acg tgg gag tcg   307
Trp Cys Pro Ala Val Glu Val Ile Ala Ala Pro Gly Thr Trp Glu Ser
     55                  60                  65

gct gct aat gat gat ccg atc aac ccg acc gct aat ccg ctg tca ttc   355
Ala Ala Asn Asp Asp Pro Ile Asn Pro Thr Ala Asn Pro Leu Ser Phe
 70                  75                  80                  85

atg ttg agc atc act cag cca ctg cag gag cgt tat tct gcg gat gac   403
Met Leu Ser Ile Thr Gln Pro Leu Gln Glu Arg Tyr Ser Ala Asp Asp
                 90                  95                 100

gtc aag gtg tgg acg ctg ccg tac act gcg cag ttc cgc aac atc aac   451
Val Lys Val Trp Thr Leu Pro Tyr Thr Ala Gln Phe Arg Asn Ile Asn
```

```
            105                 110                 115

tcg caa aat gag atg tcc tat gat gat tcg cgc aat gaa ggc acc gcg   499
Ser Gln Asn Glu Met Ser Tyr Asp Asp Ser Arg Asn Glu Gly Thr Ala
        120                 125                 130

aag atg aat gag gaa ctg atc aac act cac aat gag tgc cct gcc acg   547
Lys Met Asn Glu Glu Leu Ile Asn Thr His Asn Glu Cys Pro Ala Thr
    135                 140                 145

gag ttc atc atc gtt ggt ttc tcc cag ggt gcg gtc att gcg ggc gat   595
Glu Phe Ile Ile Val Gly Phe Ser Gln Gly Ala Val Ile Ala Gly Asp
150                 155                 160                 165

gtg gct gct cag atc ggt tca gag caa ggt gtt att cca gct gac agc   643
Val Ala Ala Gln Ile Gly Ser Glu Gln Gly Val Ile Pro Ala Asp Ser
                170                 175                 180

gtc agg ggt gtc gcc ctg atc gct gac ggt cgc cgg gag cct ggt gtg   691
Val Arg Gly Val Ala Leu Ile Ala Asp Gly Arg Arg Glu Pro Gly Val
            185                 190                 195

ggc cag ttc cca ggc acg ttt gtg gat ggc atc ggc gcg gag gtt act   739
Gly Gln Phe Pro Gly Thr Phe Val Asp Gly Ile Gly Ala Glu Val Thr
        200                 205                 210

ctg cag cct ttg aac ttg ctg gtg cag ccg att gtt ccg ggc gca acc   787
Leu Gln Pro Leu Asn Leu Leu Val Gln Pro Ile Val Pro Gly Ala Thr
    215                 220                 225

atg cgt ggc ggg cgc gcg ggc ggt ttc ggt gtg ctc aac gac cgg gtg   835
Met Arg Gly Gly Arg Ala Gly Gly Phe Gly Val Leu Asn Asp Arg Val
230                 235                 240                 245

cag gat att tgt gct cca aat gat gcg atc tgt gat gct ccg gtg aat   883
Gln Asp Ile Cys Ala Pro Asn Asp Ala Ile Cys Asp Ala Pro Val Asn
                250                 255                 260

gtc ggc aac gcc ctt gat cgt gcg ttg gcc atg gtc tcc gcc aac ggt   931
Val Gly Asn Ala Leu Asp Arg Ala Leu Ala Met Val Ser Ala Asn Gly
            265                 270                 275

gtg cac gcg ctc tac gcc acc aat ccg gat gtt ttc cca ggc aca acc   979
Val His Ala Leu Tyr Ala Thr Asn Pro Asp Val Phe Pro Gly Thr Thr
        280                 285                 290

acc aat gcg tgg gtt gtg gat tgg gcg acc aac ctc atc gac aac gga  1027
Thr Asn Ala Trp Val Val Asp Trp Ala Thr Asn Leu Ile Asp Asn Gly
    295                 300                 305

taaagctttt tcgcttttcg acg                                       1050


<210> 1242
<211> 309
<212> PRT
<213> Corynebacterium glutamicum

<400> 1242
Met Arg Lys Thr Ile Thr Val Ile Ala Val Leu Ile Val Leu Ala Leu
  1               5                  10                  15
```

```
Ile Gly Val Gly Ile Val Gln Tyr Val Asn Thr Ser Asp Asp Ser Asp
            20                  25                  30

Phe Ile Gly Gln Pro Gly Glu Pro Thr Gly Thr Glu Thr Thr Glu Pro
        35                  40                  45

Pro Val Gln Pro Asp Trp Cys Pro Ala Val Glu Val Ile Ala Ala Pro
    50                  55                  60

Gly Thr Trp Glu Ser Ala Ala Asn Asp Asp Pro Ile Asn Pro Thr Ala
65                  70                  75                  80

Asn Pro Leu Ser Phe Met Leu Ser Ile Thr Gln Pro Leu Gln Glu Arg
                85                  90                  95

Tyr Ser Ala Asp Asp Val Lys Val Trp Thr Leu Pro Tyr Thr Ala Gln
            100                 105                 110

Phe Arg Asn Ile Asn Ser Gln Asn Glu Met Ser Tyr Asp Asp Ser Arg
        115                 120                 125

Asn Glu Gly Thr Ala Lys Met Asn Glu Glu Leu Ile Asn Thr His Asn
    130                 135                 140

Glu Cys Pro Ala Thr Glu Phe Ile Ile Val Gly Phe Ser Gln Gly Ala
145                 150                 155                 160

Val Ile Ala Gly Asp Val Ala Ala Gln Ile Gly Ser Glu Gln Gly Val
                165                 170                 175

Ile Pro Ala Asp Ser Val Arg Gly Val Ala Leu Ile Ala Asp Gly Arg
            180                 185                 190

Arg Glu Pro Gly Val Gly Gln Phe Pro Gly Thr Phe Val Asp Gly Ile
        195                 200                 205

Gly Ala Glu Val Thr Leu Gln Pro Leu Asn Leu Leu Val Gln Pro Ile
    210                 215                 220

Val Pro Gly Ala Thr Met Arg Gly Gly Arg Ala Gly Gly Phe Gly Val
225                 230                 235                 240

Leu Asn Asp Arg Val Gln Asp Ile Cys Ala Pro Asn Asp Ala Ile Cys
                245                 250                 255

Asp Ala Pro Val Asn Val Gly Asn Ala Leu Asp Arg Ala Leu Ala Met
            260                 265                 270

Val Ser Ala Asn Gly Val His Ala Leu Tyr Ala Thr Asn Pro Asp Val
        275                 280                 285

Phe Pro Gly Thr Thr Thr Asn Ala Trp Val Val Asp Trp Ala Thr Asn
    290                 295                 300

Leu Ile Asp Asn Gly
305
```

<210> 1243
<211> 1419

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1396)
<223> RXN02624

<400> 1243
acccggtcag atccgacgtc gccggccaaa accgcaagca cctgcgcaaa cgccacagaa 60

ggcagctcag caatcaaagt tgctgcgttt ccttccaacc gtg ctg att ccg cat 115
Val Leu Ile Pro His
1 5

ggc gtg gcg gtg ctt ttg gtt att att ctc gcc gta gcc tcc cta atg 163
Gly Val Ala Val Leu Leu Val Ile Ile Leu Ala Val Ala Ser Leu Met
10 15 20

ttc acc aat tct tca atg gtg aat ctt tcg gca acg att gca cag ctg 211
Phe Thr Asn Ser Ser Met Val Asn Leu Ser Ala Thr Ile Ala Gln Leu
25 30 35

tgg ctt tcc cta aat ctc ggt gcg gtg gac ggc agt ggg gaa gtg atc 259
Trp Leu Ser Leu Asn Leu Gly Ala Val Asp Gly Ser Gly Glu Val Ile
40 45 50

tca gta ctg ccc acg ctt ccc ggc ttt ata ttc ctc tgg gcc atc gcc 307
Ser Val Leu Pro Thr Leu Pro Gly Phe Ile Phe Leu Trp Ala Ile Ala
55 60 65

gcg cgc atc cac cgc gca gtc aaa gat cgt gtc agc atc gcc gac tta 355
Ala Arg Ile His Arg Ala Val Lys Asp Arg Val Ser Ile Ala Asp Leu
70 75 80 85

ggc gtc ctc gca gca ctc gtc ctc ggc atc ccg ctt gcg ctc acc gcc 403
Gly Val Leu Ala Ala Leu Val Leu Gly Ile Pro Leu Ala Leu Thr Ala
90 95 100

atc gca gcg ttc atg ctt ttc gac gcc tcc agc gtc ctc aac gtc gag 451
Ile Ala Ala Phe Met Leu Phe Asp Ala Ser Ser Val Leu Asn Val Glu
105 110 115

gtc ccg cca atc acg cgc ctc cta cgc gtg atg ttg ttc cac ctc agc 499
Val Pro Pro Ile Thr Arg Leu Leu Arg Val Met Leu Phe His Leu Ser
120 125 130

gcc ctc ttc ctc ggc atg ggg cca cgc ctg tgg cag gcg ttg gcg cgc 547
Ala Leu Phe Leu Gly Met Gly Pro Arg Leu Trp Gln Ala Leu Ala Arg
135 140 145

cgc tac ggt gct cca gaa tgg ctt atc gac gcc atc acc caa gct ttc 595
Arg Tyr Gly Ala Pro Glu Trp Leu Ile Asp Ala Ile Thr Gln Ala Phe
150 155 160 165

cgc ttc ctc atc gca ttt gga aca gtc tcc ttg gtt tcc gtg ctc gtg 643
Arg Phe Leu Ile Ala Phe Gly Thr Val Ser Leu Val Ser Val Leu Val
170 175 180

atg acc gcg atc aac cac agt gca ttc acc gcg acc atg cag ggt tac 691
Met Thr Ala Ile Asn His Ser Ala Phe Thr Ala Thr Met Gln Gly Tyr

```
            185                 190                 195

gac gac tcc gcc tct gtt gtg gcc ttg atc gtc ctg agc att ctg tat   739
Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val Leu Ser Ile Leu Tyr
        200                 205                 210

ctg ccc aac atg atg atc ttt gcg atg ggc aat ctg atc ggc tca ccc   787
Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn Leu Ile Gly Ser Pro
    215                 220                 225

ctt tac ttc ggt gac gcc tcc atc agc gtc ttc agc gtg cat tcc gtt   835
Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe Ser Val His Ser Val
230                 235                 240                 245

cca ttg cca ccg ctt ccc atc ctc gca gct ctc ccc agc gaa gcc ctc   883
Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu Pro Ser Glu Ala Leu
                250                 255                 260

tca tgg gca gtg gcc tta ctg gtc atc cct gca att att gcc acc tgg   931
Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala Ile Ile Ala Thr Trp
            265                 270                 275

gtc tgc gtg aga aac ccc atg cgc ctt gcc gtg aac aca aca gca gca   979
Val Cys Val Arg Asn Pro Met Arg Leu Ala Val Asn Thr Thr Ala Ala
        280                 285                 290

gtc att tca gca ctg tgt ttc ctc gtc ctg gca gtt ttc gcc ggc gga   1027
Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala Val Phe Ala Gly Gly
    295                 300                 305

acc ttg ggc gta tac aac tac gtc gga ctc aac ctc ctg gcg tca gtt   1075
Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn Leu Leu Ala Ser Val
310                 315                 320                 325

ggc cta gtt ttc gtc tat ttc gcc ctc gtt gga ctc ctc atc gcc gga   1123
Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly Leu Leu Ile Ala Gly
                330                 335                 340

atc gac aag ctg cgc aac cct gta gaa gtt aag tct gtt aag gct gtg   1171
Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys Ser Val Lys Ala Val
            345                 350                 355

gct gtt gtg gag ccc gag cct gaa gaa gtt gaa gag gac gaa gag gag   1219
Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu Glu Asp Glu Glu Glu
        360                 365                 370

cat gtt gaa gaa gaa gta gat gag gag gaa gag gaa gtt gag gaa ggg   1267
His Val Glu Glu Glu Val Asp Glu Glu Glu Glu Glu Val Glu Glu Gly
    375                 380                 385

gta gaa gag gtc gaa gaa gac gac gca gag gat cct gaa gag aat cct   1315
Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp Pro Glu Glu Asn Pro
390                 395                 400                 405

gaa gag gaa gaa tcc gac gaa gaa att gag aca gaa act gag gct gaa   1363
Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr Glu Thr Glu Ala Glu
                410                 415                 420

gaa acc aat gat ggt tcc gag gcc gaa gac cgt taacatatct gttgtgaatt 1416
Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg
            425                 430
```

ctg 1419

<210> 1244
<211> 432
<212> PRT
<213> Corynebacterium glutamicum

<400> 1244

```
Val Leu Ile Pro His Gly Val Ala Val Leu Leu Val Ile Ile Leu Ala
  1               5                  10                  15

Val Ala Ser Leu Met Phe Thr Asn Ser Ser Met Val Asn Leu Ser Ala
             20                  25                  30

Thr Ile Ala Gln Leu Trp Leu Ser Leu Asn Leu Gly Ala Val Asp Gly
         35                  40                  45

Ser Gly Glu Val Ile Ser Val Leu Pro Thr Leu Pro Gly Phe Ile Phe
     50                  55                  60

Leu Trp Ala Ile Ala Ala Arg Ile His Arg Ala Val Lys Asp Arg Val
 65                  70                  75                  80

Ser Ile Ala Asp Leu Gly Val Leu Ala Ala Leu Val Leu Gly Ile Pro
                 85                  90                  95

Leu Ala Leu Thr Ala Ile Ala Ala Phe Met Leu Phe Asp Ala Ser Ser
            100                 105                 110

Val Leu Asn Val Glu Val Pro Pro Ile Thr Arg Leu Leu Arg Val Met
        115                 120                 125

Leu Phe His Leu Ser Ala Leu Phe Leu Gly Met Gly Pro Arg Leu Trp
    130                 135                 140

Gln Ala Leu Ala Arg Arg Tyr Gly Ala Pro Glu Trp Leu Ile Asp Ala
145                 150                 155                 160

Ile Thr Gln Ala Phe Arg Phe Leu Ile Ala Phe Gly Thr Val Ser Leu
                165                 170                 175

Val Ser Val Leu Val Met Thr Ala Ile Asn His Ser Ala Phe Thr Ala
            180                 185                 190

Thr Met Gln Gly Tyr Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val
        195                 200                 205

Leu Ser Ile Leu Tyr Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn
    210                 215                 220

Leu Ile Gly Ser Pro Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe
225                 230                 235                 240

Ser Val His Ser Val Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu
                245                 250                 255

Pro Ser Glu Ala Leu Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala
            260                 265                 270
```

```
Ile Ile Ala Thr Trp Val Cys Val Arg Asn Pro Met Arg Leu Ala Val
        275                 280                 285

Asn Thr Thr Ala Ala Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala
    290                 295                 300

Val Phe Ala Gly Gly Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn
305                 310                 315                 320

Leu Leu Ala Ser Val Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly
                325                 330                 335

Leu Leu Ile Ala Gly Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys
            340                 345                 350

Ser Val Lys Ala Val Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu
        355                 360                 365

Glu Asp Glu Glu Glu His Val Glu Glu Glu Val Asp Glu Glu Glu Glu
    370                 375                 380

Glu Val Glu Glu Gly Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp
385                 390                 395                 400

Pro Glu Glu Asn Pro Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr
                405                 410                 415

Glu Thr Glu Ala Glu Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg
            420                 425                 430
```

Application Filed 2004-12-30 09:37:44

<210> 1245
<211> 737
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(714)
<223> FRXA02624

<400> 1245

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cag ggc tac gac gac tcc gcc tct gtt gtg gcc ttg atc gtc ctg agc   48
Gln Gly Tyr Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val Leu Ser
  1               5                  10                  15

att ctg tat ctg ccc aac atg atg atc ttt gcg atg ggc aat ctg atc   96
Ile Leu Tyr Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn Leu Ile
             20                  25                  30

ggc tca ccc ctt tac ttc ggt gac gcc tcc atc agc gtc ttc agc gtg   144
Gly Ser Pro Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe Ser Val
         35                  40                  45

cat tcc gtt cca ttg cca ccg ctt ccc atc ctc gca gct ctc ccc agc   192
His Ser Val Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu Pro Ser
     50                  55                  60
```

```
gaa gcc ctc tca tgg gca gtg gcc tta ctg gtc atc cct gca att att   240
Glu Ala Leu Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala Ile Ile
 65                  70                  75                  80

gcc acc tgg gtc tgc gtg aga aac ccc atg cgc ctt gcc gtg aac aca   288
Ala Thr Trp Val Cys Val Arg Asn Pro Met Arg Leu Ala Val Asn Thr
                85                  90                  95

aca gca gca gtc att tca gca ctg tgt ttc ctc gtc ctg gca gtt ttc   336
Thr Ala Ala Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala Val Phe
            100                 105                 110

gcc ggc gga acc ttg ggc gta tac aac tac gtc gga ctc aac ctc ctg   384
Ala Gly Gly Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn Leu Leu
        115                 120                 125

gcg tca gtt ggc cta gtt ttc gtc tat ttc gcc ctc gtt gga ctc ctc   432
Ala Ser Val Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly Leu Leu
    130                 135                 140

atc gcc gga atc gac aag ctg cgc aac cct gta gaa gtt aag tct gtt   480
Ile Ala Gly Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys Ser Val
145                 150                 155                 160

aag gct gtg gct gtt gtg gag ccc gag cct gaa gaa gtt gaa gag gac   528
Lys Ala Val Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu Glu Asp
                165                 170                 175

gaa gag gag cat gtt gaa gaa gaa gta gat gag gag gaa gag gaa gtt   576
Glu Glu Glu His Val Glu Glu Glu Val Asp Glu Glu Glu Glu Glu Val
            180                 185                 190

gag gaa ggg gta gaa gag gtc gaa gaa gac gac gca gag gat cct gaa   624
Glu Glu Gly Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp Pro Glu
        195                 200                 205

gag aat cct gaa gag gaa gaa tcc gac gaa gaa att gag aca gaa act   672
Glu Asn Pro Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr Glu Thr
    210                 215                 220

gag gct gaa gaa acc aat gat ggt tcc gag gcc gaa gac cgt           714
Glu Ala Glu Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg
225                 230                 235

taacatatct gttgtgaatt ctg                                        737
```

<210> 1246
<211> 238
<212> PRT
<213> Corynebacterium glutamicum

<400> 1246

```
Gln Gly Tyr Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val Leu Ser
  1               5                  10                  15

Ile Leu Tyr Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn Leu Ile
             20                  25                  30

Gly Ser Pro Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe Ser Val
         35                  40                  45
```

```
His Ser Val Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu Pro Ser
     50                  55                  60

Glu Ala Leu Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala Ile Ile
 65                  70                  75                  80

Ala Thr Trp Val Cys Val Arg Asn Pro Met Arg Leu Ala Val Asn Thr
                 85                  90                  95

Thr Ala Ala Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala Val Phe
            100                 105                 110

Ala Gly Gly Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn Leu Leu
        115                 120                 125

Ala Ser Val Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly Leu Leu
    130                 135                 140

Ile Ala Gly Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys Ser Val
145                 150                 155                 160

Lys Ala Val Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu Glu Asp
                165                 170                 175

Glu Glu Glu His Val Glu Glu Glu Val Asp Glu Glu Glu Glu Glu Val
            180                 185                 190

Glu Glu Gly Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp Pro Glu
        195                 200                 205

Glu Asn Pro Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr Glu Thr
    210                 215                 220

Glu Ala Glu Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg
225                 230                 235


<210> 1247
<211> 1128
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1105)
<223> RXN02626

<400> 1247
gtagcggtcg aattatttgc ctgtgggcat aattttgaga caaaataata gaaacgtctc 60

agatgttggg aagttcttca cgctatcagt tagggagcac atg agt act caa gtt   115
                                            Met Ser Thr Gln Val
                                              1               5

gaa ctc aaa aca ccg aaa tcg gaa gac cgg gca gca tat atc gct gca   163
Glu Leu Lys Thr Pro Lys Ser Glu Asp Arg Ala Ala Tyr Ile Ala Ala
                10                  15                  20

ttg gga ttc ccg gtc ttg gtc atc att ggc ggc atc atc gga ttc aca   211
Leu Gly Phe Pro Val Leu Val Ile Ile Gly Gly Ile Ile Gly Phe Thr
```

```
                25                  30                  35

gcc tcg gat gtt gtg ctc aat att tct tcg tgg gtc aat cct ttg ctg   259
Ala Ser Asp Val Val Leu Asn Ile Ser Ser Trp Val Asn Pro Leu Leu
         40                  45                  50

ggc atc atc atg ttc tcc atg ggc ctg acc ttg aag cca gtt gac ttc   307
Gly Ile Ile Met Phe Ser Met Gly Leu Thr Leu Lys Pro Val Asp Phe
     55                  60                  65

gcc ctt gtt gct aaa cgc cca ctc cca gtt ctt atc ggc gtg atc gcc   355
Ala Leu Val Ala Lys Arg Pro Leu Pro Val Leu Ile Gly Val Ile Ala
 70                  75                  80                  85

cag ttt gtc atc atg ccc ctg atc gca ttg ctg gtg gtc tgg gtt ttg   403
Gln Phe Val Ile Met Pro Leu Ile Ala Leu Leu Val Val Trp Val Leu
                 90                  95                 100

cag ctg cct gcg gaa att gcg gcc ggt gtc atc ttg gtt ggt tgt gca   451
Gln Leu Pro Ala Glu Ile Ala Ala Gly Val Ile Leu Val Gly Cys Ala
            105                 110                 115

cct ggc gga act tcc tcc aac gtg gtg tct tac ctg tcc cgt ggt gat   499
Pro Gly Gly Thr Ser Ser Asn Val Val Ser Tyr Leu Ser Arg Gly Asp
        120                 125                 130

gtt gcg ctg tct gtc acc atg act tcc atc tcc acg ctg ctt gct cca   547
Val Ala Leu Ser Val Thr Met Thr Ser Ile Ser Thr Leu Leu Ala Pro
    135                 140                 145

att ttc act cca ctg ctt acc ctg tgg ctg gcg ggg caa tac atg cca   595
Ile Phe Thr Pro Leu Leu Thr Leu Trp Leu Ala Gly Gln Tyr Met Pro
150                 155                 160                 165

ctt aat gcc gct gat atg gct gta tcc atc gtc caa gtt gtg ctg atc   643
Leu Asn Ala Ala Asp Met Ala Val Ser Ile Val Gln Val Val Leu Ile
                170                 175                 180

cca gtc gtg ggc gga ctt gtt gtg cgg ttg atc ttc ccg aca ctc att   691
Pro Val Val Gly Gly Leu Val Val Arg Leu Ile Phe Pro Thr Leu Ile
            185                 190                 195

ggc aag gtt ttg cct ctt ttg cca tgg att tca gtc att gcg att tca   739
Gly Lys Val Leu Pro Leu Leu Pro Trp Ile Ser Val Ile Ala Ile Ser
        200                 205                 210

ttg atc gtt gcc atc gtg gtc gct ggt tca agg gat aaa atc ctc gaa   787
Leu Ile Val Ala Ile Val Val Ala Gly Ser Arg Asp Lys Ile Leu Glu
    215                 220                 225

gca gga ctg ctc gtg ctg gct gcc gtg att att cac aac acc ctc ggc   835
Ala Gly Leu Leu Val Leu Ala Ala Val Ile Ile His Asn Thr Leu Gly
230                 235                 240                 245

tac tcc ctg gga tac ctc gct gcg aaa ttc act ggg cag cct gct gca   883
Tyr Ser Leu Gly Tyr Leu Ala Ala Lys Phe Thr Gly Gln Pro Ala Ala
                250                 255                 260

gct cga cgc act acc gcg att gag gtc ggt atg caa aac tcc ggc ctc   931
Ala Arg Arg Thr Thr Ala Ile Glu Val Gly Met Gln Asn Ser Gly Leu
            265                 270                 275
```

```
gca gat gga ctc gca tcc cag tac atg tca cca atg tct gct ctg cca   979
Ala Asp Gly Leu Ala Ser Gln Tyr Met Ser Pro Met Ser Ala Leu Pro
        280                 285                 290

ggc gct atc ttc tct gtc tgg cac aac ctt tcc gga gca ctt ctt gct   1027
Gly Ala Ile Phe Ser Val Trp His Asn Leu Ser Gly Ala Leu Leu Ala
    295                 300                 305

gca ttg tgc agg gcg tcc gat aag agg gct gcg gag aag gtg gct tca   1075
Ala Leu Cys Arg Ala Ser Asp Lys Arg Ala Ala Glu Lys Val Ala Ser
310                 315                 320                 325

gaa aag gct gcc tcg gag aag gcc gct tcc taaaaggctt cgctcctaaa     1125
Glu Lys Ala Ala Ser Glu Lys Ala Ala Ser
                330                 335

act                                                               1128
```

<210> 1248
<211> 335
<212> PRT
<213> Corynebacterium glutamicum

<400> 1248

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Met Ser Thr Gln Val Glu Leu Lys Thr Pro Lys Ser Glu Asp Arg Ala
  1               5                  10                  15

Ala Tyr Ile Ala Ala Leu Gly Phe Pro Val Leu Val Ile Ile Gly Gly
             20                  25                  30

Ile Ile Gly Phe Thr Ala Ser Asp Val Val Leu Asn Ile Ser Ser Trp
         35                  40                  45

Val Asn Pro Leu Leu Gly Ile Ile Met Phe Ser Met Gly Leu Thr Leu
     50                  55                  60

Lys Pro Val Asp Phe Ala Leu Val Ala Lys Arg Pro Leu Pro Val Leu
 65                  70                  75                  80

Ile Gly Val Ile Ala Gln Phe Val Ile Met Pro Leu Ile Ala Leu Leu
                 85                  90                  95

Val Val Trp Val Leu Gln Leu Pro Ala Glu Ile Ala Ala Gly Val Ile
            100                 105                 110

Leu Val Gly Cys Ala Pro Gly Gly Thr Ser Ser Asn Val Val Ser Tyr
        115                 120                 125

Leu Ser Arg Gly Asp Val Ala Leu Ser Val Thr Met Thr Ser Ile Ser
    130                 135                 140

Thr Leu Leu Ala Pro Ile Phe Thr Pro Leu Leu Thr Leu Trp Leu Ala
145                 150                 155                 160

Gly Gln Tyr Met Pro Leu Asn Ala Ala Asp Met Ala Val Ser Ile Val
                165                 170                 175

Gln Val Val Leu Ile Pro Val Val Gly Gly Leu Val Val Arg Leu Ile
            180                 185                 190
```

```
Phe Pro Thr Leu Ile Gly Lys Val Leu Pro Leu Leu Pro Trp Ile Ser
        195                 200                 205

Val Ile Ala Ile Ser Leu Ile Val Ala Ile Val Val Ala Gly Ser Arg
    210                 215                 220

Asp Lys Ile Leu Glu Ala Gly Leu Leu Val Leu Ala Ala Val Ile Ile
225                 230                 235                 240

His Asn Thr Leu Gly Tyr Ser Leu Gly Tyr Leu Ala Ala Lys Phe Thr
                245                 250                 255

Gly Gln Pro Ala Ala Ala Arg Arg Thr Thr Ala Ile Glu Val Gly Met
            260                 265                 270

Gln Asn Ser Gly Leu Ala Asp Gly Leu Ala Ser Gln Tyr Met Ser Pro
        275                 280                 285

Met Ser Ala Leu Pro Gly Ala Ile Phe Ser Val Trp His Asn Leu Ser
    290                 295                 300

Gly Ala Leu Leu Ala Ala Leu Cys Arg Ala Ser Asp Lys Arg Ala Ala
305                 310                 315                 320

Glu Lys Val Ala Ser Glu Lys Ala Ala Ser Glu Lys Ala Ala Ser
                325                 330                 335
```

<210> 1249
<211> 963
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(940)
<223> RXN02656

<400> 1249

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gccatgtggg acagtctagc catctcctta cacccgtgaa actcctattt cattaacgca 60

ttgatctcgg cttttctaac ctaggtataa ggtaacagct atg att ttc ggc gta   115
                                            Met Ile Phe Gly Val
                                              1               5

ctc gca tac ttg gga tgg ggc atg ttc ccg gcc ttt ttc cca cta ctt   163
Leu Ala Tyr Leu Gly Trp Gly Met Phe Pro Ala Phe Phe Pro Leu Leu
                 10                  15                  20

ctt ccg gca gga ccg ttc gaa att tta gcg cat cgg atc cta tgg act   211
Leu Pro Ala Gly Pro Phe Glu Ile Leu Ala His Arg Ile Leu Trp Thr
             25                  30                  35

gct gta tta atg atg att atc att agt ttc acg tcg gga tgg aaa gag   259
Ala Val Leu Met Met Ile Ile Ile Ser Phe Thr Ser Gly Trp Lys Glu
         40                  45                  50

ctt aag tcc gct gat cgc ggt aca tgg tta cgc att ata ttg tca tcg   307
Leu Lys Ser Ala Asp Arg Gly Thr Trp Leu Arg Ile Ile Leu Ser Ser
     55                  60                  65
```

```
ttg ttt att gcc ggg aac tgg ctg atc tat gtc atc gct gtc aat tct   355
Leu Phe Ile Ala Gly Asn Trp Leu Ile Tyr Val Ile Ala Val Asn Ser
 70                  75                  80                  85

ggg caa gtt act gaa gcc gct ctc gga tac ttt att aac ccc ctg tta   403
Gly Gln Val Thr Glu Ala Ala Leu Gly Tyr Phe Ile Asn Pro Leu Leu
                90                  95                 100

agt gtc gtg ctt ggc att gtg ttc ttc aaa gaa cag tta cga aaa ctg   451
Ser Val Val Leu Gly Ile Val Phe Phe Lys Glu Gln Leu Arg Lys Leu
            105                 110                 115

caa att agt gcg gtg gtt att gct gct gcg ggg gtt ttg gta cta aca   499
Gln Ile Ser Ala Val Val Ile Ala Ala Ala Gly Val Leu Val Leu Thr
        120                 125                 130

ttt cta ggt gat aag cca ccg tat tta gcg ata aca cta gca ttt aca   547
Phe Leu Gly Asp Lys Pro Pro Tyr Leu Ala Ile Thr Leu Ala Phe Thr
    135                 140                 145

ttc ggc atc tat gga gcg ttg aaa aaa caa gtc aag atg tct gct gct   595
Phe Gly Ile Tyr Gly Ala Leu Lys Lys Gln Val Lys Met Ser Ala Ala
150                 155                 160                 165

agt tct ttg tgc gct gaa act tta gta ctg ctg ccc atc gca gtc ata   643
Ser Ser Leu Cys Ala Glu Thr Leu Val Leu Leu Pro Ile Ala Val Ile
                170                 175                 180

tac ctg att ggg ctc gaa gct tcc ggt cac agt acc ttt ttc aac aat   691
Tyr Leu Ile Gly Leu Glu Ala Ser Gly His Ser Thr Phe Phe Asn Asn
            185                 190                 195

ggc agt ggg cac atg gcg tta tta atc tgc tcg ggt ttg gtc aca gcc   739
Gly Ser Gly His Met Ala Leu Leu Ile Cys Ser Gly Leu Val Thr Ala
        200                 205                 210

gtc ccg ctg ttg atg ttt gca ttg gcc gcc aag gca ata cct ctt tcc   787
Val Pro Leu Leu Met Phe Ala Leu Ala Ala Lys Ala Ile Pro Leu Ser
    215                 220                 225

act gtc ggc atg ctg caa tat ctg acc cca acg atg cag atg ctg tgg   835
Thr Val Gly Met Leu Gln Tyr Leu Thr Pro Thr Met Gln Met Leu Trp
230                 235                 240                 245

gca ttg ttt gtg gtc aac gaa tca gta gaa cca atg cgt tgg ttc gga   883
Ala Leu Phe Val Val Asn Glu Ser Val Glu Pro Met Arg Trp Phe Gly
                250                 255                 260

ttc gtt ttc att tgg atc gca gtt act att tac atc aca gat agc cta   931
Phe Val Phe Ile Trp Ile Ala Val Thr Ile Tyr Ile Thr Asp Ser Leu
            265                 270                 275

ctt aag aag taggtaatag cagtattgat atg                            963
Leu Lys Lys
        280
```

<210> 1250
<211> 280
<212> PRT

<213> Corynebacterium glutamicum

<400> 1250

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Met Ile Phe Gly Val Leu Ala Tyr Leu Gly Trp Gly Met Phe Pro Ala
  1               5                  10                  15

Phe Phe Pro Leu Leu Leu Pro Ala Gly Pro Phe Glu Ile Leu Ala His
             20                  25                  30

Arg Ile Leu Trp Thr Ala Val Leu Met Met Ile Ile Ile Ser Phe Thr
         35                  40                  45

Ser Gly Trp Lys Glu Leu Lys Ser Ala Asp Arg Gly Thr Trp Leu Arg
     50                  55                  60

Ile Ile Leu Ser Ser Leu Phe Ile Ala Gly Asn Trp Leu Ile Tyr Val
 65                  70                  75                  80

Ile Ala Val Asn Ser Gly Gln Val Thr Glu Ala Ala Leu Gly Tyr Phe
                 85                  90                  95

Ile Asn Pro Leu Leu Ser Val Val Leu Gly Ile Val Phe Phe Lys Glu
            100                 105                 110

Gln Leu Arg Lys Leu Gln Ile Ser Ala Val Val Ile Ala Ala Ala Gly
        115                 120                 125

Val Leu Val Leu Thr Phe Leu Gly Asp Lys Pro Pro Tyr Leu Ala Ile
    130                 135                 140

Thr Leu Ala Phe Thr Phe Gly Ile Tyr Gly Ala Leu Lys Lys Gln Val
145                 150                 155                 160

Lys Met Ser Ala Ala Ser Ser Leu Cys Ala Glu Thr Leu Val Leu Leu
                165                 170                 175

Pro Ile Ala Val Ile Tyr Leu Ile Gly Leu Glu Ala Ser Gly His Ser
            180                 185                 190

Thr Phe Phe Asn Asn Gly Ser Gly His Met Ala Leu Leu Ile Cys Ser
        195                 200                 205

Gly Leu Val Thr Ala Val Pro Leu Leu Met Phe Ala Leu Ala Ala Lys
    210                 215                 220

Ala Ile Pro Leu Ser Thr Val Gly Met Leu Gln Tyr Leu Thr Pro Thr
225                 230                 235                 240

Met Gln Met Leu Trp Ala Leu Phe Val Val Asn Glu Ser Val Glu Pro
                245                 250                 255

Met Arg Trp Phe Gly Phe Val Phe Ile Trp Ile Ala Val Thr Ile Tyr
            260                 265                 270

Ile Thr Asp Ser Leu Leu Lys Lys
        275                 280
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<210> 1251
<211> 756
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(733)
<223> RXN02673

<400> 1251
acgcccaaaa cgctaatccg ctgaacaggc cgatgaaagt aatagagtgt tctgtgtggg 60

aacgccgaga cataatgaag tcatttacaa gcgccgccgc atg gca gcg ctc cta 115
Met Ala Ala Leu Leu
1 5

gtt ctg ctc gtc gtg att gcc ttg att atc tgg gca gtc gtc gcg ctt 163
Val Leu Leu Val Val Ile Ala Leu Ile Ile Trp Ala Val Val Ala Leu
10 15 20

cga ggt gga tca tcg gag cct gag gaa gag cag cca aat aat gct gta 211
Arg Gly Gly Ser Ser Glu Pro Glu Glu Glu Gln Pro Asn Asn Ala Val
25 30 35

gtg acc tcc tca atg gaa tct tcc gcg acg tct agt tct tct tct aaa 259
Val Thr Ser Ser Met Glu Ser Ser Ala Thr Ser Ser Ser Ser Ser Lys
40 45 50

gaa tcc acg act gaa gcc acc aca gaa gaa gag act tcc agt gct gaa 307
Glu Ser Thr Thr Glu Ala Thr Thr Glu Glu Glu Thr Ser Ser Ala Glu
55 60 65

cca acc gca aca tcc tcc gtt gca gca gat gca aaa aag acc tgt gag 355
Pro Thr Ala Thr Ser Ser Val Ala Ala Asp Ala Lys Lys Thr Cys Glu
70 75 80 85

ctt agt gac ttg gtg att tcc gca agc act aat cag ccg act ttc tca 403
Leu Ser Asp Leu Val Ile Ser Ala Ser Thr Asn Gln Pro Thr Phe Ser
90 95 100

ggt tct gcg cag cca gaa tta ttt atg gct gtg cat aat ccg act gct 451
Gly Ser Ala Gln Pro Glu Leu Phe Met Ala Val His Asn Pro Thr Ala
105 110 115

gtt gat tgc gaa att gac ctc gag gag aac aaa ctc cgt ttc gag gta 499
Val Asp Cys Glu Ile Asp Leu Glu Glu Asn Lys Leu Arg Phe Glu Val
120 125 130

tac aat ctc gcg acc aac gca cga atc tgg tct gat gtc gac tgc aac 547
Tyr Asn Leu Ala Thr Asn Ala Arg Ile Trp Ser Asp Val Asp Cys Asn
135 140 145

cct gca gtt gaa gac ggc acg agc gtg ttc cct gcc ggc gag gat cgc 595
Pro Ala Val Glu Asp Gly Thr Ser Val Phe Pro Ala Gly Glu Asp Arg
150 155 160 165

tac ttc cag gca aca tgg tct cgt acc act tca gcg cca aac cag tgc 643
Tyr Phe Gln Ala Thr Trp Ser Arg Thr Thr Ser Ala Pro Asn Gln Cys
170 175 180

aac aac cgc act gat gtc ccc gcc ggt ggc tac tac ttg cac act gtg 691
Asn Asn Arg Thr Asp Val Pro Ala Gly Gly Tyr Tyr Leu His Thr Val
185 190 195

gtc ggt aat aac cct tca cca gcg gtg acc ttt aac cta act 733
Val Gly Asn Asn Pro Ser Pro Ala Val Thr Phe Asn Leu Thr
200 205 210

taaacggcca agtccgtcgg tga 756

<210> 1252
<211> 211
<212> PRT
<213> Corynebacterium glutamicum

<400> 1252
Met Ala Ala Leu Leu Val Leu Leu Val Val Ile Ala Leu Ile Ile Trp
1 5 10 15

Ala Val Val Ala Leu Arg Gly Gly Ser Ser Glu Pro Glu Glu Glu Gln
20 25 30

Pro Asn Asn Ala Val Val Thr Ser Ser Met Glu Ser Ser Ala Thr Ser
35 40 45

Ser Ser Ser Ser Lys Glu Ser Thr Thr Glu Ala Thr Thr Glu Glu Glu
50 55 60

Thr Ser Ser Ala Glu Pro Thr Ala Thr Ser Ser Val Ala Ala Asp Ala
65 70 75 80

Lys Lys Thr Cys Glu Leu Ser Asp Leu Val Ile Ser Ala Ser Thr Asn
85 90 95

Gln Pro Thr Phe Ser Gly Ser Ala Gln Pro Glu Leu Phe Met Ala Val
100 105 110

His Asn Pro Thr Ala Val Asp Cys Glu Ile Asp Leu Glu Glu Asn Lys
115 120 125

Leu Arg Phe Glu Val Tyr Asn Leu Ala Thr Asn Ala Arg Ile Trp Ser
130 135 140

Asp Val Asp Cys Asn Pro Ala Val Glu Asp Gly Thr Ser Val Phe Pro
145 150 155 160

Ala Gly Glu Asp Arg Tyr Phe Gln Ala Thr Trp Ser Arg Thr Thr Ser
165 170 175

Ala Pro Asn Gln Cys Asn Asn Arg Thr Asp Val Pro Ala Gly Gly Tyr
180 185 190

Tyr Leu His Thr Val Val Gly Asn Asn Pro Ser Pro Ala Val Thr Phe
195 200 205

Asn Leu Thr
210

<210> 1253
<211> 756
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(733)
<223> FRXA02673

<400> 1253
acgcccaaaa cgctaatccg ctgaacaggc cgatgaaagt aatagagtgt tctgtgtggg 60

aacgccgaga cataatgaag tcatttacaa gcgccgccgc atg gca gcg ctc cta 115
Met Ala Ala Leu Leu
1 5

gtt ctg ctc gtc gtg att gcc ttg att atc tgg gca gtc gtc gcg ctt 163
Val Leu Leu Val Val Ile Ala Leu Ile Ile Trp Ala Val Val Ala Leu
10 15 20

cga ggt gga tca tcg gag cct gag gaa gag cag cca aat aat gct gta 211
Arg Gly Gly Ser Ser Glu Pro Glu Glu Glu Gln Pro Asn Asn Ala Val
25 30 35

gtg acc tcc tca atg gaa tct tcc gcg acg tct agt tct tct tct aaa 259
Val Thr Ser Ser Met Glu Ser Ser Ala Thr Ser Ser Ser Ser Ser Lys
40 45 50

gaa tcc acg act gaa gcc acc aca gaa gaa gag act tcc agt gct gaa 307
Glu Ser Thr Thr Glu Ala Thr Thr Glu Glu Glu Thr Ser Ser Ala Glu
55 60 65

cca acc gca aca tcc tcc gtt gca gca gat gca aaa aag acc tgt gag 355
Pro Thr Ala Thr Ser Ser Val Ala Ala Asp Ala Lys Lys Thr Cys Glu
70 75 80 85

ctt agt gac ttg gtg att tcc gca agc act aat cag ccg act ttc tca 403
Leu Ser Asp Leu Val Ile Ser Ala Ser Thr Asn Gln Pro Thr Phe Ser
90 95 100

ggt tct gcg cag cca gaa tta ttt atg gct gtg cat aat ccg act gct 451
Gly Ser Ala Gln Pro Glu Leu Phe Met Ala Val His Asn Pro Thr Ala
105 110 115

gtt gat tgc gaa att gac ctc gag gag aac aaa ctc cgt ttc gag gta 499
Val Asp Cys Glu Ile Asp Leu Glu Glu Asn Lys Leu Arg Phe Glu Val
120 125 130

tac aat ctc gcg acc aac gca cga atc tgg tct gat gtc gac tgc aac 547
Tyr Asn Leu Ala Thr Asn Ala Arg Ile Trp Ser Asp Val Asp Cys Asn
135 140 145

cct gca gtt gaa gac ggc acg agc gtg ttc cct gcc ggc gag gat cgc 595
Pro Ala Val Glu Asp Gly Thr Ser Val Phe Pro Ala Gly Glu Asp Arg
150 155 160 165

tac ttc cag gca aca tgg tct cgt acc act tca gcg cca aac cag tgc 643
Tyr Phe Gln Ala Thr Trp Ser Arg Thr Thr Ser Ala Pro Asn Gln Cys
170 175 180

aac aac cgc act gat gtc ccc gcc ggt ggc tac tac ttg cac act gtg 691
Asn Asn Arg Thr Asp Val Pro Ala Gly Gly Tyr Tyr Leu His Thr Val
185 190 195

gtc ggt aat aac cct tca cca gcg gtg acc ttt aac cta act 733
Val Gly Asn Asn Pro Ser Pro Ala Val Thr Phe Asn Leu Thr
200 205 210

taaacggcca agtccgtcgg tga 756

<210> 1254
<211> 211
<212> PRT
<213> Corynebacterium glutamicum

<400> 1254
Met Ala Ala Leu Leu Val Leu Leu Val Val Ile Ala Leu Ile Ile Trp
1 5 10 15

Ala Val Val Ala Leu Arg Gly Gly Ser Ser Glu Pro Glu Glu Glu Gln
20 25 30

Pro Asn Asn Ala Val Val Thr Ser Ser Met Glu Ser Ser Ala Thr Ser
35 40 45

Ser Ser Ser Ser Lys Glu Ser Thr Thr Glu Ala Thr Thr Glu Glu Glu
50 55 60

Thr Ser Ser Ala Glu Pro Thr Ala Thr Ser Ser Val Ala Ala Asp Ala
65 70 75 80

Lys Lys Thr Cys Glu Leu Ser Asp Leu Val Ile Ser Ala Ser Thr Asn
85 90 95

Gln Pro Thr Phe Ser Gly Ser Ala Gln Pro Glu Leu Phe Met Ala Val
100 105 110

His Asn Pro Thr Ala Val Asp Cys Glu Ile Asp Leu Glu Glu Asn Lys
115 120 125

Leu Arg Phe Glu Val Tyr Asn Leu Ala Thr Asn Ala Arg Ile Trp Ser
130 135 140

Asp Val Asp Cys Asn Pro Ala Val Glu Asp Gly Thr Ser Val Phe Pro
145 150 155 160

Ala Gly Glu Asp Arg Tyr Phe Gln Ala Thr Trp Ser Arg Thr Thr Ser
165 170 175

Ala Pro Asn Gln Cys Asn Asn Arg Thr Asp Val Pro Ala Gly Gly Tyr
180 185 190

Tyr Leu His Thr Val Val Gly Asn Asn Pro Ser Pro Ala Val Thr Phe
195 200 205

Asn Leu Thr
210

<210> 1255
<211> 1407
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1384)
<223> RXN02680

<400> 1255
aataccaggt caacacacac aggaaccgtt cagaaacctt ccagattgct cacttttaa 60

tttcactttt ttgagaagtt ttacttttat attagttctc atg cgc ctc aac aaa 115
Met Arg Leu Asn Lys
1 5

cga ctc cca gcg gca ctc tcc gga ctg ctc tct gct gcc ctt ctt 163
Arg Leu Pro Ala Ala Leu Ser Gly Leu Leu Leu Ser Ala Ala Leu Leu
10 15 20

gcc gga tgc tcc act tct gga acc gcc gag acc acg aca aca acc gtt 211
Ala Gly Cys Ser Thr Ser Gly Thr Ala Glu Thr Thr Thr Thr Thr Val
25 30 35

tca tct gct gcg gca tca aca acc act tcc acc tcc tct gct tcg tct 259
Ser Ser Ala Ala Ala Ser Thr Thr Thr Ser Thr Ser Ser Ala Ser Ser
40 45 50

tcc tct tcc tcc tcc tct tcc tcc tct tcc tcc gac tca agc acc acc 307
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Thr Thr
55 60 65

gcc gaa acc atc tcc aac acc gcg gaa gct gcc caa gct ttc ttg tcc 355
Ala Glu Thr Ile Ser Asn Thr Ala Glu Ala Ala Gln Ala Phe Leu Ser
70 75 80 85

acc ctg tcc acc gaa gaa caa gac gcc gta ctc tac gac tac gac gcc 403
Thr Leu Ser Thr Glu Glu Gln Asp Ala Val Leu Tyr Asp Tyr Asp Ala
90 95 100

gaa gaa aag tcc acc ggc tgg tct aac ttc cca gtc acc ttc gtg cag 451
Glu Glu Lys Ser Thr Gly Trp Ser Asn Phe Pro Val Thr Phe Val Gln
105 110 115

cgt tcc ggc gtg aac ctc acc gac ctc act gag gaa cag caa gca gct 499
Arg Ser Gly Val Asn Leu Thr Asp Leu Thr Glu Glu Gln Gln Ala Ala
120 125 130

gcc ctc aac gtg ctg aag aac ctg ctc aac gac gac gcc tac caa atg 547
Ala Leu Asn Val Leu Lys Asn Leu Leu Asn Asp Asp Ala Tyr Gln Met
135 140 145

atc gaa gac atc atg gct agc gat cag tac ctc aac gac gaa agc aac 595
Ile Glu Asp Ile Met Ala Ser Asp Gln Tyr Leu Asn Asp Glu Ser Asn
150 155 160 165

acc acc gag gat tcc ctc ggc cag tac tac atc gca ttc ttc ggc gat 643
Thr Thr Glu Asp Ser Leu Gly Gln Tyr Tyr Ile Ala Phe Phe Gly Asp
170 175 180

cca agc agc gac tcc gac tgg tcc atc caa ttc ggc gga cac cac atc 691
Pro Ser Ser Asp Ser Asp Trp Ser Ile Gln Phe Gly Gly His His Ile
185 190 195

ggc atc aac acc acc ttc tcc gac ggt gcc atc acc ttc gcc cca acc 739

```
Gly Ile Asn Thr Thr Phe Ser Asp Gly Ala Ile Thr Phe Ala Pro Thr
        200                 205                 210

cac ctt ggc acc cag cct tcc gag tgg acc aac gag gac ggc gaa acc   787
His Leu Gly Thr Gln Pro Ser Glu Trp Thr Asn Glu Asp Gly Glu Thr
    215                 220                 225

gtt gca gca cta agc aac atg tac gaa acc gcc ttc gcc ttc tac gac   835
Val Ala Ala Leu Ser Asn Met Tyr Glu Thr Ala Phe Ala Phe Tyr Asp
230                 235                 240                 245

agc ctc gcc gaa gag cag caa gca cag ctc tac cag ggt gaa gag ttg   883
Ser Leu Ala Glu Glu Gln Gln Ala Gln Leu Tyr Gln Gly Glu Glu Leu
                250                 255                 260

gat tcc atg gtg tgc gca ccg ggc agc acg tgc gac tac cca acc ggc   931
Asp Ser Met Val Cys Ala Pro Gly Ser Thr Cys Asp Tyr Pro Thr Gly
            265                 270                 275

acc ggc ttg aaa ggc tct gac ctc acc gat gag caa aaa gaa ttg ctc   979
Thr Gly Leu Lys Gly Ser Asp Leu Thr Asp Glu Gln Lys Glu Leu Leu
        280                 285                 290

atc gat gtc atc gca aac tgg gtt ggc ctc gcc gat gag gaa acc acc   1027
Ile Asp Val Ile Ala Asn Trp Val Gly Leu Ala Asp Glu Glu Thr Thr
    295                 300                 305

gaa act gaa ctc gat gcc atc cgc gaa acc ctg gat gac acc tac atc   1075
Glu Thr Glu Leu Asp Ala Ile Arg Glu Thr Leu Asp Asp Thr Tyr Ile
310                 315                 320                 325

aac tgg tcc ggc gcc acc gag tac gac acc tcc acc ggc gac ggc atc   1123
Asn Trp Ser Gly Ala Thr Glu Tyr Asp Thr Ser Thr Gly Asp Gly Ile
                330                 335                 340

tac ttc cag atc agt ggc cca aag gtc tac att gag ttc gct aac cag   1171
Tyr Phe Gln Ile Ser Gly Pro Lys Val Tyr Ile Glu Phe Ala Asn Gln
            345                 350                 355

caa ggt tct gca ggt gcc gac atc gac ggt gtc atc acc gct gga tgg   1219
Gln Gly Ser Ala Gly Ala Asp Ile Asp Gly Val Ile Thr Ala Gly Trp
        360                 365                 370

ggc cac att cac acc atc tac cgc gac cca acc aat gac tac gct aac   1267
Gly His Ile His Thr Ile Tyr Arg Asp Pro Thr Asn Asp Tyr Ala Asn
    375                 380                 385

tcc gta act cag gaa gca gcc agc gga atg atg ggc ggc ggc cct ggt   1315
Ser Val Thr Gln Glu Ala Ala Ser Gly Met Met Gly Gly Gly Pro Gly
390                 395                 400                 405

ggt aat ggt ggc gag atg cct agc ggt gac atg cct act ggt gag atg   1363
Gly Asn Gly Gly Glu Met Pro Ser Gly Asp Met Pro Thr Gly Glu Met
                410                 415                 420

cct tct ggc gct cca tca aac taacgccatt taagaggccg aac             1407
Pro Ser Gly Ala Pro Ser Asn
            425
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<210> 1256

<211> 428
<212> PRT
<213> Corynebacterium glutamicum

<400> 1256

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Met Arg Leu Asn Lys Arg Leu Pro Ala Ala Leu Ser Gly Leu Leu Leu
  1               5                  10                  15

Ser Ala Ala Leu Leu Ala Gly Cys Ser Thr Ser Gly Thr Ala Glu Thr
             20                  25                  30

Thr Thr Thr Thr Val Ser Ser Ala Ala Ala Ser Thr Thr Thr Ser Thr
         35                  40                  45

Ser Ser Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
     50                  55                  60

Asp Ser Ser Thr Thr Ala Glu Thr Ile Ser Asn Thr Ala Glu Ala Ala
 65                  70                  75                  80

Gln Ala Phe Leu Ser Thr Leu Ser Thr Glu Glu Gln Asp Ala Val Leu
                 85                  90                  95

Tyr Asp Tyr Asp Ala Glu Glu Lys Ser Thr Gly Trp Ser Asn Phe Pro
            100                 105                 110

Val Thr Phe Val Gln Arg Ser Gly Val Asn Leu Thr Asp Leu Thr Glu
        115                 120                 125

Glu Gln Gln Ala Ala Ala Leu Asn Val Leu Lys Asn Leu Leu Asn Asp
    130                 135                 140

Asp Ala Tyr Gln Met Ile Glu Asp Ile Met Ala Ser Asp Gln Tyr Leu
145                 150                 155                 160

Asn Asp Glu Ser Asn Thr Thr Glu Asp Ser Leu Gly Gln Tyr Tyr Ile
                165                 170                 175

Ala Phe Phe Gly Asp Pro Ser Ser Asp Ser Asp Trp Ser Ile Gln Phe
            180                 185                 190

Gly Gly His His Ile Gly Ile Asn Thr Thr Phe Ser Asp Gly Ala Ile
        195                 200                 205

Thr Phe Ala Pro Thr His Leu Gly Thr Gln Pro Ser Glu Trp Thr Asn
    210                 215                 220

Glu Asp Gly Glu Thr Val Ala Ala Leu Ser Asn Met Tyr Glu Thr Ala
225                 230                 235                 240

Phe Ala Phe Tyr Asp Ser Leu Ala Glu Glu Gln Gln Ala Gln Leu Tyr
                245                 250                 255

Gln Gly Glu Glu Leu Asp Ser Met Val Cys Ala Pro Gly Ser Thr Cys
            260                 265                 270

Asp Tyr Pro Thr Gly Thr Gly Leu Lys Gly Ser Asp Leu Thr Asp Glu
        275                 280                 285

Gln Lys Glu Leu Leu Ile Asp Val Ile Ala Asn Trp Val Gly Leu Ala
    290                 295                 300
```

```
Asp Glu Glu Thr Thr Glu Thr Glu Leu Asp Ala Ile Arg Glu Thr Leu
305                 310                 315                 320

Asp Asp Thr Tyr Ile Asn Trp Ser Gly Ala Thr Glu Tyr Asp Thr Ser
                325                 330                 335

Thr Gly Asp Gly Ile Tyr Phe Gln Ile Ser Gly Pro Lys Val Tyr Ile
            340                 345                 350

Glu Phe Ala Asn Gln Gln Gly Ser Ala Gly Ala Asp Ile Asp Gly Val
        355                 360                 365

Ile Thr Ala Gly Trp Gly His Ile His Thr Ile Tyr Arg Asp Pro Thr
    370                 375                 380

Asn Asp Tyr Ala Asn Ser Val Thr Gln Glu Ala Ala Ser Gly Met Met
385                 390                 395                 400

Gly Gly Gly Pro Gly Gly Asn Gly Gly Glu Met Pro Ser Gly Asp Met
                405                 410                 415

Pro Thr Gly Glu Met Pro Ser Gly Ala Pro Ser Asn
            420                 425


<210> 1257
<211> 1407
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1384)
<223> FRXA02680

<400> 1257
aataccaggt caacacacac aggaaccgtt cagaaacctt ccagattgct cacttttaa 60

tttcactttt ttgagaagtt ttacttttat attagttctc atg cgc ctc aac aaa   115
                                            Met Arg Leu Asn Lys
                                              1               5

cga ctc cca gcg gca ctc tcc gga ctg ctg ctc tct gct gcc ctt ctt   163
Arg Leu Pro Ala Ala Leu Ser Gly Leu Leu Leu Ser Ala Ala Leu Leu
                10                  15                  20

gcc gga tgc tcc act tct gga acc gcc gag acc acg aca aca acc gtt   211
Ala Gly Cys Ser Thr Ser Gly Thr Ala Glu Thr Thr Thr Thr Thr Val
            25                  30                  35

tca tct gct gcg gca tca aca acc act tcc acc tcc tct gct tcg tct   259
Ser Ser Ala Ala Ala Ser Thr Thr Thr Ser Thr Ser Ser Ala Ser Ser
        40                  45                  50

tcc tct tcc tcc tcc tct tcc tcc tct tcc tcc gac tca agc acc acc   307
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Thr Thr
    55                  60                  65

gcc gaa acc atc tcc aac acc gcg gaa gct gcc caa gct ttc ttg tcc   355
Ala Glu Thr Ile Ser Asn Thr Ala Glu Ala Ala Gln Ala Phe Leu Ser
```

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 70                  75                  80                  85

acc ctg tcc acc gaa gaa caa gac gcc gta ctc tac gac tac gac gcc   403
Thr Leu Ser Thr Glu Glu Gln Asp Ala Val Leu Tyr Asp Tyr Asp Ala
                 90                  95                 100

gaa gaa aag tcc acc ggc tgg tct aac ttc cca gtc acc ttc gtg cag   451
Glu Glu Lys Ser Thr Gly Trp Ser Asn Phe Pro Val Thr Phe Val Gln
            105                 110                 115

cgt tcc ggc gtg aac ctc acc gac ctc act gag gaa cag caa gca gct   499
Arg Ser Gly Val Asn Leu Thr Asp Leu Thr Glu Glu Gln Gln Ala Ala
        120                 125                 130

gcc ctc aac gtg ctg aag aac ctg ctc aac gac gac gcc tac caa atg   547
Ala Leu Asn Val Leu Lys Asn Leu Leu Asn Asp Asp Ala Tyr Gln Met
    135                 140                 145

atc gaa gac atc atg gct agc gat cag tac ctc aac gac gaa agc aac   595
Ile Glu Asp Ile Met Ala Ser Asp Gln Tyr Leu Asn Asp Glu Ser Asn
150                 155                 160                 165

acc acc gag gat tcc ctc ggc cag tac tac atc gca ttc ttc ggc gat   643
Thr Thr Glu Asp Ser Leu Gly Gln Tyr Tyr Ile Ala Phe Phe Gly Asp
                170                 175                 180

cca agc agc gac tcc gac tgg tcc atc caa ttc ggc gga cac cac atc   691
Pro Ser Ser Asp Ser Asp Trp Ser Ile Gln Phe Gly Gly His His Ile
            185                 190                 195

ggc atc aac acc acc ttc tcc gac ggt gcc atc acc ttc gcc cca acc   739
Gly Ile Asn Thr Thr Phe Ser Asp Gly Ala Ile Thr Phe Ala Pro Thr
        200                 205                 210

cac ctt ggc acc cag cct tcc gag tgg acc aac gag gac ggc gaa acc   787
His Leu Gly Thr Gln Pro Ser Glu Trp Thr Asn Glu Asp Gly Glu Thr
    215                 220                 225

gtt gca gca cta agc aac atg tac gaa acc gcc ttc gcc ttc tac gac   835
Val Ala Ala Leu Ser Asn Met Tyr Glu Thr Ala Phe Ala Phe Tyr Asp
230                 235                 240                 245

agc ctc gcc gaa gag cag caa gca cag ctc tac cag ggt gaa gag ttg   883
Ser Leu Ala Glu Glu Gln Gln Ala Gln Leu Tyr Gln Gly Glu Glu Leu
                250                 255                 260

gat tcc atg gtg tgc gca ccg ggc agc acg tgc gac tac cca acc ggc   931
Asp Ser Met Val Cys Ala Pro Gly Ser Thr Cys Asp Tyr Pro Thr Gly
            265                 270                 275

acc ggc ttg aaa ggc tct gac ctc acc gat gag caa aaa gaa ttg ctc   979
Thr Gly Leu Lys Gly Ser Asp Leu Thr Asp Glu Gln Lys Glu Leu Leu
        280                 285                 290

atc gat gtc atc gca aac tgg gtt ggc ctc gcc gat gag gaa acc acc   1027
Ile Asp Val Ile Ala Asn Trp Val Gly Leu Ala Asp Glu Glu Thr Thr
    295                 300                 305

gaa act gaa ctc gat gcc atc cgc gaa acc ctg gat gac acc tac atc   1075
Glu Thr Glu Leu Asp Ala Ile Arg Glu Thr Leu Asp Asp Thr Tyr Ile
310                 315                 320                 325
```

```
aac tgg tcc ggc gcc acc gag tac gac acc tcc acc ggc gac ggc atc   1123
Asn Trp Ser Gly Ala Thr Glu Tyr Asp Thr Ser Thr Gly Asp Gly Ile
                330                 335                 340

tac ttc cag atc agt ggc cca aag gtc tac att gag ttc gct aac cag   1171
Tyr Phe Gln Ile Ser Gly Pro Lys Val Tyr Ile Glu Phe Ala Asn Gln
            345                 350                 355

caa ggt tct gca ggt gcc gac atc gac ggt gtc atc acc gct gga tgg   1219
Gln Gly Ser Ala Gly Ala Asp Ile Asp Gly Val Ile Thr Ala Gly Trp
        360                 365                 370

ggc cac att cac acc atc tac cgc gac cca acc aat gac tac gct aac   1267
Gly His Ile His Thr Ile Tyr Arg Asp Pro Thr Asn Asp Tyr Ala Asn
    375                 380                 385

tcc gta act cag gaa gca gcc agc gga atg atg ggc ggc ggc cct ggt   1315
Ser Val Thr Gln Glu Ala Ala Ser Gly Met Met Gly Gly Gly Pro Gly
390                 395                 400                 405

ggt aat ggt ggc gag atg cct agc ggt gac atg cct act ggt gag atg   1363
Gly Asn Gly Gly Glu Met Pro Ser Gly Asp Met Pro Thr Gly Glu Met
                410                 415                 420

cct tct ggc gct cca tca aac taacgccatt taagaggccg aac             1407
Pro Ser Gly Ala Pro Ser Asn
            425
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<210> 1258
<211> 428
<212> PRT
<213> Corynebacterium glutamicum

<400> 1258

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Met Arg Leu Asn Lys Arg Leu Pro Ala Ala Leu Ser Gly Leu Leu Leu
  1               5                  10                  15

Ser Ala Ala Leu Leu Ala Gly Cys Ser Thr Ser Gly Thr Ala Glu Thr
             20                  25                  30

Thr Thr Thr Thr Val Ser Ser Ala Ala Ala Ser Thr Thr Thr Ser Thr
         35                  40                  45

Ser Ser Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
     50                  55                  60

Asp Ser Ser Thr Thr Ala Glu Thr Ile Ser Asn Thr Ala Glu Ala Ala
 65                  70                  75                  80

Gln Ala Phe Leu Ser Thr Leu Ser Thr Glu Glu Gln Asp Ala Val Leu
                 85                  90                  95

Tyr Asp Tyr Asp Ala Glu Glu Lys Ser Thr Gly Trp Ser Asn Phe Pro
            100                 105                 110

Val Thr Phe Val Gln Arg Ser Gly Val Asn Leu Thr Asp Leu Thr Glu
        115                 120                 125

Glu Gln Gln Ala Ala Ala Leu Asn Val Leu Lys Asn Leu Leu Asn Asp
```

```
    130                 135                 140

Asp Ala Tyr Gln Met Ile Glu Asp Ile Met Ala Ser Asp Gln Tyr Leu
145                 150                 155                 160

Asn Asp Glu Ser Asn Thr Thr Glu Asp Ser Leu Gly Gln Tyr Tyr Ile
                165                 170                 175

Ala Phe Phe Gly Asp Pro Ser Ser Asp Ser Asp Trp Ser Ile Gln Phe
            180                 185                 190

Gly Gly His His Ile Gly Ile Asn Thr Thr Phe Ser Asp Gly Ala Ile
        195                 200                 205

Thr Phe Ala Pro Thr His Leu Gly Thr Gln Pro Ser Glu Trp Thr Asn
    210                 215                 220

Glu Asp Gly Glu Thr Val Ala Ala Leu Ser Asn Met Tyr Glu Thr Ala
225                 230                 235                 240

Phe Ala Phe Tyr Asp Ser Leu Ala Glu Glu Gln Gln Ala Gln Leu Tyr
                245                 250                 255

Gln Gly Glu Glu Leu Asp Ser Met Val Cys Ala Pro Gly Ser Thr Cys
            260                 265                 270

Asp Tyr Pro Thr Gly Thr Gly Leu Lys Gly Ser Asp Leu Thr Asp Glu
        275                 280                 285

Gln Lys Glu Leu Leu Ile Asp Val Ile Ala Asn Trp Val Gly Leu Ala
    290                 295                 300

Asp Glu Glu Thr Thr Glu Thr Glu Leu Asp Ala Ile Arg Glu Thr Leu
305                 310                 315                 320

Asp Asp Thr Tyr Ile Asn Trp Ser Gly Ala Thr Glu Tyr Asp Thr Ser
                325                 330                 335

Thr Gly Asp Gly Ile Tyr Phe Gln Ile Ser Gly Pro Lys Val Tyr Ile
            340                 345                 350

Glu Phe Ala Asn Gln Gln Gly Ser Ala Gly Ala Asp Ile Asp Gly Val
        355                 360                 365

Ile Thr Ala Gly Trp Gly His Ile His Thr Ile Tyr Arg Asp Pro Thr
    370                 375                 380

Asn Asp Tyr Ala Asn Ser Val Thr Gln Glu Ala Ala Ser Gly Met Met
385                 390                 395                 400

Gly Gly Gly Pro Gly Gly Asn Gly Gly Glu Met Pro Ser Gly Asp Met
                405                 410                 415

Pro Thr Gly Glu Met Pro Ser Gly Ala Pro Ser Asn
            420                 425
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<210> 1259
<211> 549
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(526)
<223> FRXA02679

<400> 1259
caccattacc accagggccg ccgcccatca ttccgctggc tgcttcctga gttacggagt 60

tagcgtagtc attggttggg tcgcggtaga tggtgtgaat gtg gcc cca tcc agc 115
Val Ala Pro Ser Ser
1 5

ggt gat gac acc gtc gat gtc ggc acc tgc aga acc ttg ctg gtt agc 163
Gly Asp Asp Thr Val Asp Val Gly Thr Cys Arg Thr Leu Leu Val Ser
10 15 20

gaa ctc aat gta gac ctt tgg gcc act gat ctg gaa gta gat gcc gtc 211
Glu Leu Asn Val Asp Leu Trp Ala Thr Asp Leu Glu Val Asp Ala Val
25 30 35

gcc ggt gga ggt gtc gta ctc ggt ggc gcc gga cca gtt gat gta ggt 259
Ala Gly Gly Gly Val Val Leu Gly Gly Ala Gly Pro Val Asp Val Gly
40 45 50

gtc atc cag ggt ttc gcg gat ggc atc gag ttc agt ttc ggt ggt ttc 307
Val Ile Gln Gly Phe Ala Asp Gly Ile Glu Phe Ser Phe Gly Gly Phe
55 60 65

ctc atc ggc gag gcc aac cca gtt tgc gat gac atc gat gag caa ttc 355
Leu Ile Gly Glu Ala Asn Pro Val Cys Asp Asp Ile Asp Glu Gln Phe
70 75 80 85

ttt ttg ctc atc ggt gag gtc aga gcc ttt caa gcc ggt gcc ggt tgg 403
Phe Leu Leu Ile Gly Glu Val Arg Ala Phe Gln Ala Gly Ala Gly Trp
90 95 100

gta gtc gca cgt gct gcc cgg tgc gca cac cat gga atc caa ctc ttc 451
Val Val Ala Arg Ala Ala Arg Cys Ala His His Gly Ile Gln Leu Phe
105 110 115

acc ctg gta gag ctg tgc ttg ctg ctc ttc ggc gag gct gtc gta gaa 499
Thr Leu Val Glu Leu Cys Leu Leu Leu Phe Gly Glu Ala Val Val Glu
120 125 130

ggc gaa ggc ggt ttc gta cat gtt gct tagtgctgca acggtttcgc 546
Gly Glu Gly Gly Phe Val His Val Ala
135 140

cgt 549

<210> 1260
<211> 142
<212> PRT
<213> Corynebacterium glutamicum

<400> 1260
Val Ala Pro Ser Ser Gly Asp Asp Thr Val Asp Val Gly Thr Cys Arg
1 5 10 15

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Thr Leu Leu Val Ser Glu Leu Asn Val Asp Leu Trp Ala Thr Asp Leu
            20                  25                  30

Glu Val Asp Ala Val Ala Gly Gly Gly Val Val Leu Gly Gly Ala Gly
        35                  40                  45

Pro Val Asp Val Gly Val Ile Gln Gly Phe Ala Asp Gly Ile Glu Phe
    50                  55                  60

Ser Phe Gly Gly Phe Leu Ile Gly Glu Ala Asn Pro Val Cys Asp Asp
65                  70                  75                  80

Ile Asp Glu Gln Phe Phe Leu Leu Ile Gly Glu Val Arg Ala Phe Gln
                85                  90                  95

Ala Gly Ala Gly Trp Val Val Ala Arg Ala Ala Arg Cys Ala His His
            100                 105                 110

Gly Ile Gln Leu Phe Thr Leu Val Glu Leu Cys Leu Leu Leu Phe Gly
        115                 120                 125

Glu Ala Val Val Glu Gly Glu Gly Gly Phe Val His Val Ala
    130                 135                 140
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Patent Application Publication

<210> 1261
<211> 567
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(544)
<223> FRXA02681

<400> 1261

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cgccgtcctc gttggtccac tcggaaggct gggtgccaag gtg ggt tgg ggc gaa   115
                                            Val Gly Trp Gly Glu
                                              1               5

ggt gat ggc acc gtc gga gaa ggt ggt gtt gat gcc gat gtg gtg tcc   163
Gly Asp Gly Thr Val Gly Glu Gly Gly Val Asp Ala Asp Val Val Ser
                10                  15                  20

gcc gaa ttg gat gga cca gtc gga gtc gct gct tgg atc gcc gaa gaa   211
Ala Glu Leu Asp Gly Pro Val Gly Val Ala Ala Trp Ile Ala Glu Glu
            25                  30                  35

tgc gat gta gta ctg gcc gag gga atc ctc ggt ggt gtt gct ttc gtc   259
Cys Asp Val Val Leu Ala Glu Gly Ile Leu Gly Gly Val Ala Phe Val
        40                  45                  50

gtt gag gta ctg atc gct agc cat gat gtc ttc gat cat ttg gta ggc   307
Val Glu Val Leu Ile Ala Ser His Asp Val Phe Asp His Leu Val Gly
    55                  60                  65

gtc gtc gtt gag cag gtt ctt cag cac gtt gag ggc agc tgc ttg ctg   355
Val Val Val Glu Gln Val Leu Gln His Val Glu Gly Ser Cys Leu Leu
70                  75                  80                  85
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ttc ctc agt gag gtc ggt gag gtt cac gcc gga acg ctg cac gaa ggt   403
Phe Leu Ser Glu Val Gly Glu Val His Ala Gly Thr Leu His Glu Gly
                 90                  95                 100

gac tgg gaa gtt aga cca gcc ggt gga ctt ttc ttc ggc gtc gta gtc   451
Asp Trp Glu Val Arg Pro Ala Gly Gly Leu Phe Phe Gly Val Val Val
            105                 110                 115

gta gag tac ggc gtc ttg ttc ttc ggt gga cag ggt gga caa gaa agc   499
Val Glu Tyr Gly Val Leu Phe Phe Gly Gly Gln Gly Gly Gln Glu Ser
        120                 125                 130

ttg ggc agc ttc cgc ggt gtt gga gat ggt ttc ggc ggt ggt gct       544
Leu Gly Ser Phe Arg Gly Val Gly Asp Gly Phe Gly Gly Gly Ala
    135                 140                 145

tgagtcggag gaagaggagg aag                                        567
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<210> 1262
<211> 148
<212> PRT
<213> Corynebacterium glutamicum

<400> 1262

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Val Gly Trp Gly Glu Gly Asp Gly Thr Val Gly Glu Gly Gly Val Asp
  1               5                  10                  15

Ala Asp Val Val Ser Ala Glu Leu Asp Gly Pro Val Gly Val Ala Ala
             20                  25                  30

Trp Ile Ala Glu Glu Cys Asp Val Val Leu Ala Glu Gly Ile Leu Gly
         35                  40                  45

Gly Val Ala Phe Val Val Glu Val Leu Ile Ala Ser His Asp Val Phe
     50                  55                  60

Asp His Leu Val Gly Val Val Val Glu Gln Val Leu Gln His Val Glu
 65                  70                  75                  80

Gly Ser Cys Leu Leu Phe Leu Ser Glu Val Gly Glu Val His Ala Gly
                 85                  90                  95

Thr Leu His Glu Gly Asp Trp Glu Val Arg Pro Ala Gly Gly Leu Phe
            100                 105                 110

Phe Gly Val Val Val Val Glu Tyr Gly Val Leu Phe Phe Gly Gly Gln
        115                 120                 125

Gly Gly Gln Glu Ser Leu Gly Ser Phe Arg Gly Val Gly Asp Gly Phe
    130                 135                 140

Gly Gly Gly Ala
145
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<210> 1263
<211> 1899
<212> DNA
<213> Corynebacterium glutamicum

Confidential - Subject to Protective Order

<220>
<221> CDS
<222> (101)..(1876)
<223> RXN02693

<400> 1263
cagaccaagt gttatttttg ttgaaaaaat cacattgtaa atcgagcaaa accaacctat 60

gccctgcaga attgtgcatg ctctgccaag atgactcaat atg gtt tcg ctc ccc 115
Met Val Ser Leu Pro
1 5

aga cta gcg tct ctg ctc acc act cgc ctg gca acg ctt aaa ccc gca 163
Arg Leu Ala Ser Leu Leu Thr Thr Arg Leu Ala Thr Leu Lys Pro Ala
10 15 20

cta aaa cct gcc acc cac ctc gcc tcc ctc ggc gcg cag gtc att gca 211
Leu Lys Pro Ala Thr His Leu Ala Ser Leu Gly Ala Gln Val Ile Ala
25 30 35

gag cta gtt ccg ggg atc cga atg tcg cca aac cgc agg cga atc ctc 259
Glu Leu Val Pro Gly Ile Arg Met Ser Pro Asn Arg Arg Arg Ile Leu
40 45 50

cct gca aat atg ggc gct ggc ttt atc gga gcg gaa atc gca atg tgg 307
Pro Ala Asn Met Gly Ala Gly Phe Ile Gly Ala Glu Ile Ala Met Trp
55 60 65

tgg gct ctc tcg ccg tca ttg ttg ccg aaa ccg tgg tgg gtt acg gct 355
Trp Ala Leu Ser Pro Ser Leu Leu Pro Lys Pro Trp Trp Val Thr Ala
70 75 80 85

gct aac ctg gct gtt tta caa gcg gtg ggg cat gcg gca gcg acg gga 403
Ala Asn Leu Ala Val Leu Gln Ala Val Gly His Ala Ala Ala Thr Gly
90 95 100

atc cac tcg atc ctc ccc aga acc aac cgg cgg gta tcc agg aaa att 451
Ile His Ser Ile Leu Pro Arg Thr Asn Arg Arg Val Ser Arg Lys Ile
105 110 115

tac aac gcc acc cac atc gca act ggt gcc atc acg ttg acc acc acg 499
Tyr Asn Ala Thr His Ile Ala Thr Gly Ala Ile Thr Leu Thr Thr Thr
120 125 130

gtt gtg gga ttg atc agg cat cgc acc caa atc cgg ctg att ggg cag 547
Val Val Gly Leu Ile Arg His Arg Thr Gln Ile Arg Leu Ile Gly Gln
135 140 145

aag aat ttt gga ccg aag gag acg atc gcg ggc att agt gtc ggc acc 595
Lys Asn Phe Gly Pro Lys Glu Thr Ile Ala Gly Ile Ser Val Gly Thr
150 155 160 165

ttg ggg tac ggc gcg ctg ctg atc acc ggc gaa tta acc cag cac agt 643
Leu Gly Tyr Gly Ala Leu Leu Ile Thr Gly Glu Leu Thr Gln His Ser
170 175 180

att aat gag gtc aag ctc cta att gag agg ttt tta ccg ccg tgg ata 691
Ile Asn Glu Val Lys Leu Leu Ile Glu Arg Phe Leu Pro Pro Trp Ile
185 190 195

```
agt ttc atc gca gcg gtt tcg gtc att aca ttg acc act ttg acc ttg   739
Ser Phe Ile Ala Ala Val Ser Val Ile Thr Leu Thr Thr Leu Thr Leu
        200                 205                 210

gcc gat cgc gtt ttg ttg cgg cgc atc ttg cat aat tct gca att caa   787
Ala Asp Arg Val Leu Leu Arg Arg Ile Leu His Asn Ser Ala Ile Gln
    215                 220                 225

gca gcg cac ctt aat cgc atg gtg ttc cca gga act gag cag ccg tgg   835
Ala Ala His Leu Asn Arg Met Val Phe Pro Gly Thr Glu Gln Pro Trp
230                 235                 240                 245

gag ccg gag cgt tcg ggt agc ccg tgg tcg tat gaa aaa tgg ggt gcg   883
Glu Pro Glu Arg Ser Gly Ser Pro Trp Ser Tyr Glu Lys Trp Gly Ala
                250                 255                 260

gtg ggt tcg cag ggc cgt gca gtg ttg tcg gga ggc cca cgc aaa gat   931
Val Gly Ser Gln Gly Arg Ala Val Leu Ser Gly Gly Pro Arg Lys Asp
            265                 270                 275

gac atc atc acg gta acc agg ctt tct gac acg gaa aca cat gaa ccg   979
Asp Ile Ile Thr Val Thr Arg Leu Ser Asp Thr Glu Thr His Glu Pro
        280                 285                 290

att cgt att ttt atc ggt atg gtt ccg gga cga tcc tta agc gat cag   1027
Ile Arg Ile Phe Ile Gly Met Val Pro Gly Arg Ser Leu Ser Asp Gln
    295                 300                 305

gtg gat ctt gtc att cat gaa atg cgc cgc acg gga gcc ctg cgc cgc   1075
Val Asp Leu Val Ile His Glu Met Arg Arg Thr Gly Ala Leu Arg Arg
310                 315                 320                 325

gac cac atc gtg atc aac aat tcc acg ggc acc ggc tgg atc acc gat   1123
Asp His Ile Val Ile Asn Asn Ser Thr Gly Thr Gly Trp Ile Thr Asp
                330                 335                 340

tgg tcc gcc cac acc ttt gag ttc ctc acc ggc gga aac tgc gtg aca   1171
Trp Ser Ala His Thr Phe Glu Phe Leu Thr Gly Gly Asn Cys Val Thr
            345                 350                 355

att tcc atg caa tat tct tat ctt ccc agt gca ctg agc tgg tac aag   1219
Ile Ser Met Gln Tyr Ser Tyr Leu Pro Ser Ala Leu Ser Trp Tyr Lys
        360                 365                 370

gac aac gac ggc ccc att aat gcg gcg aga atg ctt atc gac gcc gtc   1267
Asp Asn Asp Gly Pro Ile Asn Ala Ala Arg Met Leu Ile Asp Ala Val
    375                 380                 385

ctc cac gag cta gac cag ctt ccc acc ggg agt cgc cca aag ctg ttc   1315
Leu His Glu Leu Asp Gln Leu Pro Thr Gly Ser Arg Pro Lys Leu Phe
390                 395                 400                 405

ctc gcg gga gag tca ctg ggg gcg tat ggg ttg gct gag gtg tgg gga   1363
Leu Ala Gly Glu Ser Leu Gly Ala Tyr Gly Leu Ala Glu Val Trp Gly
                410                 415                 420

gac gtc gaa aag ctt ctt gga acc gct gac ggc gtg ctg ctc agt ggg   1411
Asp Val Glu Lys Leu Leu Gly Thr Ala Asp Gly Val Leu Leu Ser Gly
            425                 430                 435

gcg ccg cgt ttt tcg gac gcc atg aat gcg ttg cgc acc cgg cgc gat   1459
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```
Ala Pro Arg Phe Ser Asp Ala Met Asn Ala Leu Arg Thr Arg Arg Asp
        440                 445                 450

gcg agc agc tcc gag cgg ctg ccc gtg att gat agc ggg cgg cac atc   1507
Ala Ser Ser Ser Glu Arg Leu Pro Val Ile Asp Ser Gly Arg His Ile
    455                 460                 465

cgt ttt gcg ggc gag cct gag cac ctt gat atg ccg gct acc tgg cag   1555
Arg Phe Ala Gly Glu Pro Glu His Leu Asp Met Pro Ala Thr Trp Gln
470                 475                 480                 485

ttt ccg cgc atg atc gtg gcg cag cac gcc tct gat cca att gtg tgg   1603
Phe Pro Arg Met Ile Val Ala Gln His Ala Ser Asp Pro Ile Val Trp
                490                 495                 500

tgg aac gcg gag ctg ttt att cgg cgg ccg gaa tgg ttg aaa act ccc   1651
Trp Asn Ala Glu Leu Phe Ile Arg Arg Pro Glu Trp Leu Lys Thr Pro
            505                 510                 515

aag caa gac cac caa gat gtc ttt ccc cgc ttg cga tgg atg ccg ttt   1699
Lys Gln Asp His Gln Asp Val Phe Pro Arg Leu Arg Trp Met Pro Phe
        520                 525                 530

gta acc ggc tgg cag gtg gct ttg gat ttg ttc act tca acc tcc gtt   1747
Val Thr Gly Trp Gln Val Ala Leu Asp Leu Phe Thr Ser Thr Ser Val
    535                 540                 545

ccc ggc ggg cac ggg cac aat tat cac gag gag ttt att gat tat tgg   1795
Pro Gly Gly His Gly His Asn Tyr His Glu Glu Phe Ile Asp Tyr Trp
550                 555                 560                 565

gca gct ctt ttg gac cgc gaa gtc acc ccc gag ctg cgc cac agc att   1843
Ala Ala Leu Leu Asp Arg Glu Val Thr Pro Glu Leu Arg His Ser Ile
                570                 575                 580

gct tat tgg atc cgc gcg aac cac atc aaa cgc tagagtgatt ccatgacgca 1896
Ala Tyr Trp Ile Arg Ala Asn His Ile Lys Arg
            585                 590

tgc                                                               1899
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<210> 1264
<211> 592
<212> PRT
<213> Corynebacterium glutamicum

<400> 1264

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Met Val Ser Leu Pro Arg Leu Ala Ser Leu Leu Thr Thr Arg Leu Ala
  1               5                  10                  15

Thr Leu Lys Pro Ala Leu Lys Pro Ala Thr His Leu Ala Ser Leu Gly
             20                  25                  30

Ala Gln Val Ile Ala Glu Leu Val Pro Gly Ile Arg Met Ser Pro Asn
         35                  40                  45

Arg Arg Arg Ile Leu Pro Ala Asn Met Gly Ala Gly Phe Ile Gly Ala
     50                  55                  60

Glu Ile Ala Met Trp Trp Ala Leu Ser Pro Ser Leu Leu Pro Lys Pro
```

```
65                  70                  75                  80

Trp Trp Val Thr Ala Ala Asn Leu Ala Val Leu Gln Ala Val Gly His
                85                  90                  95

Ala Ala Ala Thr Gly Ile His Ser Ile Leu Pro Arg Thr Asn Arg Arg
            100                 105                 110

Val Ser Arg Lys Ile Tyr Asn Ala Thr His Ile Ala Thr Gly Ala Ile
        115                 120                 125

Thr Leu Thr Thr Thr Val Val Gly Leu Ile Arg His Arg Thr Gln Ile
    130                 135                 140

Arg Leu Ile Gly Gln Lys Asn Phe Gly Pro Lys Glu Thr Ile Ala Gly
145                 150                 155                 160

Ile Ser Val Gly Thr Leu Gly Tyr Gly Ala Leu Leu Ile Thr Gly Glu
                165                 170                 175

Leu Thr Gln His Ser Ile Asn Glu Val Lys Leu Leu Ile Glu Arg Phe
            180                 185                 190

Leu Pro Pro Trp Ile Ser Phe Ile Ala Ala Val Ser Val Ile Thr Leu
        195                 200                 205

Thr Thr Leu Thr Leu Ala Asp Arg Val Leu Leu Arg Arg Ile Leu His
    210                 215                 220

Asn Ser Ala Ile Gln Ala Ala His Leu Asn Arg Met Val Phe Pro Gly
225                 230                 235                 240

Thr Glu Gln Pro Trp Glu Pro Glu Arg Ser Gly Ser Pro Trp Ser Tyr
                245                 250                 255

Glu Lys Trp Gly Ala Val Gly Ser Gln Gly Arg Ala Val Leu Ser Gly
            260                 265                 270

Gly Pro Arg Lys Asp Asp Ile Ile Thr Val Thr Arg Leu Ser Asp Thr
        275                 280                 285

Glu Thr His Glu Pro Ile Arg Ile Phe Ile Gly Met Val Pro Gly Arg
    290                 295                 300

Ser Leu Ser Asp Gln Val Asp Leu Val Ile His Glu Met Arg Arg Thr
305                 310                 315                 320

Gly Ala Leu Arg Arg Asp His Ile Val Ile Asn Asn Ser Thr Gly Thr
                325                 330                 335

Gly Trp Ile Thr Asp Trp Ser Ala His Thr Phe Glu Phe Leu Thr Gly
            340                 345                 350

Gly Asn Cys Val Thr Ile Ser Met Gln Tyr Ser Tyr Leu Pro Ser Ala
        355                 360                 365

Leu Ser Trp Tyr Lys Asp Asn Asp Gly Pro Ile Asn Ala Ala Arg Met
    370                 375                 380

Leu Ile Asp Ala Val Leu His Glu Leu Asp Gln Leu Pro Thr Gly Ser
385                 390                 395                 400
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```
Arg Pro Lys Leu Phe Leu Ala Gly Glu Ser Leu Gly Ala Tyr Gly Leu
                405                 410                 415

Ala Glu Val Trp Gly Asp Val Glu Lys Leu Leu Gly Thr Ala Asp Gly
            420                 425                 430

Val Leu Leu Ser Gly Ala Pro Arg Phe Ser Asp Ala Met Asn Ala Leu
        435                 440                 445

Arg Thr Arg Arg Asp Ala Ser Ser Ser Glu Arg Leu Pro Val Ile Asp
    450                 455                 460

Ser Gly Arg His Ile Arg Phe Ala Gly Glu Pro Glu His Leu Asp Met
465                 470                 475                 480

Pro Ala Thr Trp Gln Phe Pro Arg Met Ile Val Ala Gln His Ala Ser
                485                 490                 495

Asp Pro Ile Val Trp Trp Asn Ala Glu Leu Phe Ile Arg Arg Pro Glu
            500                 505                 510

Trp Leu Lys Thr Pro Lys Gln Asp His Gln Asp Val Phe Pro Arg Leu
        515                 520                 525

Arg Trp Met Pro Phe Val Thr Gly Trp Gln Val Ala Leu Asp Leu Phe
    530                 535                 540

Thr Ser Thr Ser Val Pro Gly Gly His Gly His Asn Tyr His Glu Glu
545                 550                 555                 560

Phe Ile Asp Tyr Trp Ala Ala Leu Leu Asp Arg Glu Val Thr Pro Glu
                565                 570                 575

Leu Arg His Ser Ile Ala Tyr Trp Ile Arg Ala Asn His Ile Lys Arg
            580                 585                 590
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<210> 1265
<211> 1747
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1747)
<223> FRXA02693

<400> 1265

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cagaccaagt gttatttttg ttgaaaaaat cacattgtaa atcgagcaaa accaacctat 60

gccctgcaga attgtgcatg ctctgccaag atgactcaat atg gtt tcg ctc ccc   115
                                            Met Val Ser Leu Pro
                                              1               5

aga cta gcg tct ctg ctc acc act cgc ctg gca acg ctt aaa ccc gca   163
Arg Leu Ala Ser Leu Leu Thr Thr Arg Leu Ala Thr Leu Lys Pro Ala
                10                  15                  20
```

```
cta aaa cct gcc acc cac ctc gcc tcc ctc ggc gcg cag gtc att gca   211
Leu Lys Pro Ala Thr His Leu Ala Ser Leu Gly Ala Gln Val Ile Ala
            25                  30                  35

gag cta gtt ccg ggg atc cga atg tcg cca aac cgc agg cga atc ctc   259
Glu Leu Val Pro Gly Ile Arg Met Ser Pro Asn Arg Arg Arg Ile Leu
        40                  45                  50

cct gca aat atg ggc gct ggc ttt atc gga gcg gaa atc gca atg tgg   307
Pro Ala Asn Met Gly Ala Gly Phe Ile Gly Ala Glu Ile Ala Met Trp
    55                  60                  65

tgg gct ctc tcg ccg tca ttg ttg ccg aaa ccg tgg tgg gtt acg gct   355
Trp Ala Leu Ser Pro Ser Leu Leu Pro Lys Pro Trp Trp Val Thr Ala
70                  75                  80                  85

gct aac ctg gct gtt tta caa gcg gtg ggg cat gcg gca gcg acg gga   403
Ala Asn Leu Ala Val Leu Gln Ala Val Gly His Ala Ala Ala Thr Gly
                90                  95                  100

atc cac tcg atc ctc ccc aga acc aac cgg cgg gta tcc agg aaa att   451
Ile His Ser Ile Leu Pro Arg Thr Asn Arg Arg Val Ser Arg Lys Ile
            105                 110                 115

tac aac gcc acc cac atc gca act ggt gcc atc acg ttg acc acc acg   499
Tyr Asn Ala Thr His Ile Ala Thr Gly Ala Ile Thr Leu Thr Thr Thr
        120                 125                 130

gtt gtg gga ttg atc agg cat cgc acc caa atc cgg ctg att ggg cag   547
Val Val Gly Leu Ile Arg His Arg Thr Gln Ile Arg Leu Ile Gly Gln
    135                 140                 145

aag aat ttt gga ccg aag gag acg atc gcg ggc att agt gtc ggc acc   595
Lys Asn Phe Gly Pro Lys Glu Thr Ile Ala Gly Ile Ser Val Gly Thr
150                 155                 160                 165

ttg ggg tac ggc gcg ctg ctg atc acc ggc gaa tta acc cag cac agt   643
Leu Gly Tyr Gly Ala Leu Leu Ile Thr Gly Glu Leu Thr Gln His Ser
                170                 175                 180

att aat gag gtc aag ctc cta att gag agg ttt tta ccg ccg tgg ata   691
Ile Asn Glu Val Lys Leu Leu Ile Glu Arg Phe Leu Pro Pro Trp Ile
            185                 190                 195

agt ttc atc gca gcg gtt tcg gtc att aca ttg acc act ttg acc ttg   739
Ser Phe Ile Ala Ala Val Ser Val Ile Thr Leu Thr Thr Leu Thr Leu
        200                 205                 210

gcc gat cgc gtt ttg ttg cgg cgc atc ttg cat aat tct gca att caa   787
Ala Asp Arg Val Leu Leu Arg Arg Ile Leu His Asn Ser Ala Ile Gln
    215                 220                 225

gca gcg cac ctt aat cgc atg gtg ttc cca gga act gag cag ccg tgg   835
Ala Ala His Leu Asn Arg Met Val Phe Pro Gly Thr Glu Gln Pro Trp
230                 235                 240                 245

gag ccg gag cgt tcg ggt agc ccg tgg tcg tat gaa aaa tgg ggt gcg   883
Glu Pro Glu Arg Ser Gly Ser Pro Trp Ser Tyr Glu Lys Trp Gly Ala
                250                 255                 260
```

```
gtg ggt tcg cag ggc cgt gca gtg ttg tcg gga ggc cca cgc aaa gat   931
Val Gly Ser Gln Gly Arg Ala Val Leu Ser Gly Gly Pro Arg Lys Asp
            265                 270                 275

gac atc atc acg gta acc agg ctt tct gac acg gaa aca cat gaa ccg   979
Asp Ile Ile Thr Val Thr Arg Leu Ser Asp Thr Glu Thr His Glu Pro
        280                 285                 290

att cgt att ttt atc ggt atg gtt ccg gga cga tcc tta agc gat cag   1027
Ile Arg Ile Phe Ile Gly Met Val Pro Gly Arg Ser Leu Ser Asp Gln
    295                 300                 305

gtg gat ctt gtc att cat gaa atg cgc cgc acg gga gcc ctg cgc cgc   1075
Val Asp Leu Val Ile His Glu Met Arg Arg Thr Gly Ala Leu Arg Arg
310                 315                 320                 325

gac cac atc gtg atc aac aat tcc acg ggc acc ggc tgg atc acc gat   1123
Asp His Ile Val Ile Asn Asn Ser Thr Gly Thr Gly Trp Ile Thr Asp
                330                 335                 340

tgg tcc gcc cac acc ttt gag ttc ctc acc ggc gga aac tgc gtg aca   1171
Trp Ser Ala His Thr Phe Glu Phe Leu Thr Gly Gly Asn Cys Val Thr
            345                 350                 355

att tcc atg caa tat tct tat ctt ccc agt gca ctg agc tgg tac aag   1219
Ile Ser Met Gln Tyr Ser Tyr Leu Pro Ser Ala Leu Ser Trp Tyr Lys
        360                 365                 370

gac aac gac ggc ccc att aat gcg gcg aga atg ctt atc gac gcc gtc   1267
Asp Asn Asp Gly Pro Ile Asn Ala Ala Arg Met Leu Ile Asp Ala Val
    375                 380                 385

ctc cac gag cta gac cag ctt ccc acc ggg agt cgc cca aag ctg ttc   1315
Leu His Glu Leu Asp Gln Leu Pro Thr Gly Ser Arg Pro Lys Leu Phe
390                 395                 400                 405

ctc gcg gga gag tca ctg ggg gcg tat ggg ttg gct gag gtg tgg gga   1363
Leu Ala Gly Glu Ser Leu Gly Ala Tyr Gly Leu Ala Glu Val Trp Gly
                410                 415                 420

gac gtc gaa aag ctt ctt gga acc gct gac ggc gtg ctg ctc agt ggg   1411
Asp Val Glu Lys Leu Leu Gly Thr Ala Asp Gly Val Leu Leu Ser Gly
            425                 430                 435

gcg ccg cgt ttt tcg gac gcc atg aat gcg ttg cgc acc cgg cgc gat   1459
Ala Pro Arg Phe Ser Asp Ala Met Asn Ala Leu Arg Thr Arg Arg Asp
        440                 445                 450

gcg agc agc tcc gag cgg ctg ccc gtg att gat agc ggg cgg cac atc   1507
Ala Ser Ser Ser Glu Arg Leu Pro Val Ile Asp Ser Gly Arg His Ile
    455                 460                 465

cgt ttt gcg ggc gag cct gag cac ctt gat atg ccg gct acc tgg cag   1555
Arg Phe Ala Gly Glu Pro Glu His Leu Asp Met Pro Ala Thr Trp Gln
470                 475                 480                 485

ttt ccg cgc atg atc gtg gcg cag cac gcc tct gat cca att gtg tgg   1603
Phe Pro Arg Met Ile Val Ala Gln His Ala Ser Asp Pro Ile Val Trp
                490                 495                 500

tgg aac gcg gag ctg ttt att cgg cgg ccg gaa tgg ttg aaa act ccc   1651
```

```
Trp Asn Ala Glu Leu Phe Ile Arg Arg Pro Glu Trp Leu Lys Thr Pro
            505                 510                 515

aag caa gac cac caa gat gtc ttt aac cgc ttg cga tgg atg ccg ttt   1699
Lys Gln Asp His Gln Asp Val Phe Asn Arg Leu Arg Trp Met Pro Phe
        520                 525                 530

gtt gcc ggc tgg cag gtg gct ttg gat ttg ttc act tca acc tcc gtt   1747
Val Ala Gly Trp Gln Val Ala Leu Asp Leu Phe Thr Ser Thr Ser Val
    535                 540                 545
```

<210> 1266
<211> 549
<212> PRT
<213> Corynebacterium glutamicum

<400> 1266

```
Met Val Ser Leu Pro Arg Leu Ala Ser Leu Leu Thr Thr Arg Leu Ala
  1               5                  10                  15

Thr Leu Lys Pro Ala Leu Lys Pro Ala Thr His Leu Ala Ser Leu Gly
             20                  25                  30

Ala Gln Val Ile Ala Glu Leu Val Pro Gly Ile Arg Met Ser Pro Asn
         35                  40                  45

Arg Arg Arg Ile Leu Pro Ala Asn Met Gly Ala Gly Phe Ile Gly Ala
     50                  55                  60

Glu Ile Ala Met Trp Trp Ala Leu Ser Pro Ser Leu Leu Pro Lys Pro
 65                  70                  75                  80

Trp Trp Val Thr Ala Ala Asn Leu Ala Val Leu Gln Ala Val Gly His
                 85                  90                  95

Ala Ala Ala Thr Gly Ile His Ser Ile Leu Pro Arg Thr Asn Arg Arg
            100                 105                 110

Val Ser Arg Lys Ile Tyr Asn Ala Thr His Ile Ala Thr Gly Ala Ile
        115                 120                 125

Thr Leu Thr Thr Thr Val Val Gly Leu Ile Arg His Arg Thr Gln Ile
    130                 135                 140

Arg Leu Ile Gly Gln Lys Asn Phe Gly Pro Lys Glu Thr Ile Ala Gly
145                 150                 155                 160

Ile Ser Val Gly Thr Leu Gly Tyr Gly Ala Leu Leu Ile Thr Gly Glu
                165                 170                 175

Leu Thr Gln His Ser Ile Asn Glu Val Lys Leu Leu Ile Glu Arg Phe
            180                 185                 190

Leu Pro Pro Trp Ile Ser Phe Ile Ala Ala Val Ser Val Ile Thr Leu
        195                 200                 205

Thr Thr Leu Thr Leu Ala Asp Arg Val Leu Leu Arg Arg Ile Leu His
    210                 215                 220

Asn Ser Ala Ile Gln Ala Ala His Leu Asn Arg Met Val Phe Pro Gly
```

```
225                 230                 235                 240

Thr Glu Gln Pro Trp Glu Pro Glu Arg Ser Gly Ser Pro Trp Ser Tyr
                245                 250                 255

Glu Lys Trp Gly Ala Val Gly Ser Gln Gly Arg Ala Val Leu Ser Gly
            260                 265                 270

Gly Pro Arg Lys Asp Asp Ile Ile Thr Val Thr Arg Leu Ser Asp Thr
        275                 280                 285

Glu Thr His Glu Pro Ile Arg Ile Phe Ile Gly Met Val Pro Gly Arg
    290                 295                 300

Ser Leu Ser Asp Gln Val Asp Leu Val Ile His Glu Met Arg Arg Thr
305                 310                 315                 320

Gly Ala Leu Arg Arg Asp His Ile Val Ile Asn Asn Ser Thr Gly Thr
                325                 330                 335

Gly Trp Ile Thr Asp Trp Ser Ala His Thr Phe Glu Phe Leu Thr Gly
            340                 345                 350

Gly Asn Cys Val Thr Ile Ser Met Gln Tyr Ser Tyr Leu Pro Ser Ala
        355                 360                 365

Leu Ser Trp Tyr Lys Asp Asn Asp Gly Pro Ile Asn Ala Ala Arg Met
    370                 375                 380

Leu Ile Asp Ala Val Leu His Glu Leu Asp Gln Leu Pro Thr Gly Ser
385                 390                 395                 400

Arg Pro Lys Leu Phe Leu Ala Gly Glu Ser Leu Gly Ala Tyr Gly Leu
                405                 410                 415

Ala Glu Val Trp Gly Asp Val Glu Lys Leu Leu Gly Thr Ala Asp Gly
            420                 425                 430

Val Leu Leu Ser Gly Ala Pro Arg Phe Ser Asp Ala Met Asn Ala Leu
        435                 440                 445

Arg Thr Arg Arg Asp Ala Ser Ser Ser Glu Arg Leu Pro Val Ile Asp
    450                 455                 460

Ser Gly Arg His Ile Arg Phe Ala Gly Glu Pro Glu His Leu Asp Met
465                 470                 475                 480

Pro Ala Thr Trp Gln Phe Pro Arg Met Ile Val Ala Gln His Ala Ser
                485                 490                 495

Asp Pro Ile Val Trp Trp Asn Ala Glu Leu Phe Ile Arg Arg Pro Glu
            500                 505                 510

Trp Leu Lys Thr Pro Lys Gln Asp His Gln Asp Val Phe Asn Arg Leu
        515                 520                 525

Arg Trp Met Pro Phe Val Ala Gly Trp Gln Val Ala Leu Asp Leu Phe
    530                 535                 540

Thr Ser Thr Ser Val
545
```

<210> 1267
<211> 579
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> RXN02696

<400> 1267
cttgggaacc gaccgctagc gtagaaaatc aagttaaggg tgtgacgagc accccagctg 60

cacatgaaat ttaagacatt ccaggtgaag ggaaactgcc atg tcc atg ctc aag 115
Met Ser Met Leu Lys
1 5

aag act aaa gaa ttc ttc gga ctc gct cca tac gaa gcg gag cac gag 163
Lys Thr Lys Glu Phe Phe Gly Leu Ala Pro Tyr Glu Ala Glu His Glu
10 15 20

gat gct tac tat gca gat gaa cca cgt tac gag ggc acc gct gcg tac 211
Asp Ala Tyr Tyr Ala Asp Glu Pro Arg Tyr Glu Gly Thr Ala Ala Tyr
25 30 35

gca cct gaa tac cgt gag cgt gac tac ggc tat gca cca gag gca cca 259
Ala Pro Glu Tyr Arg Glu Arg Asp Tyr Gly Tyr Ala Pro Glu Ala Pro
40 45 50

gcc cct gtt gct cca tcg cca gca cct cgc tct tac cag tcc acc atc 307
Ala Pro Val Ala Pro Ser Pro Ala Pro Arg Ser Tyr Gln Ser Thr Ile
55 60 65

gtt cca gta gag ctt cat tcc ttt gaa gac gct cag gtt att ggt gga 355
Val Pro Val Glu Leu His Ser Phe Glu Asp Ala Gln Val Ile Gly Gly
70 75 80 85

gca ttt cgc gac ggc gac gca gtt gtt ttc gac atg agc ttg ctt tcc 403
Ala Phe Arg Asp Gly Asp Ala Val Val Phe Asp Met Ser Leu Leu Ser
90 95 100

cgt gag gaa gca cgc cgc att gtg gac ttc gct gca ggc ctg tgc ttc 451
Arg Glu Glu Ala Arg Arg Ile Val Asp Phe Ala Ala Gly Leu Cys Phe
105 110 115

gca ttg cgt ggc aag atg cag aag att gac agc gtc acc ttc gct gtc 499
Ala Leu Arg Gly Lys Met Gln Lys Ile Asp Ser Val Thr Phe Ala Val
120 125 130

gtt cca gag ctg tcc aac atc agc act tcc gag ctc gag cgc gcc gca 547
Val Pro Glu Leu Ser Asn Ile Ser Thr Ser Glu Leu Glu Arg Ala Ala
135 140 145

cgc atc cgc taaacacacc ctcgtggtgt gga 579
Arg Ile Arg
150

<210> 1268

<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 1268
Met Ser Met Leu Lys Lys Thr Lys Glu Phe Phe Gly Leu Ala Pro Tyr
1 5 10 15

Glu Ala Glu His Glu Asp Ala Tyr Tyr Ala Asp Glu Pro Arg Tyr Glu
20 25 30

Gly Thr Ala Ala Tyr Ala Pro Glu Tyr Arg Glu Arg Asp Tyr Gly Tyr
35 40 45

Ala Pro Glu Ala Pro Ala Pro Val Ala Pro Ser Pro Ala Pro Arg Ser
50 55 60

Tyr Gln Ser Thr Ile Val Pro Val Glu Leu His Ser Phe Glu Asp Ala
65 70 75 80

Gln Val Ile Gly Gly Ala Phe Arg Asp Gly Asp Ala Val Val Phe Asp
85 90 95

Met Ser Leu Leu Ser Arg Glu Glu Ala Arg Arg Ile Val Asp Phe Ala
100 105 110

Ala Gly Leu Cys Phe Ala Leu Arg Gly Lys Met Gln Lys Ile Asp Ser
115 120 125

Val Thr Phe Ala Val Val Pro Glu Leu Ser Asn Ile Ser Thr Ser Glu
130 135 140

Leu Glu Arg Ala Ala Arg Ile Arg
145 150

<210> 1269
<211> 578
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (100)..(555)
<223> FRXA02696

<400> 1269
ngcttnaaga aataaagccc tncccagtta anggtgngna tgggtaccag ccctgtggac 60

gctgtacatn taagtcattn ctggttnagg tganctgccatg tcc atg ctc aag aag 117
Met Ser Met Leu Lys Lys
1 5

act aaa gaa ttc ttc gga ctc gct cca tac gaa gcg gag cac gag gat 165
Thr Lys Glu Phe Phe Gly Leu Ala Pro Tyr Glu Ala Glu His Glu Asp
10 15 20

gct tac tat gca gat gaa cca cgt tac gag ggc acc gct gcg tac gca 213
Ala Tyr Tyr Ala Asp Glu Pro Arg Tyr Glu Gly Thr Ala Ala Tyr Ala
25 30 35

```
cct gaa tac cgt gag cgt gac tac ggc tat gca cca gag gca cca gcc   261
Pro Glu Tyr Arg Glu Arg Asp Tyr Gly Tyr Ala Pro Glu Ala Pro Ala
     40                  45                  50

cct gtt gct cca tcg cca gca cct cgc tct tac cag tcc acc atc gtt   309
Pro Val Ala Pro Ser Pro Ala Pro Arg Ser Tyr Gln Ser Thr Ile Val
 55                  60                  65                  70

cca gta gag ctt cat tcc ttt gaa gac gct cag gtt att ggt gga gca   357
Pro Val Glu Leu His Ser Phe Glu Asp Ala Gln Val Ile Gly Gly Ala
                75                  80                  85

ttt cgc gac ggc gac gca gtt gtt ttc gac atg agc ttg ctt tcc cgt   405
Phe Arg Asp Gly Asp Ala Val Val Phe Asp Met Ser Leu Leu Ser Arg
            90                  95                  100

gag gaa gca cgc cgc att gtg gac ttc gct gca ggc ctg tgc ttc gca   453
Glu Glu Ala Arg Arg Ile Val Asp Phe Ala Ala Gly Leu Cys Phe Ala
        105                 110                 115

ttg cgt ggc aag atg cag aag att gac agc gtc acc ttc gct gtc gtt   501
Leu Arg Gly Lys Met Gln Lys Ile Asp Ser Val Thr Phe Ala Val Val
    120                 125                 130

cca gag ctg tcc aac atc agc act tcc gag ctc gag cgc gcc gca cgc   549
Pro Glu Leu Ser Asn Ile Ser Thr Ser Glu Leu Glu Arg Ala Ala Arg
135                 140                 145                 150

atc cgc taaacacacc ctcgtggtgt gga                                578
Ile Arg
```

<210> 1270
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 1270

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Met Ser Met Leu Lys Lys Thr Lys Glu Phe Phe Gly Leu Ala Pro Tyr
  1               5                  10                  15

Glu Ala Glu His Glu Asp Ala Tyr Tyr Ala Asp Glu Pro Arg Tyr Glu
            20                  25                  30

Gly Thr Ala Ala Tyr Ala Pro Glu Tyr Arg Glu Arg Asp Tyr Gly Tyr
        35                  40                  45

Ala Pro Glu Ala Pro Ala Pro Val Ala Pro Ser Pro Ala Pro Arg Ser
    50                  55                  60

Tyr Gln Ser Thr Ile Val Pro Val Glu Leu His Ser Phe Glu Asp Ala
65                  70                  75                  80

Gln Val Ile Gly Gly Ala Phe Arg Asp Gly Asp Ala Val Val Phe Asp
                85                  90                  95

Met Ser Leu Leu Ser Arg Glu Glu Ala Arg Arg Ile Val Asp Phe Ala
            100                 105                 110

Ala Gly Leu Cys Phe Ala Leu Arg Gly Lys Met Gln Lys Ile Asp Ser
```

```
        115                 120                 125

Val Thr Phe Ala Val Val Pro Glu Leu Ser Asn Ile Ser Thr Ser Glu
    130                 135                 140

Leu Glu Arg Ala Ala Arg Ile Arg
145                 150


<210> 1271
<211> 1650
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1627)
<223> RXN02697

<400> 1271
tttggctcac ctcgatgatg tagacatccc cgatgaggtg cgcgcacagt tgcgggcact 60

ggctatccgc tcaaccgaac gtcggatgta gtagacgcgt atg aca ctt ttt caa   115
                                              Met Thr Leu Phe Gln
                                                1               5

cgt tta acc aac cct gta gtg ctc ggc ggc cta gca ggt gtt ttg ctt   163
Arg Leu Thr Asn Pro Val Val Leu Gly Gly Leu Ala Gly Val Leu Leu
                10                  15                  20

ctg ctc ggc tct ttc ggt ggc ggt gcc att cgg tac cgt ggc gga gtg   211
Leu Leu Gly Ser Phe Gly Gly Gly Ala Ile Arg Tyr Arg Gly Gly Val
            25                  30                  35

ctc gat gcg ttg ggg ctt aac ttc ctt gct ttt ggc cac gcg cag ggt   259
Leu Asp Ala Leu Gly Leu Asn Phe Leu Ala Phe Gly His Ala Gln Gly
        40                  45                  50

att tcc aat acc gtg ttg tgg gtt ggg cag ctg ctg ctg att ggc gcg   307
Ile Ser Asn Thr Val Leu Trp Val Gly Gln Leu Leu Leu Ile Gly Ala
    55                  60                  65

tgg gtt cac ctt gga cgt cgg ttg ttc aag aaa aaa gtc gct gat gac   355
Trp Val His Leu Gly Arg Arg Leu Phe Lys Lys Lys Val Ala Asp Asp
70                  75                  80                  85

acc gca gac gct gct gac tta ggt ctt gta aag cgc acg ttg tat gcc   403
Thr Ala Asp Ala Ala Asp Leu Gly Leu Val Lys Arg Thr Leu Tyr Ala
                90                  95                  100

atg gtg gtg ccc ctc att ttt gcg gca cca atg atg tcg cgt gat gtt   451
Met Val Val Pro Leu Ile Phe Ala Ala Pro Met Met Ser Arg Asp Val
            105                 110                 115

tat tcc tat ctc atg cag ggc gcg atg ctg cgt gat ggc ttc gat ccc   499
Tyr Ser Tyr Leu Met Gln Gly Ala Met Leu Arg Asp Gly Phe Asp Pro
        120                 125                 130

tac act gag ggc gct gcg gta aac cct ggc ccc atg ttg ctt gag gtc   547
Tyr Thr Glu Gly Ala Ala Val Asn Pro Gly Pro Met Leu Leu Glu Val
    135                 140                 145
```

```
tct cat gat tgg cgc aac acc acg acg ccg tat ggt cca cta cac ctg   595
Ser His Asp Trp Arg Asn Thr Thr Thr Pro Tyr Gly Pro Leu His Leu
150                 155                 160                 165

tgg att gga gac atg atc acc acg gtt gtg ggc gat aat gtc acc ttg   643
Trp Ile Gly Asp Met Ile Thr Thr Val Val Gly Asp Asn Val Thr Leu
                170                 175                 180

ggc gtc gtc gct tac aag atc ttg tcg atc att ggc ctt gct gtg aca   691
Gly Val Val Ala Tyr Lys Ile Leu Ser Ile Ile Gly Leu Ala Val Thr
            185                 190                 195

ggc tgg agc att gtc cgc att gca caa cat ttt gga gcc aac cca gca   739
Gly Trp Ser Ile Val Arg Ile Ala Gln His Phe Gly Ala Asn Pro Ala
        200                 205                 210

att gca ttg tgg att ggt gtg gcc aat cct gtg atg atc atc cac atg   787
Ile Ala Leu Trp Ile Gly Val Ala Asn Pro Val Met Ile Ile His Met
    215                 220                 225

atc ggc ggc atg cac aat gaa tcc ctc atg gtg gga ttg gtc agc gtc   835
Ile Gly Gly Met His Asn Glu Ser Leu Met Val Gly Leu Val Ser Val
230                 235                 240                 245

ggc ttg ttg cta gca ctg aag aag cgt ttc gtg gca ggt gtg gca ctc   883
Gly Leu Leu Leu Ala Leu Lys Lys Arg Phe Val Ala Gly Val Ala Leu
                250                 255                 260

att gca gtg gct gtg tcg ctg aaa gct aca gcg gcg att gca ctt cct   931
Ile Ala Val Ala Val Ser Leu Lys Ala Thr Ala Ala Ile Ala Leu Pro
            265                 270                 275

ttt gtg gtg tgg atc ggc atg cat cat ttc gca gga ttc tta gcc acc   979
Phe Val Val Trp Ile Gly Met His His Phe Ala Gly Phe Leu Ala Thr
        280                 285                 290

aaa aag ggc aaa gac tcc cct acc ctt aag caa cag gtc ccc gcg ttc  1027
Lys Lys Gly Lys Asp Ser Pro Thr Leu Lys Gln Gln Val Pro Ala Phe
    295                 300                 305

ttt gcc act gga gct gca ggt gtt gct gtc act ggt gtt gtt gtc agt  1075
Phe Ala Thr Gly Ala Ala Gly Val Ala Val Thr Gly Val Val Val Ser
310                 315                 320                 325

gcg atc act tgg gcg tct ggc gct tcg tgg ggc tgg atc agt gag atc  1123
Ala Ile Thr Trp Ala Ser Gly Ala Ser Trp Gly Trp Ile Ser Glu Ile
                330                 335                 340

agt ggc aac agc aag gta atc aac ccg ctg gct ttc cct tct ttg gtg  1171
Ser Gly Asn Ser Lys Val Ile Asn Pro Leu Ala Phe Pro Ser Leu Val
            345                 350                 355

gcc agt gtg atc acc atg gtg gct gaa gtg ttc gtt gac gat ttc gac  1219
Ala Ser Val Ile Thr Met Val Ala Glu Val Phe Val Asp Asp Phe Asp
        360                 365                 370

tac aac gca gtg gtt aat gtt gtg cgc tca atc tcc atg ctg atc atg  1267
Tyr Asn Ala Val Val Asn Val Val Arg Ser Ile Ser Met Leu Ile Met
    375                 380                 385
```

```
ctt ggc ggg ttg gtc gta tgt tgg tgg ctg ttc cgc cag aac gaa cgc   1315
Leu Gly Gly Leu Val Val Cys Trp Trp Leu Phe Arg Gln Asn Glu Arg
390                 395                 400                 405

agg gcg gtc act ggt aca gca gcg gct tat gcc gtg gct ttt gtg ttc   1363
Arg Ala Val Thr Gly Thr Ala Ala Ala Tyr Ala Val Ala Phe Val Phe
                410                 415                 420

aat tct gtg acc ttg ccg tgg tac tac gcc agc ttg atc tct ttg ctc   1411
Asn Ser Val Thr Leu Pro Trp Tyr Tyr Ala Ser Leu Ile Ser Leu Leu
            425                 430                 435

ggc aca ttt aaa cca ccg atg tgg ttg att cgc ttc gca gcg ggt gct   1459
Gly Thr Phe Lys Pro Pro Met Trp Leu Ile Arg Phe Ala Ala Gly Ala
        440                 445                 450

tcg gtg ttt atc gcg ctg atg ttt acc gga agt gga aac cac cag ctg   1507
Ser Val Phe Ile Ala Leu Met Phe Thr Gly Ser Gly Asn His Gln Leu
    455                 460                 465

tac aac atc gtt acg gtg atc atc gca gca att atc gcg tgg ctt gcc   1555
Tyr Asn Ile Val Thr Val Ile Ile Ala Ala Ile Ile Ala Trp Leu Ala
470                 475                 480                 485

acc gtg gtg atc ttt gat gac act gac cct gca aca acg gcc acg gag   1603
Thr Val Val Ile Phe Asp Asp Thr Asp Pro Ala Thr Thr Ala Thr Glu
                490                 495                 500

aaa ccc tcc ccg cat acc gtt tcc tagttgcata aggtaaaccg cca         1650
Lys Pro Ser Pro His Thr Val Ser
            505
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<210> 1272
<211> 509
<212> PRT
<213> Corynebacterium glutamicum

<400> 1272

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Met Thr Leu Phe Gln Arg Leu Thr Asn Pro Val Val Leu Gly Gly Leu
  1               5                  10                  15

Ala Gly Val Leu Leu Leu Leu Gly Ser Phe Gly Gly Gly Ala Ile Arg
             20                  25                  30

Tyr Arg Gly Gly Val Leu Asp Ala Leu Gly Leu Asn Phe Leu Ala Phe
         35                  40                  45

Gly His Ala Gln Gly Ile Ser Asn Thr Val Leu Trp Val Gly Gln Leu
     50                  55                  60

Leu Leu Ile Gly Ala Trp Val His Leu Gly Arg Arg Leu Phe Lys Lys
 65                  70                  75                  80

Lys Val Ala Asp Asp Thr Ala Asp Ala Ala Asp Leu Gly Leu Val Lys
                 85                  90                  95

Arg Thr Leu Tyr Ala Met Val Val Pro Leu Ile Phe Ala Ala Pro Met
            100                 105                 110

Met Ser Arg Asp Val Tyr Ser Tyr Leu Met Gln Gly Ala Met Leu Arg
```

```
        115                 120                 125

Asp Gly Phe Asp Pro Tyr Thr Glu Gly Ala Ala Val Asn Pro Gly Pro
    130                 135                 140

Met Leu Leu Glu Val Ser His Asp Trp Arg Asn Thr Thr Thr Pro Tyr
145                 150                 155                 160

Gly Pro Leu His Leu Trp Ile Gly Asp Met Ile Thr Thr Val Val Gly
                165                 170                 175

Asp Asn Val Thr Leu Gly Val Val Ala Tyr Lys Ile Leu Ser Ile Ile
            180                 185                 190

Gly Leu Ala Val Thr Gly Trp Ser Ile Val Arg Ile Ala Gln His Phe
        195                 200                 205

Gly Ala Asn Pro Ala Ile Ala Leu Trp Ile Gly Val Ala Asn Pro Val
    210                 215                 220

Met Ile Ile His Met Ile Gly Gly Met His Asn Glu Ser Leu Met Val
225                 230                 235                 240

Gly Leu Val Ser Val Gly Leu Leu Leu Ala Leu Lys Lys Arg Phe Val
                245                 250                 255

Ala Gly Val Ala Leu Ile Ala Val Ala Val Ser Leu Lys Ala Thr Ala
            260                 265                 270

Ala Ile Ala Leu Pro Phe Val Val Trp Ile Gly Met His His Phe Ala
        275                 280                 285

Gly Phe Leu Ala Thr Lys Lys Gly Lys Asp Ser Pro Thr Leu Lys Gln
    290                 295                 300

Gln Val Pro Ala Phe Phe Ala Thr Gly Ala Ala Gly Val Ala Val Thr
305                 310                 315                 320

Gly Val Val Val Ser Ala Ile Thr Trp Ala Ser Gly Ala Ser Trp Gly
                325                 330                 335

Trp Ile Ser Glu Ile Ser Gly Asn Ser Lys Val Ile Asn Pro Leu Ala
            340                 345                 350

Phe Pro Ser Leu Val Ala Ser Val Ile Thr Met Val Ala Glu Val Phe
        355                 360                 365

Val Asp Asp Phe Asp Tyr Asn Ala Val Val Asn Val Val Arg Ser Ile
    370                 375                 380

Ser Met Leu Ile Met Leu Gly Gly Leu Val Val Cys Trp Trp Leu Phe
385                 390                 395                 400

Arg Gln Asn Glu Arg Arg Ala Val Thr Gly Thr Ala Ala Ala Tyr Ala
                405                 410                 415

Val Ala Phe Val Phe Asn Ser Val Thr Leu Pro Trp Tyr Tyr Ala Ser
            420                 425                 430

Leu Ile Ser Leu Leu Gly Thr Phe Lys Pro Pro Met Trp Leu Ile Arg
        435                 440                 445
```

```
Phe Ala Ala Gly Ala Ser Val Phe Ile Ala Leu Met Phe Thr Gly Ser
    450                 455                 460

Gly Asn His Gln Leu Tyr Asn Ile Val Thr Val Ile Ile Ala Ala Ile
465                 470                 475                 480

Ile Ala Trp Leu Ala Thr Val Val Ile Phe Asp Asp Thr Asp Pro Ala
                485                 490                 495

Thr Thr Ala Thr Glu Lys Pro Ser Pro His Thr Val Ser
            500                 505
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<210> 1273
<211> 722
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(699)
<223> FRXA02697

<400> 1273

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cct ttt gtg gtg tgg atc ggc atg cat cat ttc gca gga ttc tta gcc   48
Pro Phe Val Val Trp Ile Gly Met His His Phe Ala Gly Phe Leu Ala
  1               5                  10                  15

acc aaa aag ggc aaa gac tcc cct acc ctt aag caa cag gtc ccc gcg   96
Thr Lys Lys Gly Lys Asp Ser Pro Thr Leu Lys Gln Gln Val Pro Ala
             20                  25                  30

ttc ttt gcc act gga gct gca ggt gtt gct gtc act ggt gtt gtt gtc   144
Phe Phe Ala Thr Gly Ala Ala Gly Val Ala Val Thr Gly Val Val Val
         35                  40                  45

agt gcg atc act tgg gcg tct ggc gct tcg tgg ggc tgg atc agt gag   192
Ser Ala Ile Thr Trp Ala Ser Gly Ala Ser Trp Gly Trp Ile Ser Glu
     50                  55                  60

atc agt ggc aac agc aag gta atc aac ccg ctg gct ttc cct tct ttg   240
Ile Ser Gly Asn Ser Lys Val Ile Asn Pro Leu Ala Phe Pro Ser Leu
 65                  70                  75                  80

gtg gcc agt gtg atc acc atg gtg gct gaa gtg ttc gtt gac gat ttc   288
Val Ala Ser Val Ile Thr Met Val Ala Glu Val Phe Val Asp Asp Phe
                 85                  90                  95

gac tac aac gca gtg gtt aat gtt gtg cgc tca atc tcc atg ctg atc   336
Asp Tyr Asn Ala Val Val Asn Val Val Arg Ser Ile Ser Met Leu Ile
            100                 105                 110

atg ctt ggc ggg ttg gtc gta tgt tgg tgg ctg ttc cgc cag aac gaa   384
Met Leu Gly Gly Leu Val Val Cys Trp Trp Leu Phe Arg Gln Asn Glu
        115                 120                 125

cgc agg gcg gtc act ggt aca gcg gcg gct tat gcc gtg gct ttt gtg   432
Arg Arg Ala Val Thr Gly Thr Ala Ala Ala Tyr Ala Val Ala Phe Val
    130                 135                 140
```

```
ttc aat tct gtg acc ttg ccg tgg tac tac gcc agc ttg atc tct ttg   480
Phe Asn Ser Val Thr Leu Pro Trp Tyr Tyr Ala Ser Leu Ile Ser Leu
145                 150                 155                 160

ctc ggc aca ttt aaa cca ccg atg tgg ttg att cgc ttc gca gcg ggt   528
Leu Gly Thr Phe Lys Pro Pro Met Trp Leu Ile Arg Phe Ala Ala Gly
                165                 170                 175

gct tcg gtg ttt atc gcg ctg atg ttt acc gga agt gga aac cac cag   576
Ala Ser Val Phe Ile Ala Leu Met Phe Thr Gly Ser Gly Asn His Gln
            180                 185                 190

ctg tac aac atc gtt acg gtg atc atc gca gca att atc gcg tgg ctt   624
Leu Tyr Asn Ile Val Thr Val Ile Ile Ala Ala Ile Ile Ala Trp Leu
        195                 200                 205

gcc acc gtg gtg atc ttt gat gac act gac cct gca aca acg gcc acg   672
Ala Thr Val Val Ile Phe Asp Asp Thr Asp Pro Ala Thr Thr Ala Thr
    210                 215                 220

gag aaa ccc tcc ccg cat acc gtt tcc tagttgcata aggtaaaccg         719
Glu Lys Pro Ser Pro His Thr Val Ser
225                 230

cca                                                               722


<210> 1274
<211> 233
<212> PRT
<213> Corynebacterium glutamicum

<400> 1274
Pro Phe Val Val Trp Ile Gly Met His His Phe Ala Gly Phe Leu Ala
  1               5                  10                  15

Thr Lys Lys Gly Lys Asp Ser Pro Thr Leu Lys Gln Gln Val Pro Ala
             20                  25                  30

Phe Phe Ala Thr Gly Ala Ala Gly Val Ala Val Thr Gly Val Val Val
         35                  40                  45

Ser Ala Ile Thr Trp Ala Ser Gly Ala Ser Trp Gly Trp Ile Ser Glu
     50                  55                  60

Ile Ser Gly Asn Ser Lys Val Ile Asn Pro Leu Ala Phe Pro Ser Leu
 65                  70                  75                  80

Val Ala Ser Val Ile Thr Met Val Ala Glu Val Phe Val Asp Asp Phe
                 85                  90                  95

Asp Tyr Asn Ala Val Val Asn Val Val Arg Ser Ile Ser Met Leu Ile
            100                 105                 110

Met Leu Gly Gly Leu Val Val Cys Trp Trp Leu Phe Arg Gln Asn Glu
        115                 120                 125

Arg Arg Ala Val Thr Gly Thr Ala Ala Ala Tyr Ala Val Ala Phe Val
    130                 135                 140

Phe Asn Ser Val Thr Leu Pro Trp Tyr Tyr Ala Ser Leu Ile Ser Leu
```

```
145                 150                 155                 160

Leu Gly Thr Phe Lys Pro Pro Met Trp Leu Ile Arg Phe Ala Ala Gly
                165                 170                 175

Ala Ser Val Phe Ile Ala Leu Met Phe Thr Gly Ser Gly Asn His Gln
            180                 185                 190

Leu Tyr Asn Ile Val Thr Val Ile Ile Ala Ala Ile Ile Ala Trp Leu
        195                 200                 205

Ala Thr Val Val Ile Phe Asp Asp Thr Asp Pro Ala Thr Thr Ala Thr
    210                 215                 220

Glu Lys Pro Ser Pro His Thr Val Ser
225                 230
```

<210> 1275
<211> 748
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(748)
<223> FRXA02719

<400> 1275

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tttggctcac ctcgatgatg tagacatccc cgatgaggtg cgcgcacagt tgcgggcact 60

ggctatccgc tcaaccgaac gtcggatgta gtagacgcgt atg aca ctt ttt caa   115
                                            Met Thr Leu Phe Gln
                                              1               5

cgt tta acc aac cct gta gtg ctc ggc ggc cta gca ggt gtt ttg ctt   163
Arg Leu Thr Asn Pro Val Val Leu Gly Gly Leu Ala Gly Val Leu Leu
                  10                  15                  20

ctg ctc ggc tct ttc ggt ggc ggt gcc att cgg tac cgt ggc gga gtg   211
Leu Leu Gly Ser Phe Gly Gly Gly Ala Ile Arg Tyr Arg Gly Gly Val
              25                  30                  35

ctc gat gcg ttg ggg ctt aac ttc ctt gct ttt ggc cac gcg cag ggt   259
Leu Asp Ala Leu Gly Leu Asn Phe Leu Ala Phe Gly His Ala Gln Gly
          40                  45                  50

att tcc aat acc gtg ttg tgg gtt ggg cag ctg ctg ctg att ggc gcg   307
Ile Ser Asn Thr Val Leu Trp Val Gly Gln Leu Leu Leu Ile Gly Ala
      55                  60                  65

tgg gtt cac ctt gga cgt cgg ttg ttc aag aaa aaa gtc gct gat gac   355
Trp Val His Leu Gly Arg Arg Leu Phe Lys Lys Lys Val Ala Asp Asp
  70                  75                  80                  85

acc gca gac gct gct gac tta ggt ctt gta aag cgc acg ttg tat gcc   403
Thr Ala Asp Ala Ala Asp Leu Gly Leu Val Lys Arg Thr Leu Tyr Ala
                  90                  95                 100

atg gtg gtg ccc ctc att ttt gcg gca cca atg atg tcg cgt gat gtt   451
Met Val Val Pro Leu Ile Phe Ala Ala Pro Met Met Ser Arg Asp Val
```

```
            105                 110                 115

tat tcc tat ctc atg cag ggc gcg atg ctg cgt gat ggc ttc gat ccc   499
Tyr Ser Tyr Leu Met Gln Gly Ala Met Leu Arg Asp Gly Phe Asp Pro
        120                 125                 130

tac act gag ggc gct gcg gta aac cct ggc ccc atg ttg ctt gag gtc   547
Tyr Thr Glu Gly Ala Ala Val Asn Pro Gly Pro Met Leu Leu Glu Val
    135                 140                 145

tct cat gat tgg cgc aac acc acg acg ccg tat ggt cca cta cac ctg   595
Ser His Asp Trp Arg Asn Thr Thr Thr Pro Tyr Gly Pro Leu His Leu
150                 155                 160                 165

tgg att gga gac atg atc acc acg gtt gtg ggc gat aat gtc acc ttg   643
Trp Ile Gly Asp Met Ile Thr Thr Val Val Gly Asp Asn Val Thr Leu
                170                 175                 180

ggc gtc gtc gct tac aag atc ttg tcg atc att ggc ctt gct gtg aca   691
Gly Val Val Ala Tyr Lys Ile Leu Ser Ile Ile Gly Leu Ala Val Thr
            185                 190                 195

ggc tgg agc att gtc cgc att gca caa cat ttt gga gcc aac cca gca   739
Gly Trp Ser Ile Val Arg Ile Ala Gln His Phe Gly Ala Asn Pro Ala
        200                 205                 210

att gca ttg                                                       748
Ile Ala Leu
    215
```

Sequence Listing.ST25.txt

<210> 1276
<211> 216
<212> PRT
<213> Corynebacterium glutamicum

<400> 1276

```
Met Thr Leu Phe Gln Arg Leu Thr Asn Pro Val Val Leu Gly Gly Leu
  1               5                  10                  15

Ala Gly Val Leu Leu Leu Leu Gly Ser Phe Gly Gly Gly Ala Ile Arg
             20                  25                  30

Tyr Arg Gly Gly Val Leu Asp Ala Leu Gly Leu Asn Phe Leu Ala Phe
         35                  40                  45

Gly His Ala Gln Gly Ile Ser Asn Thr Val Leu Trp Val Gly Gln Leu
     50                  55                  60

Leu Leu Ile Gly Ala Trp Val His Leu Gly Arg Arg Leu Phe Lys Lys
 65                  70                  75                  80

Lys Val Ala Asp Asp Thr Ala Asp Ala Ala Asp Leu Gly Leu Val Lys
                 85                  90                  95

Arg Thr Leu Tyr Ala Met Val Val Pro Leu Ile Phe Ala Ala Pro Met
            100                 105                 110

Met Ser Arg Asp Val Tyr Ser Tyr Leu Met Gln Gly Ala Met Leu Arg
        115                 120                 125
```

```
Asp Gly Phe Asp Pro Tyr Thr Glu Gly Ala Ala Val Asn Pro Gly Pro
    130                 135                 140

Met Leu Leu Glu Val Ser His Asp Trp Arg Asn Thr Thr Thr Pro Tyr
145                 150                 155                 160

Gly Pro Leu His Leu Trp Ile Gly Asp Met Ile Thr Thr Val Val Gly
                165                 170                 175

Asp Asn Val Thr Leu Gly Val Val Ala Tyr Lys Ile Leu Ser Ile Ile
            180                 185                 190

Gly Leu Ala Val Thr Gly Trp Ser Ile Val Arg Ile Ala Gln His Phe
        195                 200                 205

Gly Ala Asn Pro Ala Ile Ala Leu
    210                 215


<210> 1277
<211> 825
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(802)
<223> RXN02720

<400> 1277
ccacgctgca ccatcgaaga cgaagatctg ttttcttacc gccgcgaagg cacgacaggc 60

cgccaggccg gcgtggtgtg gctgccaaag gaggcataaa ttg gag cgc cgc gaa   115
                                              Leu Glu Arg Arg Glu
                                                1               5

gag ctg cag gta cga ctg cag cag gtg caa gcg cgt atc gac gcg acc   163
Glu Leu Gln Val Arg Leu Gln Gln Val Gln Ala Arg Ile Asp Ala Thr
                10                  15                  20

ctc aac gaa cac aac cgc ccc gag ggc agt gta cgt ctg ttg ccg gtc   211
Leu Asn Glu His Asn Arg Pro Glu Gly Ser Val Arg Leu Leu Pro Val
            25                  30                  35

acc aaa ttc cac ccc gtg gaa gac atc aag atc tta caa gag ttt ggt   259
Thr Lys Phe His Pro Val Glu Asp Ile Lys Ile Leu Gln Glu Phe Gly
        40                  45                  50

gtc acc gca gtg gga gag aac cgc gaa caa gaa gca cgc gcc aaa gca   307
Val Thr Ala Val Gly Glu Asn Arg Glu Gln Glu Ala Arg Ala Lys Ala
    55                  60                  65

ctc gaa ctt ccc gac atg gac ttt cat atg att ggc caa atc caa tca   355
Leu Glu Leu Pro Asp Met Asp Phe His Met Ile Gly Gln Ile Gln Ser
70                  75                  80                  85

aag aaa gcc aac tcg atc gcc agg tgg gca gct gca gtg cac tcc gtt   403
Lys Lys Ala Asn Ser Ile Ala Arg Trp Ala Ala Ala Val His Ser Val
                90                  95                  100

gat agc gag aaa atc gcc gaa gca ttg ggc agg gga gta gcc ctt gca   451
```

```
Asp Ser Glu Lys Ile Ala Glu Ala Leu Gly Arg Gly Val Ala Leu Ala
          105                 110                 115

ttg gat aga ggc gac cgc acc agt gac gag ctt ccg tgt ttt att caa   499
Leu Asp Arg Gly Asp Arg Thr Ser Asp Glu Leu Pro Cys Phe Ile Gln
        120                 125                 130

ctg agt ttg gat ggt gac ccg agc cga ggt gga act cca ttg agc cag   547
Leu Ser Leu Asp Gly Asp Pro Ser Arg Gly Gly Thr Pro Leu Ser Gln
    135                 140                 145

gtc aca caa ctt gcc gat tgc atc agt gac acc aca cat ctg cgt ttt   595
Val Thr Gln Leu Ala Asp Cys Ile Ser Asp Thr Thr His Leu Arg Phe
150                 155                 160                 165

gag ggc ctc atg tgc gtc cca ccg ctt ggt tgg ggc cct gaa aaa gct   643
Glu Gly Leu Met Cys Val Pro Pro Leu Gly Trp Gly Pro Glu Lys Ala
                170                 175                 180

ttt tcc cag gca aga gac gta ctt tca ggt tta gag gaa cac ttt gac   691
Phe Ser Gln Ala Arg Asp Val Leu Ser Gly Leu Glu Glu His Phe Asp
            185                 190                 195

agg tct ttg gaa ttt tcg gca ggt atg tct gga gac cta gtt gct gcg   739
Arg Ser Leu Glu Phe Ser Ala Gly Met Ser Gly Asp Leu Val Ala Ala
        200                 205                 210

att aaa cac ggc tca aca atc gtg cgt gtc gga act gaa att ctt ggg   787
Ile Lys His Gly Ser Thr Ile Val Arg Val Gly Thr Glu Ile Leu Gly
    215                 220                 225

aac cga ccg cta gcg tagaaaatca agttaagggt gtg                    825
Asn Arg Pro Leu Ala
230
```

US 09/847,218 Filed May 3, 2001

<210> 1278
<211> 234
<212> PRT
<213> Corynebacterium glutamicum

<400> 1278

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Leu Glu Arg Arg Glu Glu Leu Gln Val Arg Leu Gln Gln Val Gln Ala
  1               5                  10                  15

Arg Ile Asp Ala Thr Leu Asn Glu His Asn Arg Pro Glu Gly Ser Val
             20                  25                  30

Arg Leu Leu Pro Val Thr Lys Phe His Pro Val Glu Asp Ile Lys Ile
         35                  40                  45

Leu Gln Glu Phe Gly Val Thr Ala Val Gly Glu Asn Arg Glu Gln Glu
     50                  55                  60

Ala Arg Ala Lys Ala Leu Glu Leu Pro Asp Met Asp Phe His Met Ile
 65                  70                  75                  80

Gly Gln Ile Gln Ser Lys Lys Ala Asn Ser Ile Ala Arg Trp Ala Ala
                 85                  90                  95

Ala Val His Ser Val Asp Ser Glu Lys Ile Ala Glu Ala Leu Gly Arg
```

```
            100                 105                 110

Gly Val Ala Leu Ala Leu Asp Arg Gly Asp Arg Thr Ser Asp Glu Leu
        115                 120                 125

Pro Cys Phe Ile Gln Leu Ser Leu Asp Gly Asp Pro Ser Arg Gly Gly
    130                 135                 140

Thr Pro Leu Ser Gln Val Thr Gln Leu Ala Asp Cys Ile Ser Asp Thr
145                 150                 155                 160

Thr His Leu Arg Phe Glu Gly Leu Met Cys Val Pro Pro Leu Gly Trp
                165                 170                 175

Gly Pro Glu Lys Ala Phe Ser Gln Ala Arg Asp Val Leu Ser Gly Leu
            180                 185                 190

Glu Glu His Phe Asp Arg Ser Leu Glu Phe Ser Ala Gly Met Ser Gly
        195                 200                 205

Asp Leu Val Ala Ala Ile Lys His Gly Ser Thr Ile Val Arg Val Gly
    210                 215                 220

Thr Glu Ile Leu Gly Asn Arg Pro Leu Ala
225                 230


<210> 1279
<211> 727
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(727)
<223> FRXA02720

<400> 1279
ccacgctgca ccatcgaaga cgaagatctg ttttcttacc gccgcgaagg cacgacaggc 60

cgccaggccg gcgtggtgtg gctgccaaag gaggcataaa ttg gag cgc cgc gaa   115
                                              Leu Glu Arg Arg Glu
                                                1               5

gag ctg cag gta cga ctg cag cag gtg caa gcg cgt atc gac gcg acc   163
Glu Leu Gln Val Arg Leu Gln Gln Val Gln Ala Arg Ile Asp Ala Thr
                10                  15                  20

ctc aac gaa cac aac cgc ccc gag ggc agt gta cgt ctg ttg ccg gtc   211
Leu Asn Glu His Asn Arg Pro Glu Gly Ser Val Arg Leu Leu Pro Val
            25                  30                  35

acc aaa ttc cac ccc gtg gaa gac atc aag atc tta caa gag ttt ggt   259
Thr Lys Phe His Pro Val Glu Asp Ile Lys Ile Leu Gln Glu Phe Gly
        40                  45                  50

gtc acc gca gtg gga gag aac cgc gaa caa gaa gca cgc gcc aaa gca   307
Val Thr Ala Val Gly Glu Asn Arg Glu Gln Glu Ala Arg Ala Lys Ala
    55                  60                  65

ctc gaa ctt ccc gac atg gac ttt cat atg att ggc caa atc caa tca   355
```

```
Leu Glu Leu Pro Asp Met Asp Phe His Met Ile Gly Gln Ile Gln Ser
 70                  75                  80                  85

aag aaa gcc aac tcg atc gcc agg tgg gca gct gca gtg cac tcc gtt   403
Lys Lys Ala Asn Ser Ile Ala Arg Trp Ala Ala Ala Val His Ser Val
                90                  95                 100

gat agc gag aaa atc gcc gaa gca ttg ggc agg gga gta gcc ctt gca   451
Asp Ser Glu Lys Ile Ala Glu Ala Leu Gly Arg Gly Val Ala Leu Ala
            105                 110                 115

ttg gat aga ggc gac cgc acc agt gac gag ctt ccg tgt ttt att caa   499
Leu Asp Arg Gly Asp Arg Thr Ser Asp Glu Leu Pro Cys Phe Ile Gln
        120                 125                 130

ctg agt ttg gat ggt gac ccg agc cga ggt gga act cca ttg agc cag   547
Leu Ser Leu Asp Gly Asp Pro Ser Arg Gly Gly Thr Pro Leu Ser Gln
    135                 140                 145

gtc aca caa ctt gcc gat tgc atc agt gac acc aca cat ctg cgt ttt   595
Val Thr Gln Leu Ala Asp Cys Ile Ser Asp Thr Thr His Leu Arg Phe
150                 155                 160                 165

gag ggc ctc atg tgc gtc cca ccg ctt ggt tgg ggc cct gaa aaa gct   643
Glu Gly Leu Met Cys Val Pro Pro Leu Gly Trp Gly Pro Glu Lys Ala
                170                 175                 180

ttt tcc cag gca aga gac gta ctt tca ggt tta gag gaa cac ttt gac   691
Phe Ser Gln Ala Arg Asp Val Leu Ser Gly Leu Glu Glu His Phe Asp
            185                 190                 195

agg tct ttg gaa ttt tcg gca ggt atg tct gga gac                   727
Arg Ser Leu Glu Phe Ser Ala Gly Met Ser Gly Asp
        200                 205
```

Application Filed with the Patent Office

<210> 1280
<211> 209
<212> PRT
<213> Corynebacterium glutamicum

<400> 1280

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Leu Glu Arg Arg Glu Glu Leu Gln Val Arg Leu Gln Gln Val Gln Ala
  1               5                  10                  15

Arg Ile Asp Ala Thr Leu Asn Glu His Asn Arg Pro Glu Gly Ser Val
             20                  25                  30

Arg Leu Leu Pro Val Thr Lys Phe His Pro Val Glu Asp Ile Lys Ile
         35                  40                  45

Leu Gln Glu Phe Gly Val Thr Ala Val Gly Glu Asn Arg Glu Gln Glu
     50                  55                  60

Ala Arg Ala Lys Ala Leu Glu Leu Pro Asp Met Asp Phe His Met Ile
 65                  70                  75                  80

Gly Gln Ile Gln Ser Lys Lys Ala Asn Ser Ile Ala Arg Trp Ala Ala
                 85                  90                  95

Ala Val His Ser Val Asp Ser Glu Lys Ile Ala Glu Ala Leu Gly Arg
```

```
            100                 105                 110

Gly Val Ala Leu Ala Leu Asp Arg Gly Asp Arg Thr Ser Asp Glu Leu
        115                 120                 125

Pro Cys Phe Ile Gln Leu Ser Leu Asp Gly Asp Pro Ser Arg Gly Gly
    130                 135                 140

Thr Pro Leu Ser Gln Val Thr Gln Leu Ala Asp Cys Ile Ser Asp Thr
145                 150                 155                 160

Thr His Leu Arg Phe Glu Gly Leu Met Cys Val Pro Pro Leu Gly Trp
                165                 170                 175

Gly Pro Glu Lys Ala Phe Ser Gln Ala Arg Asp Val Leu Ser Gly Leu
            180                 185                 190

Glu Glu His Phe Asp Arg Ser Leu Glu Phe Ser Ala Gly Met Ser Gly
        195                 200                 205

Asp
```

US 2004/0137578 A1 May 15, 2004

<210> 1281
<211> 927
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(904)
<223> RXN02744

<400> 1281
gccaaaacgt catgattcgc tctttggata cgggacaccg ctcattggaa gatgtcttcc 60

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tggacatcac cggaaaagaa ctgaggagtt aacgcacacc atg tct aaa cct ttt   115
                                              Met Ser Lys Pro Phe
                                                1               5

gaa aac tct gcg ctc cgc ggt tct tct cga ttc cca gct gga acg ttc   163
Glu Asn Ser Ala Leu Arg Gly Ser Ser Arg Phe Pro Ala Gly Thr Phe
                10                  15                  20

acc cct gct ccc aaa cga gcc acc ccg gca aaa atg ttg gct gct cag   211
Thr Pro Ala Pro Lys Arg Ala Thr Pro Ala Lys Met Leu Ala Ala Gln
            25                  30                  35

ggc aag atg gaa tcc ctg ctg ttt ctt cgc cac ggc gaa cag caa ctg   259
Gly Lys Met Glu Ser Leu Leu Phe Leu Arg His Gly Glu Gln Gln Leu
        40                  45                  50

ctc agc atc atc att ccc ttg gtc gcg ctc atc gca cta gcg aat ttt   307
Leu Ser Ile Ile Ile Pro Leu Val Ala Leu Ile Ala Leu Ala Asn Phe
    55                  60                  65

gat ttc atc cct ggt gag aac tcc ctc gac aag act ttc ccc ttc gcg   355
Asp Phe Ile Pro Gly Glu Asn Ser Leu Asp Lys Thr Phe Pro Phe Ala
70                  75                  80                  85
```

```
ctg gcc aca gca gcc atg agc gct ggt ttt aca ggt caa gcc atc agc   403
Leu Ala Thr Ala Ala Met Ser Ala Gly Phe Thr Gly Gln Ala Ile Ser
                 90                  95                 100

cta gct ttt gac cgc cgc tat ggt gcc ctc aag cgc acc ggc gcc agc   451
Leu Ala Phe Asp Arg Arg Tyr Gly Ala Leu Lys Arg Thr Gly Ala Ser
            105                 110                 115

ggt gtt ccc gcc tgg acg att att ttt ggc aaa gtc atc gca gtc att   499
Gly Val Pro Ala Trp Thr Ile Ile Phe Gly Lys Val Ile Ala Val Ile
        120                 125                 130

gca gtc acc att gtg cag atc atc ttt ctc ggt gtg act gca ctg ctg   547
Ala Val Thr Ile Val Gln Ile Ile Phe Leu Gly Val Thr Ala Leu Leu
    135                 140                 145

ttg ggc tgg tcc gca cct gtc ggt ggt gtg ctc ttt ggc atc gtg acc   595
Leu Gly Trp Ser Ala Pro Val Gly Gly Val Leu Phe Gly Ile Val Thr
150                 155                 160                 165

cta ttt gtg ggt gtt tcc agc ttc acc gcg ctc ggc atg ctg atg ggc   643
Leu Phe Val Gly Val Ser Ser Phe Thr Ala Leu Gly Met Leu Met Gly
                170                 175                 180

gga acg ttg tcc tcc gaa ttg gta ttg gca ctg gct aac ttg att tgg   691
Gly Thr Leu Ser Ser Glu Leu Val Leu Ala Leu Ala Asn Leu Ile Trp
            185                 190                 195

att gta ctg tcc ggc ctt gca gca tgg gcg gtc ttt tcc cct tcc gtc   739
Ile Val Leu Ser Gly Leu Ala Ala Trp Ala Val Phe Ser Pro Ser Val
        200                 205                 210

aac gct gaa gga gtg ctg tcc atc atc cca tcc gtt gcg ctg tcc caa   787
Asn Ala Glu Gly Val Leu Ser Ile Ile Pro Ser Val Ala Leu Ser Gln
    215                 220                 225

ggt atg gtt gac gca ttc aac ggc gaa ctt ccg tgg ctc cag cta gga   835
Gly Met Val Asp Ala Phe Asn Gly Glu Leu Pro Trp Leu Gln Leu Gly
230                 235                 240                 245

att ttg gtg ggc tgg cta att atc acc ggc gtg gcc gca aac aag cta   883
Ile Leu Val Gly Trp Leu Ile Ile Thr Gly Val Ala Ala Asn Lys Leu
                250                 255                 260

ttt aac ttc tct gcg agc cgc tagatatacc cttagtcgga aaa             927
Phe Asn Phe Ser Ala Ser Arg
            265
```

<210> 1282
<211> 268
<212> PRT
<213> Corynebacterium glutamicum

<400> 1282

```
Met Ser Lys Pro Phe Glu Asn Ser Ala Leu Arg Gly Ser Ser Arg Phe
  1               5                  10                  15

Pro Ala Gly Thr Phe Thr Pro Ala Pro Lys Arg Ala Thr Pro Ala Lys
             20                  25                  30
```

```
Met Leu Ala Ala Gln Gly Lys Met Glu Ser Leu Leu Phe Leu Arg His
         35                  40                  45

Gly Glu Gln Gln Leu Leu Ser Ile Ile Ile Pro Leu Val Ala Leu Ile
     50                  55                  60

Ala Leu Ala Asn Phe Asp Phe Ile Pro Gly Glu Asn Ser Leu Asp Lys
 65                  70                  75                  80

Thr Phe Pro Phe Ala Leu Ala Thr Ala Ala Met Ser Ala Gly Phe Thr
                 85                  90                  95

Gly Gln Ala Ile Ser Leu Ala Phe Asp Arg Arg Tyr Gly Ala Leu Lys
            100                 105                 110

Arg Thr Gly Ala Ser Gly Val Pro Ala Trp Thr Ile Ile Phe Gly Lys
        115                 120                 125

Val Ile Ala Val Ile Ala Val Thr Ile Val Gln Ile Ile Phe Leu Gly
    130                 135                 140

Val Thr Ala Leu Leu Leu Gly Trp Ser Ala Pro Val Gly Gly Val Leu
145                 150                 155                 160

Phe Gly Ile Val Thr Leu Phe Val Gly Val Ser Ser Phe Thr Ala Leu
                165                 170                 175

Gly Met Leu Met Gly Gly Thr Leu Ser Ser Glu Leu Val Leu Ala Leu
            180                 185                 190

Ala Asn Leu Ile Trp Ile Val Leu Ser Gly Leu Ala Ala Trp Ala Val
        195                 200                 205

Phe Ser Pro Ser Val Asn Ala Glu Gly Val Leu Ser Ile Ile Pro Ser
    210                 215                 220

Val Ala Leu Ser Gln Gly Met Val Asp Ala Phe Asn Gly Glu Leu Pro
225                 230                 235                 240

Trp Leu Gln Leu Gly Ile Leu Val Gly Trp Leu Ile Ile Thr Gly Val
                245                 250                 255

Ala Ala Asn Lys Leu Phe Asn Phe Ser Ala Ser Arg
            260                 265
```

<210> 1283
<211> 927
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(904)
<223> FRXA02744

<400> 1283
gccaaaacgt catgattcgc tctttggata cgggacaccg ctcattggaa gatgtcttcc 60

tggacatcac cggaaaagaa ctgaggagtt aacgcacacc atg tct aaa cct ttt 115
Met Ser Lys Pro Phe

```
                                                    1               5

gaa aac tct gcg ctc cgc ggt tct tct cga ttc cca gct gga acg ttc   163
Glu Asn Ser Ala Leu Arg Gly Ser Ser Arg Phe Pro Ala Gly Thr Phe
                10                  15                  20

acc cct gct ccc aaa cga gcc acc ccg gca aaa atg ttg gct gct cag   211
Thr Pro Ala Pro Lys Arg Ala Thr Pro Ala Lys Met Leu Ala Ala Gln
            25                  30                  35

ggc aag atg gaa tcc ctg ctg ttt ctt cgc cac ggc gaa cag caa ctg   259
Gly Lys Met Glu Ser Leu Leu Phe Leu Arg His Gly Glu Gln Gln Leu
        40                  45                  50

ctc agc atc atc att ccc ttg gtc gcg ctc atc gca cta gcg aat ttt   307
Leu Ser Ile Ile Ile Pro Leu Val Ala Leu Ile Ala Leu Ala Asn Phe
    55                  60                  65

gat ttc atc cct ggt gag aac tcc ctc gac aag act ttc ccc ttc gcg   355
Asp Phe Ile Pro Gly Glu Asn Ser Leu Asp Lys Thr Phe Pro Phe Ala
70                  75                  80                  85

ctg gcc aca gca gcc atg agc gct ggt ttt aca ggt caa gcc atc agc   403
Leu Ala Thr Ala Ala Met Ser Ala Gly Phe Thr Gly Gln Ala Ile Ser
                90                  95                  100

cta gct ttt gac cgc cgc tat ggt gcc ctc aag cgc acc ggc gcc agc   451
Leu Ala Phe Asp Arg Arg Tyr Gly Ala Leu Lys Arg Thr Gly Ala Ser
            105                 110                 115

ggt gtt ccc gcc tgg acg att att ttt ggc aaa gtc atc gca gtc att   499
Gly Val Pro Ala Trp Thr Ile Ile Phe Gly Lys Val Ile Ala Val Ile
        120                 125                 130

gca gtc acc att gtg cag atc atc ttt ctc ggt gtg act gca ctg ctg   547
Ala Val Thr Ile Val Gln Ile Ile Phe Leu Gly Val Thr Ala Leu Leu
    135                 140                 145

ttg ggc tgg tcc gca cct gtc ggt ggt gtg ctc ttt ggc atc gtg acc   595
Leu Gly Trp Ser Ala Pro Val Gly Gly Val Leu Phe Gly Ile Val Thr
150                 155                 160                 165

cta ttt gtg ggt gtt tcc agc ttc acc gcg ctc ggc atg ctg atg ggc   643
Leu Phe Val Gly Val Ser Ser Phe Thr Ala Leu Gly Met Leu Met Gly
                170                 175                 180

gga acg ttg tcc tcc gaa ttg gta ttg gca ctg gct aac ttg att tgg   691
Gly Thr Leu Ser Ser Glu Leu Val Leu Ala Leu Ala Asn Leu Ile Trp
            185                 190                 195

att gta ctg tcc ggc ctt gca gca tgg gcg gtc ttt tcc cct tcc gtc   739
Ile Val Leu Ser Gly Leu Ala Ala Trp Ala Val Phe Ser Pro Ser Val
        200                 205                 210

aac gct gaa gga gtg ctg tcc atc atc cca tcc gtt gcg ctg tcc caa   787
Asn Ala Glu Gly Val Leu Ser Ile Ile Pro Ser Val Ala Leu Ser Gln
    215                 220                 225

ggt atg gtt gac gca ttc aac ggc gaa ctt ccg tgg ctc cag cta gga   835
Gly Met Val Asp Ala Phe Asn Gly Glu Leu Pro Trp Leu Gln Leu Gly
230                 235                 240                 245
```

```
att ttg gtg ggc tgg cta att atc acc ggc gtg gcc gca aac aag cta   883
Ile Leu Val Gly Trp Leu Ile Ile Thr Gly Val Ala Ala Asn Lys Leu
                250                 255                 260

ttt aac ttc tct gcg agc cgc tagatatacc cttagtcgga aaa             927
Phe Asn Phe Ser Ala Ser Arg
            265
```

<210> 1284
<211> 268
<212> PRT
<213> Corynebacterium glutamicum

<400> 1284

```
Met Ser Lys Pro Phe Glu Asn Ser Ala Leu Arg Gly Ser Ser Arg Phe
  1               5                  10                  15

Pro Ala Gly Thr Phe Thr Pro Ala Pro Lys Arg Ala Thr Pro Ala Lys
             20                  25                  30

Met Leu Ala Ala Gln Gly Lys Met Glu Ser Leu Leu Phe Leu Arg His
         35                  40                  45

Gly Glu Gln Gln Leu Leu Ser Ile Ile Ile Pro Leu Val Ala Leu Ile
     50                  55                  60

Ala Leu Ala Asn Phe Asp Phe Ile Pro Gly Glu Asn Ser Leu Asp Lys
 65                  70                  75                  80

Thr Phe Pro Phe Ala Leu Ala Thr Ala Ala Met Ser Ala Gly Phe Thr
                 85                  90                  95

Gly Gln Ala Ile Ser Leu Ala Phe Asp Arg Arg Tyr Gly Ala Leu Lys
            100                 105                 110

Arg Thr Gly Ala Ser Gly Val Pro Ala Trp Thr Ile Ile Phe Gly Lys
        115                 120                 125

Val Ile Ala Val Ile Ala Val Thr Ile Val Gln Ile Ile Phe Leu Gly
    130                 135                 140

Val Thr Ala Leu Leu Leu Gly Trp Ser Ala Pro Val Gly Gly Val Leu
145                 150                 155                 160

Phe Gly Ile Val Thr Leu Phe Val Gly Val Ser Ser Phe Thr Ala Leu
                165                 170                 175

Gly Met Leu Met Gly Gly Thr Leu Ser Ser Glu Leu Val Leu Ala Leu
            180                 185                 190

Ala Asn Leu Ile Trp Ile Val Leu Ser Gly Leu Ala Ala Trp Ala Val
        195                 200                 205

Phe Ser Pro Ser Val Asn Ala Glu Gly Val Leu Ser Ile Ile Pro Ser
    210                 215                 220

Val Ala Leu Ser Gln Gly Met Val Asp Ala Phe Asn Gly Glu Leu Pro
225                 230                 235                 240
```

```
Trp Leu Gln Leu Gly Ile Leu Val Gly Trp Leu Ile Ile Thr Gly Val
                245                 250                 255

Ala Ala Asn Lys Leu Phe Asn Phe Ser Ala Ser Arg
            260                 265


<210> 1285
<211> 1689
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1666)
<223> RXN02770

<400> 1285
tcgccggggc aaaaaccgta taattacagt cctattacga ttcggggaaa ggctgggtac 60

ttcacacatg ttgtttcgga agtcacgcag cgcggtaatc atg ttg gtt gca gcg   115
                                            Met Leu Val Ala Ala
                                              1               5

tta gtg atg aca agc tgt ggt gat ggg gaa ccg gaa cca acc agc cac   163
Leu Val Met Thr Ser Cys Gly Asp Gly Glu Pro Glu Pro Thr Ser His
                10                  15                  20

caa aca agc ctt ttc ggc tac gca gtt aac tct tcg ctg gct aca acc   211
Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser Ser Leu Ala Thr Thr
            25                  30                  35

aac gcg gcg tcg ctg ttg gga gtg gct aat gat gct ggt ctt ttg gct   259
Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp Ala Gly Leu Leu Ala
        40                  45                  50

gcc aga gtg tat ccg ggt gtg tat gtt cag ggt cct tct ggg cag atg   307
Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly Pro Ser Gly Gln Met
    55                  60                  65

att ccc aac act gat ctt gct tcc acg cag gta ttg ccg ggt att aac   355
Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val Leu Pro Gly Ile Asn
70                  75                  80                  85

cgc cag gtg att tac act atc aat gaa gat gcc acc tac tca gat ggt   403
Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala Thr Tyr Ser Asp Gly
                90                  95                  100

cag cct gtg gtg tgt gat gat ttt ctg ctc tct gcg aca gct ggg cag   451
Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser Ala Thr Ala Gly Gln
            105                 110                 115

atg ccg gaa ctg ttc cag tcc cat gtg cca ttg acc tcg cag att gag   499
Met Pro Glu Leu Phe Gln Ser His Val Pro Leu Thr Ser Gln Ile Glu
        120                 125                 130

cga gtg gac tgt gta tct ggt tct aaa gta gcc acc gtg gtg ttc aag   547
Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala Thr Val Val Phe Lys
    135                 140                 145

gaa gac ctc ggt gag cgt tgg cgt tat ctt ttt gag cag ggc gat ttg   595
```

```
Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe Glu Gln Gly Asp Leu
150                 155                 160                 165

ttg cca gcc cat gcc gtt gct tcc aaa gca ggt atg acc ttg gag gag   643
Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly Met Thr Leu Glu Glu
                170                 175                 180

ctt aat cag gcg ttg aag gat aag gat cct gaa gcg ttg act gaa cct   691
Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu Ala Leu Thr Glu Pro
            185                 190                 195

gct cgt gtg tgg agc gaa ggt ttc cag ctg tcc cag ttt gat cca gag   739
Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser Gln Phe Asp Pro Glu
        200                 205                 210

ctg cag acg gct ttt ggc ccg tac aag gtg gat tct gtg ggt gaa ttc   787
Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp Ser Val Gly Glu Phe
    215                 220                 225

ggc gaa gtc aag ctg gta cgc aat gag ttt tac agt ggc gac cag gcg   835
Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr Ser Gly Asp Gln Ala
230                 235                 240                 245

gtt gaa gca gaa atc acg atg tgg cct aaa ggc tcg gat ctc agc gcc   883
Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly Ser Asp Leu Ser Ala
                250                 255                 260

att gcg gat aat gga aac ctt cag atc gca cat gtt gtg gcg tgg gag   931
Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His Val Val Ala Trp Glu
            265                 270                 275

agc gag ccg tgg gta aat cgc gat gac cca ttg aat cct tat gac att   979
Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu Asn Pro Tyr Asp Ile
        280                 285                 290

aag gaa gag gtc ggt gtt ttg act gag cag ctc acc ttg gcc agt gcc  1027
Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu Thr Leu Ala Ser Ala
    295                 300                 305

ggt gtg ttt tac gct gcg gag gcc cgg cag gcg ttt gcg gcc tgc gtt  1075
Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala Phe Ala Ala Cys Val
310                 315                 320                 325

gac cag gaa gcg gtg gct gcg gcg tcg tca agc atc tct gga atc gat  1123
Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser Ile Ser Gly Ile Asp
                330                 335                 340

gtg cct gcc gta ggt gtg cac tcg gtg cgt cac caa aat ccg gtc gtg  1171
Val Pro Ala Val Gly Val His Ser Val Arg His Gln Asn Pro Val Val
            345                 350                 355

cac caa atc ggt gat ctg cca gca cag cac atg gcg gtg gat att aat  1219
His Gln Ile Gly Asp Leu Pro Ala Gln His Met Ala Val Asp Ile Asn
        360                 365                 370

gcc gca tca gcg ttg gcg ggt caa tcc atc cgc att ggc tac gac gga  1267
Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg Ile Gly Tyr Asp Gly
    375                 380                 385

ccc gat gag cgc aag gct gca atg gtg gag gcg att cgc caa agt tgt  1315
Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala Ile Arg Gln Ser Cys
```

```
390                 395                 400                 405

gag cct gcc ggt atc acc gtt atc gat gcg tcg cag gag gct gtt agt   1363
Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser Gln Glu Ala Val Ser
                410                 415                 420

ctt aat gat ctc agt cga acc gaa gtc agt gaa tgg ggc tat gag cag   1411
Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu Trp Gly Tyr Glu Gln
            425                 430                 435

tac ttc gaa ggg aca ctt gac gct gtt ctg cgt aca gtg gat cca cat   1459
Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg Thr Val Asp Pro His
        440                 445                 450

cgg gag tat gaa aat gcc aat acc att gga act gat gcg gag tcg acg   1507
Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr Asp Ala Glu Ser Thr
    455                 460                 465

agg cgc act gaa gaa caa ttg tgg gct gaa gtc cca tca att cca cta   1555
Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val Pro Ser Ile Pro Leu
470                 475                 480                 485

gca gcg caa ccc cga gtg ttt gtg ata gat cgc aca gtc ggt aac gtt   1603
Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg Thr Val Gly Asn Val
                490                 495                 500

gtt gtt aat aca gac cta gcc ggt atc gga tgg aac atg gac cgt tgg   1651
Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp Asn Met Asp Arg Trp
            505                 510                 515

tcc aga agt gag gaa taagtagtga gcgaacaagc tct                    1689
Ser Arg Ser Glu Glu
        520
```

<210> 1286
<211> 522
<212> PRT
<213> Corynebacterium glutamicum

<400> 1286

```
Met Leu Val Ala Ala Leu Val Met Thr Ser Cys Gly Asp Gly Glu Pro
  1               5                  10                  15

Glu Pro Thr Ser His Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser
             20                  25                  30

Ser Leu Ala Thr Thr Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp
         35                  40                  45

Ala Gly Leu Leu Ala Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly
     50                  55                  60

Pro Ser Gly Gln Met Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val
 65                  70                  75                  80

Leu Pro Gly Ile Asn Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala
                 85                  90                  95

Thr Tyr Ser Asp Gly Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser
            100                 105                 110
```

Ala Thr Ala Gly Gln Met Pro Glu Leu Phe Gln Ser His Val Pro Leu
115 120 125

Thr Ser Gln Ile Glu Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala
130 135 140

Thr Val Val Phe Lys Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe
145 150 155 160

Glu Gln Gly Asp Leu Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly
165 170 175

Met Thr Leu Glu Glu Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu
180 185 190

Ala Leu Thr Glu Pro Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser
195 200 205

Gln Phe Asp Pro Glu Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp
210 215 220

Ser Val Gly Glu Phe Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr
225 230 235 240

Ser Gly Asp Gln Ala Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly
245 250 255

Ser Asp Leu Ser Ala Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His
260 265 270

Val Val Ala Trp Glu Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu
275 280 285

Asn Pro Tyr Asp Ile Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu
290 295 300

Thr Leu Ala Ser Ala Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala
305 310 315 320

Phe Ala Ala Cys Val Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser
325 330 335

Ile Ser Gly Ile Asp Val Pro Ala Val Gly Val His Ser Val Arg His
340 345 350

Gln Asn Pro Val Val His Gln Ile Gly Asp Leu Pro Ala Gln His Met
355 360 365

Ala Val Asp Ile Asn Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg
370 375 380

Ile Gly Tyr Asp Gly Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala
385 390 395 400

Ile Arg Gln Ser Cys Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser
405 410 415

Gln Glu Ala Val Ser Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu
420 425 430

```
Trp Gly Tyr Glu Gln Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg
        435                 440                 445

Thr Val Asp Pro His Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr
    450                 455                 460

Asp Ala Glu Ser Thr Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val
465                 470                 475                 480

Pro Ser Ile Pro Leu Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg
                485                 490                 495

Thr Val Gly Asn Val Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp
            500                 505                 510

Asn Met Asp Arg Trp Ser Arg Ser Glu Glu
        515                 520
```

<210> 1287
<211> 1343
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1320)
<223> FRXA02770

<400> 1287

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ggt att aac cgc cag gtg att tac act atc aat gaa gat gcc acc tac   48
Gly Ile Asn Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala Thr Tyr
  1               5                  10                  15

tca gat ggt cag cct gtg gtg tgt gat gat ttt ctg ctc tct gcg aca   96
Ser Asp Gly Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser Ala Thr
             20                  25                  30

gct ggg cag atg ccg gaa ctg ttc cag tcc cat gtg cca ttg acc tcg   144
Ala Gly Gln Met Pro Glu Leu Phe Gln Ser His Val Pro Leu Thr Ser
         35                  40                  45

cag att gag cga gtg gac tgt gta tct ggt tct aaa gta gcc acc gtg   192
Gln Ile Glu Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala Thr Val
     50                  55                  60

gtg ttc aag gaa gac ctc ggt gag cgt tgg cgt tat ctt ttt gag cag   240
Val Phe Lys Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe Glu Gln
 65                  70                  75                  80

ggc gat ttg ttg cca gcc cat gcc gtt gct tcc aaa gca ggt atg acc   288
Gly Asp Leu Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly Met Thr
                 85                  90                  95

ttg gag gag ctt aat cag gcg ttg aag gat aag gat cct gaa gcg ttg   336
Leu Glu Glu Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu Ala Leu
            100                 105                 110

act gaa cct gct cgt gtg tgg agc gaa ggt ttc cag ctg tcc cag ttt   384
Thr Glu Pro Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser Gln Phe
        115                 120                 125
```

```
gat cca gag ctg cag acg gct ttt ggc ccg tac aag gtg gat tct gtg   432
Asp Pro Glu Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp Ser Val
    130                 135                 140

ggt gaa ttc ggc gaa gtc aag ctg gta cgc aat gag ttt tac agt ggc   480
Gly Glu Phe Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr Ser Gly
145                 150                 155                 160

gac cag gcg gtt gaa gca gaa atc acg atg tgg cct aaa ggc tcg gat   528
Asp Gln Ala Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly Ser Asp
                165                 170                 175

ctc agc gcc att gcg gat aat gga aac ctt cag atc gca cat gtt gtg   576
Leu Ser Ala Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His Val Val
            180                 185                 190

gcg tgg gag agc gag ccg tgg gta aat cgc gat gac cca ttg aat cct   624
Ala Trp Glu Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu Asn Pro
        195                 200                 205

tat gac att aag gaa gag gtc ggt gtt ttg act gag cag ctc acc ttg   672
Tyr Asp Ile Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu Thr Leu
    210                 215                 220

gcc agt gcc ggt gtg ttt tac gct gcg gag gcc cgg cag gcg ttt gcg   720
Ala Ser Ala Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala Phe Ala
225                 230                 235                 240

gcc tgc gtt gac cag gaa gcg gtg gct gcg gcg tcg tca agc atc tct   768
Ala Cys Val Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser Ile Ser
                245                 250                 255

gga atc gat gtg cct gcc gta ggt gtg cac tcg gtg cgt cac caa aat   816
Gly Ile Asp Val Pro Ala Val Gly Val His Ser Val Arg His Gln Asn
            260                 265                 270

ccg gtc gtg cac caa atc ggt gat ctg cca gca cag cac atg gcg gtg   864
Pro Val Val His Gln Ile Gly Asp Leu Pro Ala Gln His Met Ala Val
        275                 280                 285

gat att aat gcc gca tca gcg ttg gcg ggt caa tcc atc cgc att ggc   912
Asp Ile Asn Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg Ile Gly
    290                 295                 300

tac gac gga ccc gat gag cgc aag gct gca atg gtg gag gcg att cgc   960
Tyr Asp Gly Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala Ile Arg
305                 310                 315                 320

caa agt tgt gag cct gcc ggt atc acc gtt atc gat gcg tcg cag gag  1008
Gln Ser Cys Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser Gln Glu
                325                 330                 335

gct gtt agt ctt aat gat ctc agt cga acc gaa gtc agt gaa tgg ggc  1056
Ala Val Ser Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu Trp Gly
            340                 345                 350

tat gag cag tac ttc gaa ggg aca ctt gac gct gtt ctg cgt aca gtg  1104
Tyr Glu Gln Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg Thr Val
        355                 360                 365
```

```
gat cca cat cgg gag tat gaa aat gcc aat acc att gga act gat gcg   1152
Asp Pro His Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr Asp Ala
    370                 375                 380

gag tcg acg agg cgc act gaa gaa caa ttg tgg gct gaa gtc cca tca   1200
Glu Ser Thr Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val Pro Ser
385                 390                 395                 400

att cca cta gca gcg caa ccc cga gtg ttt gtg ata gat cgc aca gtc   1248
Ile Pro Leu Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg Thr Val
                405                 410                 415

ggt aac gtt gtt gtt aat aca gac cta gcc ggt atc gga tgg aac atg   1296
Gly Asn Val Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp Asn Met
            420                 425                 430

gac cgt tgg tcc aga agt gag gaa taagtagtga gcgaacaagc tct         1343
Asp Arg Trp Ser Arg Ser Glu Glu
        435                 440
```

<210> 1288
<211> 440
<212> PRT
<213> Corynebacterium glutamicum

<400> 1288

```
Gly Ile Asn Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala Thr Tyr
  1               5                  10                  15

Ser Asp Gly Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser Ala Thr
             20                  25                  30

Ala Gly Gln Met Pro Glu Leu Phe Gln Ser His Val Pro Leu Thr Ser
         35                  40                  45

Gln Ile Glu Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala Thr Val
     50                  55                  60

Val Phe Lys Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe Glu Gln
 65                  70                  75                  80

Gly Asp Leu Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly Met Thr
                 85                  90                  95

Leu Glu Glu Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu Ala Leu
            100                 105                 110

Thr Glu Pro Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser Gln Phe
        115                 120                 125

Asp Pro Glu Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp Ser Val
    130                 135                 140

Gly Glu Phe Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr Ser Gly
145                 150                 155                 160

Asp Gln Ala Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly Ser Asp
                165                 170                 175

Leu Ser Ala Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His Val Val
```

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            180                 185                 190

Ala Trp Glu Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu Asn Pro
        195                 200                 205

Tyr Asp Ile Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu Thr Leu
    210                 215                 220

Ala Ser Ala Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala Phe Ala
225                 230                 235                 240

Ala Cys Val Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser Ile Ser
                245                 250                 255

Gly Ile Asp Val Pro Ala Val Gly Val His Ser Val Arg His Gln Asn
            260                 265                 270

Pro Val Val His Gln Ile Gly Asp Leu Pro Ala Gln His Met Ala Val
        275                 280                 285

Asp Ile Asn Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg Ile Gly
    290                 295                 300

Tyr Asp Gly Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala Ile Arg
305                 310                 315                 320

Gln Ser Cys Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser Gln Glu
                325                 330                 335

Ala Val Ser Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu Trp Gly
            340                 345                 350

Tyr Glu Gln Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg Thr Val
        355                 360                 365

Asp Pro His Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr Asp Ala
    370                 375                 380

Glu Ser Thr Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val Pro Ser
385                 390                 395                 400

Ile Pro Leu Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg Thr Val
                405                 410                 415

Gly Asn Val Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp Asn Met
            420                 425                 430

Asp Arg Trp Ser Arg Ser Glu Glu
        435                 440


<210> 1289
<211> 1314
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1291)
<223> RXN02781
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<400> 1289
ctccgagagt ttccgcatcc gcggttcgat cccggacgtt ccccgggaga cgcggtggga 60

ccggctgtgg cggcccttct gggcgatacc ggctgccagc gtg gtc gcg gcc ctg 115
Val Val Ala Ala Leu
1 5

gtt ttc ggt ttc ctg ctt ccc acg tgg gaa cgt ggg ttg tcc gac gcc 163
Val Phe Gly Phe Leu Leu Pro Thr Trp Glu Arg Gly Leu Ser Asp Ala
10 15 20

gcg ctc aaa ttc gtt ttt gag ggt ggg cct gat gcc gcc cgc gag gtg 211
Ala Leu Lys Phe Val Phe Glu Gly Gly Pro Asp Ala Ala Arg Glu Val
25 30 35

ctg ggc acc atc gcc gcc tcc acg atc tca gtg acc ggt ctc atc ttc 259
Leu Gly Thr Ile Ala Ala Ser Thr Ile Ser Val Thr Gly Leu Ile Phe
40 45 50

tcc atc act ctc gtt gtt ctg cag ctg gtg agc agc cag ttc agc ccg 307
Ser Ile Thr Leu Val Val Leu Gln Leu Val Ser Ser Gln Phe Ser Pro
55 60 65

cga atg ctc aac ggc ttt ctg cgc aac cgc atc gtg cag gcc acc ctg 355
Arg Met Leu Asn Gly Phe Leu Arg Asn Arg Ile Val Gln Ala Thr Leu
70 75 80 85

gcg atg ttc ctg ggg acg ttc gtg ttc tcc ctg acg gtc atc cgg tac 403
Ala Met Phe Leu Gly Thr Phe Val Phe Ser Leu Thr Val Ile Arg Tyr
90 95 100

gtg tgg agc gag gac gag gac atc acc gga ttc gtc ccc cgt gct tca 451
Val Trp Ser Glu Asp Glu Asp Ile Thr Gly Phe Val Pro Arg Ala Ser
105 110 115

gtg tcg gtt gcc ttc ctg ctg gtg ctc ggg tgt ctg gga ctg ttc ctg 499
Val Ser Val Ala Phe Leu Leu Val Leu Gly Cys Leu Gly Leu Phe Leu
120 125 130

gcg ttc atc cgg ctc atc acc ttc tcg atg cgg gtg gcc aac gcc atc 547
Ala Phe Ile Arg Leu Ile Thr Phe Ser Met Arg Val Ala Asn Ala Ile
135 140 145

tcc gag atc ggg gag gag acg atg gct ctg gcc gca cgt atc tat ccc 595
Ser Glu Ile Gly Glu Glu Thr Met Ala Leu Ala Ala Arg Ile Tyr Pro
150 155 160 165

gtg cag agc gac gac gca ggc cca gtc cag ggg ccg ggc tgg tca ccg 643
Val Gln Ser Asp Asp Ala Gly Pro Val Gln Gly Pro Gly Trp Ser Pro
170 175 180

cgg ccc ggt gac ccc cgg gaa gaa atc cgg gtg ggc aac cat ggt tcg 691
Arg Pro Gly Asp Pro Arg Glu Glu Ile Arg Val Gly Asn His Gly Ser
185 190 195

ctg gtg tgg atc gac tac cgg aag ctg gtg tcc tgg tcg acg gaa cac 739
Leu Val Trp Ile Asp Tyr Arg Lys Leu Val Ser Trp Ser Thr Glu His
200 205 210

cag gcg gtg atc acg gtc gac cgg ccg gtg ggg gac ttc ctc gtc gag 787
Gln Ala Val Ile Thr Val Asp Arg Pro Val Gly Asp Phe Leu Val Glu

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    215                 220                 225

ggc cag ccg ctg ctg cgg gtc tgg tgg gac ggg gaa ctc agc gac cgg   835
Gly Gln Pro Leu Leu Arg Val Trp Trp Asp Gly Glu Leu Ser Asp Arg
230                 235                 240                 245

gac cga cgc gtt ctg cac tcg gcc atc gag gtg cgg acc gag cgg gaa   883
Asp Arg Arg Val Leu His Ser Ala Ile Glu Val Arg Thr Glu Arg Glu
                250                 255                 260

ctt cac cag gat gtg gcg ttc gga ctg cgt caa ctg gtc gac att gcc   931
Leu His Gln Asp Val Ala Phe Gly Leu Arg Gln Leu Val Asp Ile Ala
            265                 270                 275

gat cgt gcg ttg tcc ccg ggc atc aat gat ccg gcc acg gcg gcc cag   979
Asp Arg Ala Leu Ser Pro Gly Ile Asn Asp Pro Ala Thr Ala Ala Gln
        280                 285                 290

tgt gtc cag gag atc cac cgg atc ttc cgc tat ttg gtc acc gtc atc   1027
Cys Val Gln Glu Ile His Arg Ile Phe Arg Tyr Leu Val Thr Val Ile
    295                 300                 305

gag ccc agc ccc tac atc gcc gat gac gac ggt cgg gtc cgt gtg gtg   1075
Glu Pro Ser Pro Tyr Ile Ala Asp Asp Asp Gly Arg Val Arg Val Val
310                 315                 320                 325

cac cag ccg caa cgt atc gcg gac atg ctc tat gag gtg atc cgt gag   1123
His Gln Pro Gln Arg Ile Ala Asp Met Leu Tyr Glu Val Ile Arg Glu
                330                 335                 340

atc cat ctc tac ggg gcg gat tct gcg atg att ccg agg ctg ctg cgc   1171
Ile His Leu Tyr Gly Ala Asp Ser Ala Met Ile Pro Arg Leu Leu Arg
            345                 350                 355

acc atg gtc gag gac ctg gtg acg gcc gct gcc gat cat tcc ctg cct   1219
Thr Met Val Glu Asp Leu Val Thr Ala Ala Ala Asp His Ser Leu Pro
        360                 365                 370

gcc gtc gag cgt gcc cgc ggc atc ctg gac gat gag acg gac gag gac   1267
Ala Val Glu Arg Ala Arg Gly Ile Leu Asp Asp Glu Thr Asp Glu Asp
    375                 380                 385

cgc gac agt gac acc gcg aac gtc tgatccggga tcaggtggcg gtg         1314
Arg Asp Ser Asp Thr Ala Asn Val
390                 395


<210> 1290
<211> 397
<212> PRT
<213> Corynebacterium glutamicum

<400> 1290
Val Val Ala Ala Leu Val Phe Gly Phe Leu Leu Pro Thr Trp Glu Arg
  1               5                  10                  15

Gly Leu Ser Asp Ala Ala Leu Lys Phe Val Phe Glu Gly Gly Pro Asp
             20                  25                  30

Ala Ala Arg Glu Val Leu Gly Thr Ile Ala Ala Ser Thr Ile Ser Val
         35                  40                  45
```

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Thr Gly Leu Ile Phe Ser Ile Thr Leu Val Val Leu Gln Leu Val Ser
     50                  55                  60

Ser Gln Phe Ser Pro Arg Met Leu Asn Gly Phe Leu Arg Asn Arg Ile
 65                  70                  75                  80

Val Gln Ala Thr Leu Ala Met Phe Leu Gly Thr Phe Val Phe Ser Leu
                85                  90                  95

Thr Val Ile Arg Tyr Val Trp Ser Glu Asp Glu Asp Ile Thr Gly Phe
            100                 105                 110

Val Pro Arg Ala Ser Val Ser Val Ala Phe Leu Leu Val Leu Gly Cys
        115                 120                 125

Leu Gly Leu Phe Leu Ala Phe Ile Arg Leu Ile Thr Phe Ser Met Arg
    130                 135                 140

Val Ala Asn Ala Ile Ser Glu Ile Gly Glu Glu Thr Met Ala Leu Ala
145                 150                 155                 160

Ala Arg Ile Tyr Pro Val Gln Ser Asp Asp Ala Gly Pro Val Gln Gly
                165                 170                 175

Pro Gly Trp Ser Pro Arg Pro Gly Asp Pro Arg Glu Glu Ile Arg Val
            180                 185                 190

Gly Asn His Gly Ser Leu Val Trp Ile Asp Tyr Arg Lys Leu Val Ser
        195                 200                 205

Trp Ser Thr Glu His Gln Ala Val Ile Thr Val Asp Arg Pro Val Gly
    210                 215                 220

Asp Phe Leu Val Glu Gly Gln Pro Leu Leu Arg Val Trp Trp Asp Gly
225                 230                 235                 240

Glu Leu Ser Asp Arg Asp Arg Arg Val Leu His Ser Ala Ile Glu Val
                245                 250                 255

Arg Thr Glu Arg Glu Leu His Gln Asp Val Ala Phe Gly Leu Arg Gln
            260                 265                 270

Leu Val Asp Ile Ala Asp Arg Ala Leu Ser Pro Gly Ile Asn Asp Pro
        275                 280                 285

Ala Thr Ala Ala Gln Cys Val Gln Glu Ile His Arg Ile Phe Arg Tyr
    290                 295                 300

Leu Val Thr Val Ile Glu Pro Ser Pro Tyr Ile Ala Asp Asp Asp Gly
305                 310                 315                 320

Arg Val Arg Val Val His Gln Pro Gln Arg Ile Ala Asp Met Leu Tyr
                325                 330                 335

Glu Val Ile Arg Glu Ile His Leu Tyr Gly Ala Asp Ser Ala Met Ile
            340                 345                 350

Pro Arg Leu Leu Arg Thr Met Val Glu Asp Leu Val Thr Ala Ala Ala
        355                 360                 365
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Asp His Ser Leu Pro Ala Val Glu Arg Ala Arg Gly Ile Leu Asp Asp
    370                 375                 380

Glu Thr Asp Glu Asp Arg Asp Ser Asp Thr Ala Asn Val
385                 390                 395


<210> 1291
<211> 1314
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1291)
<223> FRXA02781

<400> 1291
ctccgagagt ttccgcatcc gcggttcgat cccggacgtt ccccgggaga cgcggtggga 60

ccggctgtgg cggcccttct gggcgatacc ggctgccagc gtg gtc gcg gcc ctg   115
                                            Val Val Ala Ala Leu
                                              1               5

gtt ttc ggt ttc ctg ctt ccc acg tgg gaa cgt ggg ttg tcc gac gcc   163
Val Phe Gly Phe Leu Leu Pro Thr Trp Glu Arg Gly Leu Ser Asp Ala
                 10                  15                  20

gcg ctc aaa ttc gtt ttt gag ggt ggg cct gat gcc gcc cgc gag gtg   211
Ala Leu Lys Phe Val Phe Glu Gly Gly Pro Asp Ala Ala Arg Glu Val
             25                  30                  35

ctg ggc acc atc gcc gcc tcc acg atc tca gtg acc ggt ctc atc ttc   259
Leu Gly Thr Ile Ala Ala Ser Thr Ile Ser Val Thr Gly Leu Ile Phe
         40                  45                  50

tcc atc act ctc gtt gtt ctg cag ctg gtg agc agc cag ttc agc ccg   307
Ser Ile Thr Leu Val Val Leu Gln Leu Val Ser Ser Gln Phe Ser Pro
     55                  60                  65

cga atg ctc aac ggc ttt ctg cgc aac cgc atc gtg cag gcc acc ctg   355
Arg Met Leu Asn Gly Phe Leu Arg Asn Arg Ile Val Gln Ala Thr Leu
 70                  75                  80                  85

gcg atg ttc ctg ggg acg ttc gtg ttc tcc ctg acg gtc atc cgg tac   403
Ala Met Phe Leu Gly Thr Phe Val Phe Ser Leu Thr Val Ile Arg Tyr
                 90                  95                 100

gtg tgg agc gag gac gag gac atc acc gga ttc gtc ccc cgt gct tca   451
Val Trp Ser Glu Asp Glu Asp Ile Thr Gly Phe Val Pro Arg Ala Ser
            105                 110                 115

gtg tcg gtt gcc ttc ctg ctg gtg ctc ggg tgt ctg gga ctg ttc ctg   499
Val Ser Val Ala Phe Leu Leu Val Leu Gly Cys Leu Gly Leu Phe Leu
        120                 125                 130

gcg ttc atc cgg ctc atc acc ttc tcg atg cgg gtg gcc aac gcc atc   547
Ala Phe Ile Arg Leu Ile Thr Phe Ser Met Arg Val Ala Asn Ala Ile
    135                 140                 145

tcc gag atc ggg gag gag acg atg gct ctg gcc gca cgt atc tat ccc   595
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Ser Glu Ile Gly Glu Glu Thr Met Ala Leu Ala Ala Arg Ile Tyr Pro
150                 155                 160                 165

gtg cag agc gac gac gca ggc cca gtc cag ggg ccg ggc tgg tca ccg   643
Val Gln Ser Asp Asp Ala Gly Pro Val Gln Gly Pro Gly Trp Ser Pro
                170                 175                 180

cgg ccc ggt gac ccc cgg gaa gaa atc cgg gtg ggc aac cat ggt tcg   691
Arg Pro Gly Asp Pro Arg Glu Glu Ile Arg Val Gly Asn His Gly Ser
            185                 190                 195

ctg gtg tgg atc gac tac cgg aag ctg gtg tcc tgg tcg acg gaa cac   739
Leu Val Trp Ile Asp Tyr Arg Lys Leu Val Ser Trp Ser Thr Glu His
        200                 205                 210

cag gcg gtg atc acg gtc gac cgg ccg gtg ggg gac ttc ctc gtc gag   787
Gln Ala Val Ile Thr Val Asp Arg Pro Val Gly Asp Phe Leu Val Glu
    215                 220                 225

ggc cag ccg ctg ctg cgg gtc tgg tgg gac ggg gaa ctc agc gac cgg   835
Gly Gln Pro Leu Leu Arg Val Trp Trp Asp Gly Glu Leu Ser Asp Arg
230                 235                 240                 245

gac cga cgc gtt ctg cac tcg gcc atc gag gtg cgg acc gag cgg gaa   883
Asp Arg Arg Val Leu His Ser Ala Ile Glu Val Arg Thr Glu Arg Glu
                250                 255                 260

ctt cac cag gat gtg gcg ttc gga ctg cgt caa ctg gtc gac att gcc   931
Leu His Gln Asp Val Ala Phe Gly Leu Arg Gln Leu Val Asp Ile Ala
            265                 270                 275

gat cgt gcg ttg tcc ccg ggc atc aat gat ccg gcc acg gcg gcc cag   979
Asp Arg Ala Leu Ser Pro Gly Ile Asn Asp Pro Ala Thr Ala Ala Gln
        280                 285                 290

tgt gtc cag gag atc cac cgg atc ttc cgc tat ttg gtc acc gtc atc  1027
Cys Val Gln Glu Ile His Arg Ile Phe Arg Tyr Leu Val Thr Val Ile
    295                 300                 305

gag ccc agc ccc tac atc gcc gat gac gac ggt cgg gtc cgt gtg gtg  1075
Glu Pro Ser Pro Tyr Ile Ala Asp Asp Asp Gly Arg Val Arg Val Val
310                 315                 320                 325

cac cag ccg caa cgt atc gcg gac atg ctc tat gag gtg atc cgt gag  1123
His Gln Pro Gln Arg Ile Ala Asp Met Leu Tyr Glu Val Ile Arg Glu
                330                 335                 340

atc cat ctc tac ggg gcg gat tct gcg atg att ccg agg ctg ctg cgc  1171
Ile His Leu Tyr Gly Ala Asp Ser Ala Met Ile Pro Arg Leu Leu Arg
            345                 350                 355

acc atg gtc gag gac ctg gtg acg gcc gct gcc gat cat tcc ctg cct  1219
Thr Met Val Glu Asp Leu Val Thr Ala Ala Ala Asp His Ser Leu Pro
        360                 365                 370

gcc gtc gag cgt gcc cgc ggc atc ctg gac gat gag acg gac gag gac  1267
Ala Val Glu Arg Ala Arg Gly Ile Leu Asp Asp Glu Thr Asp Glu Asp
    375                 380                 385

cgc gac agt gac acc gcg aac gtc tgatccggga tcaggtggcg gtg        1314
Arg Asp Ser Asp Thr Ala Asn Val
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390 395

<210> 1292
<211> 397
<212> PRT
<213> Corynebacterium glutamicum

<400> 1292
Val Val Ala Ala Leu Val Phe Gly Phe Leu Leu Pro Thr Trp Glu Arg
1 5 10 15

Gly Leu Ser Asp Ala Ala Leu Lys Phe Val Phe Glu Gly Gly Pro Asp
20 25 30

Ala Ala Arg Glu Val Leu Gly Thr Ile Ala Ala Ser Thr Ile Ser Val
35 40 45

Thr Gly Leu Ile Phe Ser Ile Thr Leu Val Val Leu Gln Leu Val Ser
50 55 60

Ser Gln Phe Ser Pro Arg Met Leu Asn Gly Phe Leu Arg Asn Arg Ile
65 70 75 80

Val Gln Ala Thr Leu Ala Met Phe Leu Gly Thr Phe Val Phe Ser Leu
85 90 95

Thr Val Ile Arg Tyr Val Trp Ser Glu Asp Glu Asp Ile Thr Gly Phe
100 105 110

Val Pro Arg Ala Ser Val Ser Val Ala Phe Leu Leu Val Leu Gly Cys
115 120 125

Leu Gly Leu Phe Leu Ala Phe Ile Arg Leu Ile Thr Phe Ser Met Arg
130 135 140

Val Ala Asn Ala Ile Ser Glu Ile Gly Glu Glu Thr Met Ala Leu Ala
145 150 155 160

Ala Arg Ile Tyr Pro Val Gln Ser Asp Asp Ala Gly Pro Val Gln Gly
165 170 175

Pro Gly Trp Ser Pro Arg Pro Gly Asp Pro Arg Glu Glu Ile Arg Val
180 185 190

Gly Asn His Gly Ser Leu Val Trp Ile Asp Tyr Arg Lys Leu Val Ser
195 200 205

Trp Ser Thr Glu His Gln Ala Val Ile Thr Val Asp Arg Pro Val Gly
210 215 220

Asp Phe Leu Val Glu Gly Gln Pro Leu Leu Arg Val Trp Trp Asp Gly
225 230 235 240

Glu Leu Ser Asp Arg Asp Arg Arg Val Leu His Ser Ala Ile Glu Val
245 250 255

Arg Thr Glu Arg Glu Leu His Gln Asp Val Ala Phe Gly Leu Arg Gln
260 265 270

Leu Val Asp Ile Ala Asp Arg Ala Leu Ser Pro Gly Ile Asn Asp Pro

```
        275                 280                 285

Ala Thr Ala Ala Gln Cys Val Gln Glu Ile His Arg Ile Phe Arg Tyr
    290                 295                 300

Leu Val Thr Val Ile Glu Pro Ser Pro Tyr Ile Ala Asp Asp Asp Gly
305                 310                 315                 320

Arg Val Arg Val Val His Gln Pro Gln Arg Ile Ala Asp Met Leu Tyr
                325                 330                 335

Glu Val Ile Arg Glu Ile His Leu Tyr Gly Ala Asp Ser Ala Met Ile
            340                 345                 350

Pro Arg Leu Leu Arg Thr Met Val Glu Asp Leu Val Thr Ala Ala Ala
        355                 360                 365

Asp His Ser Leu Pro Ala Val Glu Arg Ala Arg Gly Ile Leu Asp Asp
    370                 375                 380

Glu Thr Asp Glu Asp Arg Asp Ser Asp Thr Ala Asn Val
385                 390                 395


<210> 1293
<211> 1422
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1399)
<223> RXN02782

<400> 1293
accccacccg gtcccccttt tttcctcact gacaccggag ccgcctcaag caccacgctg 60

caatcacaga agctagttga gcatattgta gaatataact atg cca aca ctg ctt   115
                                            Met Pro Thr Leu Leu
                                              1               5

att gac acc cat ccg cat ctt gca gcg caa ctt ctt gac cct ggt tta   163
Ile Asp Thr His Pro His Leu Ala Ala Gln Leu Leu Asp Pro Gly Leu
                10                  15                  20

ggt gaa ctt ctt aca gcc ggt tcc aac aaa aaa gtg cag tgg cag tgc   211
Gly Glu Leu Leu Thr Ala Gly Ser Asn Lys Lys Val Gln Trp Gln Cys
            25                  30                  35

cct aag cac tcc aat cac atc tgg acg gcc tcg gtt aat aac cgc acc   259
Pro Lys His Ser Asn His Ile Trp Thr Ala Ser Val Asn Asn Arg Thr
        40                  45                  50

aat gca aag aac ccg cgc tgc ccc tat tgt gcc gga aca cga gtg ttg   307
Asn Ala Lys Asn Pro Arg Cys Pro Tyr Cys Ala Gly Thr Arg Val Leu
    55                  60                  65

gca ggt ttt aat gat ctc gcc acc act cac ccg cat ctt gct gta cag   355
Ala Gly Phe Asn Asp Leu Ala Thr Thr His Pro His Leu Ala Val Gln
70                  75                  80                  85
```

```
ctg gtt gac caa gat att gcc gtc acc att tcc gct ggt tct ggc aaa   403
Leu Val Asp Gln Asp Ile Ala Val Thr Ile Ser Ala Gly Ser Gly Lys
                 90                  95                 100

aga caa ctg tgg cag tgt gta gta aac cca aaa cac cag tgg ttg gct   451
Arg Gln Leu Trp Gln Cys Val Val Asn Pro Lys His Gln Trp Leu Ala
            105                 110                 115

acg cca aat aat cgc acg agt act aaa tct gcg agt tct ggt tgc ccc   499
Thr Pro Asn Asn Arg Thr Ser Thr Lys Ser Ala Ser Ser Gly Cys Pro
        120                 125                 130

tac tgt gcc aac cga gcg gta tta gtc ggt gac aat gac ttt gca aca   547
Tyr Cys Ala Asn Arg Ala Val Leu Val Gly Asp Asn Asp Phe Ala Thr
    135                 140                 145

acc tac ccc gaa ctt gca gcg caa tta gta gat caa tct gca gcg aca   595
Thr Tyr Pro Glu Leu Ala Ala Gln Leu Val Asp Gln Ser Ala Ala Thr
150                 155                 160                 165

acc ttt aca gcc ggc cac aac aag cct gtt gag tgg atc tgt tgc aag   643
Thr Phe Thr Ala Gly His Asn Lys Pro Val Glu Trp Ile Cys Cys Lys
                170                 175                 180

cat gaa cca cca ttt atc tgg aaa acc tca cca att ttg cgt gta cga   691
His Glu Pro Pro Phe Ile Trp Lys Thr Ser Pro Ile Leu Arg Val Arg
            185                 190                 195

cag aac acc cag tgc cct gtg tgc tca gag cga act gtg gcg ccg gcg   739
Gln Asn Thr Gln Cys Pro Val Cys Ser Glu Arg Thr Val Ala Pro Ala
        200                 205                 210

ctt aat gat ctt gca acc act cac cct aaa ctt gcc gag caa att gca   787
Leu Asn Asp Leu Ala Thr Thr His Pro Lys Leu Ala Glu Gln Ile Ala
    215                 220                 225

gat cct caa cca agt ggt gtg agc gcc gcg gcc att atc ccc acc att   835
Asp Pro Gln Pro Ser Gly Val Ser Ala Ala Ala Ile Ile Pro Thr Ile
230                 235                 240                 245

agc agg ggt tcc cat acg caa tta aca tgg caa tgt tct aaa aat cat   883
Ser Arg Gly Ser His Thr Gln Leu Thr Trp Gln Cys Ser Lys Asn His
                250                 255                 260

gac cac caa tgg gtc gcc aca gta aag gat cgt gtt cgc gga aca gac   931
Asp His Gln Trp Val Ala Thr Val Lys Asp Arg Val Arg Gly Thr Asp
            265                 270                 275

tgc ccc acc tgc gca aat aca gga act tca cgc aaa gag gct gaa ctt   979
Cys Pro Thr Cys Ala Asn Thr Gly Thr Ser Arg Lys Glu Ala Glu Leu
        280                 285                 290

att gag gtc atc cgt gca tta ttc cca aac act gat gtc cag caa ggt   1027
Ile Glu Val Ile Arg Ala Leu Phe Pro Asn Thr Asp Val Gln Gln Gly
    295                 300                 305

gcg ctc att aat gga cgt acc ggt aat caa ggt gca tcg ccg tca acc   1075
Ala Leu Ile Asn Gly Arg Thr Gly Asn Gln Gly Ala Ser Pro Ser Thr
310                 315                 320                 325

gat gta ctc ata ccg tcc aaa aat ctc gct atc gag ttc aac ggc ctg   1123
```

```
Asp Val Leu Ile Pro Ser Lys Asn Leu Ala Ile Glu Phe Asn Gly Leu
                330                 335                 340

tac tgg cac tct gag ctt ttc atc aaa gat aag cat tat cat gcg aac   1171
Tyr Trp His Ser Glu Leu Phe Ile Lys Asp Lys His Tyr His Ala Asn
            345                 350                 355

aaa tca gct ctc gca gaa caa gcc ggt gtg cag ctc att cat gtg tgg   1219
Lys Ser Ala Leu Ala Glu Gln Ala Gly Val Gln Leu Ile His Val Trp
        360                 365                 370

gag gac gac tgg aat ctt cgc cgc gac att gtg atc cgc atg atc gca   1267
Glu Asp Asp Trp Asn Leu Arg Arg Asp Ile Val Ile Arg Met Ile Ala
    375                 380                 385

cac aag ctt cat gca acc cat aac ctc agt gct gtt ttg cct acc gaa   1315
His Lys Leu His Ala Thr His Asn Leu Ser Ala Val Leu Pro Thr Glu
390                 395                 400                 405

act act gac tca cgt gtg gca acc acc gct ttc gcc gta cac tca cac   1363
Thr Thr Asp Ser Arg Val Ala Thr Thr Ala Phe Ala Val His Ser His
                410                 415                 420

tgt cgg tgg tct ctg gtt cac gcg ctg ctg cat tct tgaacagcaa        1409
Cys Arg Trp Ser Leu Val His Ala Leu Leu His Ser
            425                 430

ccatattcag ggt                                                   1422


<210> 1294
<211> 433
<212> PRT
<213> Corynebacterium glutamicum

<400> 1294
Met Pro Thr Leu Leu Ile Asp Thr His Pro His Leu Ala Ala Gln Leu
  1               5                  10                  15

Leu Asp Pro Gly Leu Gly Glu Leu Leu Thr Ala Gly Ser Asn Lys Lys
             20                  25                  30

Val Gln Trp Gln Cys Pro Lys His Ser Asn His Ile Trp Thr Ala Ser
         35                  40                  45

Val Asn Asn Arg Thr Asn Ala Lys Asn Pro Arg Cys Pro Tyr Cys Ala
     50                  55                  60

Gly Thr Arg Val Leu Ala Gly Phe Asn Asp Leu Ala Thr Thr His Pro
 65                  70                  75                  80

His Leu Ala Val Gln Leu Val Asp Gln Asp Ile Ala Val Thr Ile Ser
                 85                  90                  95

Ala Gly Ser Gly Lys Arg Gln Leu Trp Gln Cys Val Val Asn Pro Lys
            100                 105                 110

His Gln Trp Leu Ala Thr Pro Asn Asn Arg Thr Ser Thr Lys Ser Ala
        115                 120                 125

Ser Ser Gly Cys Pro Tyr Cys Ala Asn Arg Ala Val Leu Val Gly Asp
```

```
    130                 135                 140

Asn Asp Phe Ala Thr Thr Tyr Pro Glu Leu Ala Ala Gln Leu Val Asp
145                 150                 155                 160

Gln Ser Ala Ala Thr Thr Phe Thr Ala Gly His Asn Lys Pro Val Glu
                165                 170                 175

Trp Ile Cys Cys Lys His Glu Pro Pro Phe Ile Trp Lys Thr Ser Pro
            180                 185                 190

Ile Leu Arg Val Arg Gln Asn Thr Gln Cys Pro Val Cys Ser Glu Arg
        195                 200                 205

Thr Val Ala Pro Ala Leu Asn Asp Leu Ala Thr Thr His Pro Lys Leu
    210                 215                 220

Ala Glu Gln Ile Ala Asp Pro Gln Pro Ser Gly Val Ser Ala Ala Ala
225                 230                 235                 240

Ile Ile Pro Thr Ile Ser Arg Gly Ser His Thr Gln Leu Thr Trp Gln
                245                 250                 255

Cys Ser Lys Asn His Asp His Gln Trp Val Ala Thr Val Lys Asp Arg
            260                 265                 270

Val Arg Gly Thr Asp Cys Pro Thr Cys Ala Asn Thr Gly Thr Ser Arg
        275                 280                 285

Lys Glu Ala Glu Leu Ile Glu Val Ile Arg Ala Leu Phe Pro Asn Thr
    290                 295                 300

Asp Val Gln Gln Gly Ala Leu Ile Asn Gly Arg Thr Gly Asn Gln Gly
305                 310                 315                 320

Ala Ser Pro Ser Thr Asp Val Leu Ile Pro Ser Lys Asn Leu Ala Ile
                325                 330                 335

Glu Phe Asn Gly Leu Tyr Trp His Ser Glu Leu Phe Ile Lys Asp Lys
            340                 345                 350

His Tyr His Ala Asn Lys Ser Ala Leu Ala Glu Gln Ala Gly Val Gln
        355                 360                 365

Leu Ile His Val Trp Glu Asp Asp Trp Asn Leu Arg Arg Asp Ile Val
    370                 375                 380

Ile Arg Met Ile Ala His Lys Leu His Ala Thr His Asn Leu Ser Ala
385                 390                 395                 400

Val Leu Pro Thr Glu Thr Thr Asp Ser Arg Val Ala Thr Thr Ala Phe
                405                 410                 415

Ala Val His Ser His Cys Arg Trp Ser Leu Val His Ala Leu Leu His
            420                 425                 430

Ser
```

<210> 1295

<211> 795
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(772)
<223> FRXA02782

<400> 1295
gtggatctgt tgcaagcatg aaccaccatt tatctggaaa acctcaccaa ttttgcgtgt 60

acgacagaac acccagtgcc ctgtgtgctc agagcgaact gtg gcg ccg gcg ctt 115
Val Ala Pro Ala Leu
1 5

aat gat ctt gca acc act cac cct aaa ctt gcc gag caa att gca gat 163
Asn Asp Leu Ala Thr Thr His Pro Lys Leu Ala Glu Gln Ile Ala Asp
10 15 20

cct caa cca agt ggt gtg agc gcc gcg gcc att atc ccc acc att agc 211
Pro Gln Pro Ser Gly Val Ser Ala Ala Ala Ile Ile Pro Thr Ile Ser
25 30 35

agg ggt tcc cat acg caa tta aca tgg caa tgt tct aaa aat cat gac 259
Arg Gly Ser His Thr Gln Leu Thr Trp Gln Cys Ser Lys Asn His Asp
40 45 50

cac caa tgg gtc gcc aca gta aag gat cgt gtt cgc gga aca gac tgc 307
His Gln Trp Val Ala Thr Val Lys Asp Arg Val Arg Gly Thr Asp Cys
55 60 65

ccc acc tgc gca aat aca gga act tca cgc aaa gag gct gaa ctt att 355
Pro Thr Cys Ala Asn Thr Gly Thr Ser Arg Lys Glu Ala Glu Leu Ile
70 75 80 85

gag gtc atc cgt gca tta ttc cca aac act gat gtc cag caa ggt gcg 403
Glu Val Ile Arg Ala Leu Phe Pro Asn Thr Asp Val Gln Gln Gly Ala
90 95 100

ctc att aat gga cgt acc ggt aat caa ggt gca tcg ccg tca acc gat 451
Leu Ile Asn Gly Arg Thr Gly Asn Gln Gly Ala Ser Pro Ser Thr Asp
105 110 115

gta ctc ata ccg tcc aaa aat ctc gct atc gag ttc aac ggc ctg tac 499
Val Leu Ile Pro Ser Lys Asn Leu Ala Ile Glu Phe Asn Gly Leu Tyr
120 125 130

tgg cac tct gag ctt ttc atc aaa gat aag cat tat cat gcg aac aaa 547
Trp His Ser Glu Leu Phe Ile Lys Asp Lys His Tyr His Ala Asn Lys
135 140 145

tca gct ctc gca gaa caa gcc ggt gtg cag ctc att cat gtg tgg gag 595
Ser Ala Leu Ala Glu Gln Ala Gly Val Gln Leu Ile His Val Trp Glu
150 155 160 165

gac gac tgg aat ctt cgc cgc gac att gtg atc cgc atg atc gca cac 643
Asp Asp Trp Asn Leu Arg Arg Asp Ile Val Ile Arg Met Ile Ala His
170 175 180

aag ctt cat gca acc cat aac ctc agt gct gtt ttg cct acc gaa act 691

```
Lys Leu His Ala Thr His Asn Leu Ser Ala Val Leu Pro Thr Glu Thr
            185                 190                 195

act gac tca cgt gtg gca acc acc gct ttc gcc gta cac tca cac tgt   739
Thr Asp Ser Arg Val Ala Thr Thr Ala Phe Ala Val His Ser His Cys
        200                 205                 210

cgg tgg tct ctg gtt cac gcg ctg ctg cat tct tgaacagcaa ccatattcag 792
Arg Trp Ser Leu Val His Ala Leu Leu His Ser
    215                 220

ggt                                                               795


<210> 1296
<211> 224
<212> PRT
<213> Corynebacterium glutamicum

<400> 1296
Val Ala Pro Ala Leu Asn Asp Leu Ala Thr Thr His Pro Lys Leu Ala
  1               5                  10                  15

Glu Gln Ile Ala Asp Pro Gln Pro Ser Gly Val Ser Ala Ala Ala Ile
             20                  25                  30

Ile Pro Thr Ile Ser Arg Gly Ser His Thr Gln Leu Thr Trp Gln Cys
         35                  40                  45

Ser Lys Asn His Asp His Gln Trp Val Ala Thr Val Lys Asp Arg Val
     50                  55                  60

Arg Gly Thr Asp Cys Pro Thr Cys Ala Asn Thr Gly Thr Ser Arg Lys
 65                  70                  75                  80

Glu Ala Glu Leu Ile Glu Val Ile Arg Ala Leu Phe Pro Asn Thr Asp
                 85                  90                  95

Val Gln Gln Gly Ala Leu Ile Asn Gly Arg Thr Gly Asn Gln Gly Ala
            100                 105                 110

Ser Pro Ser Thr Asp Val Leu Ile Pro Ser Lys Asn Leu Ala Ile Glu
        115                 120                 125

Phe Asn Gly Leu Tyr Trp His Ser Glu Leu Phe Ile Lys Asp Lys His
    130                 135                 140

Tyr His Ala Asn Lys Ser Ala Leu Ala Glu Gln Ala Gly Val Gln Leu
145                 150                 155                 160

Ile His Val Trp Glu Asp Asp Trp Asn Leu Arg Arg Asp Ile Val Ile
                165                 170                 175

Arg Met Ile Ala His Lys Leu His Ala Thr His Asn Leu Ser Ala Val
            180                 185                 190

Leu Pro Thr Glu Thr Thr Asp Ser Arg Val Ala Thr Thr Ala Phe Ala
        195                 200                 205

Val His Ser His Cys Arg Trp Ser Leu Val His Ala Leu Leu His Ser
    210                 215                 220
```

<210> 1297
<211> 439
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(439)
<223> RXN02812

<400> 1297
cgcaactgga gctgccgact cccctgcgtt tgccaccgtt gaaggagcag aacttccaga 60

gggctacacc tttgaagcag tagacagcgc agaagtacct gtg tgg gct gtt gcc 115
Val Trp Ala Val Ala
1 5

atc aac gct gga aac ggt atc tct gaa gac caa gcc cgc gcc gcc tct 163
Ile Asn Ala Gly Asn Gly Ile Ser Glu Asp Gln Ala Arg Ala Ala Ser
10 15 20

gat ttc agt agc ttc agc ttc gac acc ggc aac gcc gat aac tcc gcg 211
Asp Phe Ser Ser Phe Ser Phe Asp Thr Gly Asn Ala Asp Asn Ser Ala
25 30 35

ctt gaa agt gtt ctc acc caa gct tca agc gaa tcc gcg gca gaa act 259
Leu Glu Ser Val Leu Thr Gln Ala Ser Ser Glu Ser Ala Ala Glu Thr
40 45 50

act gag gcg caa cca agc gag acc ccg gtc gag ccc gcc gct gct tcc 307
Thr Glu Ala Gln Pro Ser Glu Thr Pro Val Glu Pro Ala Ala Ala Ser
55 60 65

cca tcc gat acc atc atc aac ctg gat acc tca tcc aac atg gat cga 355
Pro Ser Asp Thr Ile Ile Asn Leu Asp Thr Ser Ser Asn Met Asp Arg
70 75 80 85

gtt gtt gac ggc agc cag gaa acc tac cac acg gtt act tcc cgg act 403
Val Val Asp Gly Ser Gln Glu Thr Tyr His Thr Val Thr Ser Arg Thr
90 95 100

ctg gcc aac ctc gcc cgc gaa act ggt gca cag ggc 439
Leu Ala Asn Leu Ala Arg Glu Thr Gly Ala Gln Gly
105 110

<210> 1298
<211> 113
<212> PRT
<213> Corynebacterium glutamicum

<400> 1298
Val Trp Ala Val Ala Ile Asn Ala Gly Asn Gly Ile Ser Glu Asp Gln
1 5 10 15

Ala Arg Ala Ala Ser Asp Phe Ser Ser Phe Ser Phe Asp Thr Gly Asn

```
            20                  25                  30

Ala Asp Asn Ser Ala Leu Glu Ser Val Leu Thr Gln Ala Ser Ser Glu
         35                  40                  45

Ser Ala Ala Glu Thr Thr Glu Ala Gln Pro Ser Glu Thr Pro Val Glu
     50                  55                  60

Pro Ala Ala Ala Ser Pro Ser Asp Thr Ile Ile Asn Leu Asp Thr Ser
 65                  70                  75                  80

Ser Asn Met Asp Arg Val Val Asp Gly Ser Gln Glu Thr Tyr His Thr
                 85                  90                  95

Val Thr Ser Arg Thr Leu Ala Asn Leu Ala Arg Glu Thr Gly Ala Gln
            100                 105                 110

Gly
```

<210> 1299
<211> 567
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(567)
<223> FRXA02812

<400> 1299

```
gct tca ggc acc gac gcc tca aca atc acc ctt gac cag gta gct ctt   48
Ala Ser Gly Thr Asp Ala Ser Thr Ile Thr Leu Asp Gln Val Ala Leu
  1               5                  10                  15

ccc gtt gcc act aac tcc gga gca tcc gca gcc gta gcg ctg gcg ctg   96
Pro Val Ala Thr Asn Ser Gly Ala Ser Ala Ala Val Ala Leu Ala Leu
             20                  25                  30

gct gaa acc cca gaa gct gcc gct gct gcg ctc aac cgt gac gcc gat   144
Ala Glu Thr Pro Glu Ala Ala Ala Ala Ala Leu Asn Arg Asp Ala Asp
         35                  40                  45

gtc acc gca act gga gct gcc gac tcc cct gcg ttt gcc acc gtt gaa   192
Val Thr Ala Thr Gly Ala Ala Asp Ser Pro Ala Phe Ala Thr Val Glu
     50                  55                  60

gga gca gaa ctt cca gag ggc tac acc ttt gaa gca gta gac agc gca   240
Gly Ala Glu Leu Pro Glu Gly Tyr Thr Phe Glu Ala Val Asp Ser Ala
 65                  70                  75                  80

gaa gta cct gtg tgg gct gtt gcc atc aac gct gga aac ggt atc tct   288
Glu Val Pro Val Trp Ala Val Ala Ile Asn Ala Gly Asn Gly Ile Ser
                 85                  90                  95

gaa gac caa gcc cgc gcc gcc tct gat ttc agt agc ttc agc ttc gac   336
Glu Asp Gln Ala Arg Ala Ala Ser Asp Phe Ser Ser Phe Ser Phe Asp
            100                 105                 110

acc ggc aac gcc gat aac tcc gcg ctt gaa agt gtt ctc acc caa gct   384
```

```
Thr Gly Asn Ala Asp Asn Ser Ala Leu Glu Ser Val Leu Thr Gln Ala
        115                 120                 125

tca agc gaa tcc gcg gca gaa act act gag gcg caa cca agc gag acc   432
Ser Ser Glu Ser Ala Ala Glu Thr Thr Glu Ala Gln Pro Ser Glu Thr
    130                 135                 140

ccg gtc gag ccc gcc gct gct tcc cca tcc gat acc atc atc aac ctg   480
Pro Val Glu Pro Ala Ala Ala Ser Pro Ser Asp Thr Ile Ile Asn Leu
145                 150                 155                 160

gat acc tca tcc aac atg gat cga gtt gtt gac ggc agc cag gaa acc   528
Asp Thr Ser Ser Asn Met Asp Arg Val Val Asp Gly Ser Gln Glu Thr
                165                 170                 175

tac cac acg gtt act tcc cgg act ctg gcc aac ctc gcc               567
Tyr His Thr Val Thr Ser Arg Thr Leu Ala Asn Leu Ala
            180                 185


<210> 1300
<211> 189
<212> PRT
<213> Corynebacterium glutamicum

<400> 1300
Ala Ser Gly Thr Asp Ala Ser Thr Ile Thr Leu Asp Gln Val Ala Leu
  1               5                  10                  15

Pro Val Ala Thr Asn Ser Gly Ala Ser Ala Ala Val Ala Leu Ala Leu
             20                  25                  30

Ala Glu Thr Pro Glu Ala Ala Ala Ala Ala Ala Leu Asn Arg Asp Ala Asp
         35                  40                  45

Val Thr Ala Thr Gly Ala Ala Asp Ser Pro Ala Phe Ala Thr Val Glu
     50                  55                  60

Gly Ala Glu Leu Pro Glu Gly Tyr Thr Phe Glu Ala Val Asp Ser Ala
 65                  70                  75                  80

Glu Val Pro Val Trp Ala Val Ala Ile Asn Ala Gly Asn Gly Ile Ser
                85                  90                  95

Glu Asp Gln Ala Arg Ala Ala Ser Asp Phe Ser Ser Phe Ser Phe Asp
            100                 105                 110

Thr Gly Asn Ala Asp Asn Ser Ala Leu Glu Ser Val Leu Thr Gln Ala
        115                 120                 125

Ser Ser Glu Ser Ala Ala Glu Thr Thr Glu Ala Gln Pro Ser Glu Thr
    130                 135                 140

Pro Val Glu Pro Ala Ala Ala Ser Pro Ser Asp Thr Ile Ile Asn Leu
145                 150                 155                 160

Asp Thr Ser Ser Asn Met Asp Arg Val Val Asp Gly Ser Gln Glu Thr
                165                 170                 175

Tyr His Thr Val Thr Ser Arg Thr Leu Ala Asn Leu Ala
            180                 185
```

<210> 1301
<211> 499
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(499)
<223> RXN02817

<400> 1301
aaaattccca cccccaaaac tcccccactt cggttaagga atcaggattc tcacaaagtt 60

caggcaggct cccgctactt ttcagcgcta atcttggctc atg att tta ggc gta 115
Met Ile Leu Gly Val
1 5

ccc att caa tat ttg ctc tat tca ttg tgg aat tgg att gtc gat acc 163
Pro Ile Gln Tyr Leu Leu Tyr Ser Leu Trp Asn Trp Ile Val Asp Thr
10 15 20

ggt ttt gat gta gca att atc ctg gtc ttg gcg ttt ttg att cca cgt 211
Gly Phe Asp Val Ala Ile Ile Leu Val Leu Ala Phe Leu Ile Pro Arg
25 30 35

atc ggc cga ctg gcc atg cgt att atc aag cgc cga gtg gag tct gca 259
Ile Gly Arg Leu Ala Met Arg Ile Ile Lys Arg Arg Val Glu Ser Ala
40 45 50

gcc gat gcg gac acc act aag aac cag ctc gcg ttc gcc ggc gtt ggc 307
Ala Asp Ala Asp Thr Thr Lys Asn Gln Leu Ala Phe Ala Gly Val Gly
55 60 65

gtt tat atc gcg caa att gtg gcg ttt ttc atg ctt gcc gtc tcc gcg 355
Val Tyr Ile Ala Gln Ile Val Ala Phe Phe Met Leu Ala Val Ser Ala
70 75 80 85

atg cag gct ttt ggt ttc tct ctc gcg ggc gct gcg att ccg gca acc 403
Met Gln Ala Phe Gly Phe Ser Leu Ala Gly Ala Ala Ile Pro Ala Thr
90 95 100

att gcg tca gct gcc att ggc ctt ggt gcg cag tcg att gtt gcg gac 451
Ile Ala Ser Ala Ala Ile Gly Leu Gly Ala Gln Ser Ile Val Ala Asp
105 110 115

ttc ttg gcc gga ttt ttc atc ctg acg gaa aag caa ttc ggc gtg ggt 499
Phe Leu Ala Gly Phe Phe Ile Leu Thr Glu Lys Gln Phe Gly Val Gly
120 125 130

<210> 1302
<211> 133
<212> PRT
<213> Corynebacterium glutamicum

<400> 1302
Met Ile Leu Gly Val Pro Ile Gln Tyr Leu Leu Tyr Ser Leu Trp Asn
1 5 10 15

```
Trp Ile Val Asp Thr Gly Phe Asp Val Ala Ile Ile Leu Val Leu Ala
            20                  25                  30

Phe Leu Ile Pro Arg Ile Gly Arg Leu Ala Met Arg Ile Ile Lys Arg
        35                  40                  45

Arg Val Glu Ser Ala Ala Asp Ala Asp Thr Thr Lys Asn Gln Leu Ala
    50                  55                  60

Phe Ala Gly Val Gly Val Tyr Ile Ala Gln Ile Val Ala Phe Phe Met
65                  70                  75                  80

Leu Ala Val Ser Ala Met Gln Ala Phe Gly Phe Ser Leu Ala Gly Ala
                85                  90                  95

Ala Ile Pro Ala Thr Ile Ala Ser Ala Ala Ile Gly Leu Gly Ala Gln
            100                 105                 110

Ser Ile Val Ala Asp Phe Leu Ala Gly Phe Phe Ile Leu Thr Glu Lys
        115                 120                 125

Gln Phe Gly Val Gly
    130
```

Substitute Sheet (Rule 26)

<210> 1303
<211> 499
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(499)
<223> FRXA02817

<400> 1303

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aaaattccca cccccaaaac tcccccactt cggttaagga atcaggattc tcacaaagtt 60

caggcaggct cccgctactt ttcagcgcta atcttggctc atg att tta ggc gta   115
                                            Met Ile Leu Gly Val
                                              1               5

ccc att caa tat ttg ctc tat tca ttg tgg aat tgg att gtc gat acc   163
Pro Ile Gln Tyr Leu Leu Tyr Ser Leu Trp Asn Trp Ile Val Asp Thr
                10                  15                  20

ggt ttt gat gta gca att atc ctg gtc ttg gcg ttt ttg att cca cgt   211
Gly Phe Asp Val Ala Ile Ile Leu Val Leu Ala Phe Leu Ile Pro Arg
            25                  30                  35

atc ggc cga ctg gcc atg cgt att atc aag cgc cga gtg gag tct gca   259
Ile Gly Arg Leu Ala Met Arg Ile Ile Lys Arg Arg Val Glu Ser Ala
        40                  45                  50

gcc gat gcg gac acc act aag aac cag ctc gcg ttc gcc ggc gtt ggc   307
Ala Asp Ala Asp Thr Thr Lys Asn Gln Leu Ala Phe Ala Gly Val Gly
    55                  60                  65

gtt tat atc gcg caa att gtg gcg ttt ttc atg ctt gcc gtc tcc gcg   355
Val Tyr Ile Ala Gln Ile Val Ala Phe Phe Met Leu Ala Val Ser Ala
70                  75                  80                  85
```

```
atg cag gct ttt ggt ttc tct ctc gcg ggc gct gcg att ccg gca acc   403
Met Gln Ala Phe Gly Phe Ser Leu Ala Gly Ala Ala Ile Pro Ala Thr
                 90                  95                 100

att gcg tca gct gcc att ggc ctt ggt gcg cag tcg att gtt gcg gac   451
Ile Ala Ser Ala Ala Ile Gly Leu Gly Ala Gln Ser Ile Val Ala Asp
            105                 110                 115

ttc ttg gcc gga ttt ttc atc ctg acg gaa aag caa ttc ggc gtg ggt   499
Phe Leu Ala Gly Phe Phe Ile Leu Thr Glu Lys Gln Phe Gly Val Gly
        120                 125                 130
```

<210> 1304
<211> 133
<212> PRT
<213> Corynebacterium glutamicum

<400> 1304

```
Met Ile Leu Gly Val Pro Ile Gln Tyr Leu Leu Tyr Ser Leu Trp Asn
  1               5                  10                  15

Trp Ile Val Asp Thr Gly Phe Asp Val Ala Ile Ile Leu Val Leu Ala
             20                  25                  30

Phe Leu Ile Pro Arg Ile Gly Arg Leu Ala Met Arg Ile Ile Lys Arg
         35                  40                  45

Arg Val Glu Ser Ala Ala Asp Ala Asp Thr Thr Lys Asn Gln Leu Ala
     50                  55                  60

Phe Ala Gly Val Gly Val Tyr Ile Ala Gln Ile Val Ala Phe Phe Met
 65                  70                  75                  80

Leu Ala Val Ser Ala Met Gln Ala Phe Gly Phe Ser Leu Ala Gly Ala
                 85                  90                  95

Ala Ile Pro Ala Thr Ile Ala Ser Ala Ala Ile Gly Leu Gly Ala Gln
            100                 105                 110

Ser Ile Val Ala Asp Phe Leu Ala Gly Phe Phe Ile Leu Thr Glu Lys
        115                 120                 125

Gln Phe Gly Val Gly
    130
```

<210> 1305
<211> 606
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(606)
<223> RXN02818

<400> 1305

```
tcc tat tcc cgg aag ttt ttg acc cag gtg tgg att cga gac aat gtc   48
Ser Tyr Ser Arg Lys Phe Leu Thr Gln Val Trp Ile Arg Asp Asn Val
```

```
  1               5                  10                  15

ggc gat tat aaa ggc ctt acc gat acg gcg ttc cgt aag aag ctg cag   96
Gly Asp Tyr Lys Gly Leu Thr Asp Thr Ala Phe Arg Lys Lys Leu Gln
            20                  25                  30

cgc gat ctt gcc tac ctg cgc aga gtt ggc gtt ccg att gag cag ttc   144
Arg Asp Leu Ala Tyr Leu Arg Arg Val Gly Val Pro Ile Glu Gln Phe
         35                  40                  45

acg gtc acc tca ggc ata gct gaa ggc cag cag gcg tac cgt ctg gcc   192
Thr Val Thr Ser Gly Ile Ala Glu Gly Gln Gln Ala Tyr Arg Leu Ala
     50                  55                  60

cag gat tct tat aag ctc ccc gag gtc gaa ttc acc cca gat gag gcc   240
Gln Asp Ser Tyr Lys Leu Pro Glu Val Glu Phe Thr Pro Asp Glu Ala
 65                  70                  75                  80

gcc gtg ctg ggc atg gca ggg gag atg ggc cat aat cag gaa ctc ggc   288
Ala Val Leu Gly Met Ala Gly Glu Met Gly His Asn Gln Glu Leu Gly
                85                  90                  95

gcc ttc gcg cgt tcg ggg tgg acc aaa ttg gcg gcc ggc ggc gcg cag   336
Ala Phe Ala Arg Ser Gly Trp Thr Lys Leu Ala Ala Gly Gly Ala Gln
            100                 105                 110

cgt gat ctg tcc acg tcc aca gcc ttg acc aat gcg ggc gat tta ggt   384
Arg Asp Leu Ser Thr Ser Thr Ala Leu Thr Asn Ala Gly Asp Leu Gly
        115                 120                 125

tcc ttg tct gca aaa acc ctc gat gcg atc atc aaa gcc cgc caa ttg   432
Ser Leu Ser Ala Lys Thr Leu Asp Ala Ile Ile Lys Ala Arg Gln Leu
    130                 135                 140

ggc aag caa atc agc ttc gaa tac cgg cgc gcc ccc aaa gac gcc ccc   480
Gly Lys Gln Ile Ser Phe Glu Tyr Arg Arg Ala Pro Lys Asp Ala Pro
145                 150                 155                 160

tcg ctt cga cac atg gat cct tgg ggt ctg gtc cct gag cgc gac cgc   528
Ser Leu Arg His Met Asp Pro Trp Gly Leu Val Pro Glu Arg Asp Arg
                165                 170                 175

atc tac ctg gtc gga ttc gac ctc gac cgc caa gaa gca cgc acc ttc   576
Ile Tyr Leu Val Gly Phe Asp Leu Asp Arg Gln Glu Ala Arg Thr Phe
            180                 185                 190

cgc atc acc cgc gtc cgc aac atc aaa ctc                          606
Arg Ile Thr Arg Val Arg Asn Ile Lys Leu
        195                 200
```

<210> 1306
<211> 202
<212> PRT
<213> Corynebacterium glutamicum

<400> 1306

```
Ser Tyr Ser Arg Lys Phe Leu Thr Gln Val Trp Ile Arg Asp Asn Val
  1               5                  10                  15

Gly Asp Tyr Lys Gly Leu Thr Asp Thr Ala Phe Arg Lys Lys Leu Gln
```

```
            20                  25                  30

Arg Asp Leu Ala Tyr Leu Arg Arg Val Gly Val Pro Ile Glu Gln Phe
         35                  40                  45

Thr Val Thr Ser Gly Ile Ala Glu Gly Gln Gln Ala Tyr Arg Leu Ala
     50                  55                  60

Gln Asp Ser Tyr Lys Leu Pro Glu Val Glu Phe Thr Pro Asp Glu Ala
 65                  70                  75                  80

Ala Val Leu Gly Met Ala Gly Glu Met Gly His Asn Gln Glu Leu Gly
                 85                  90                  95

Ala Phe Ala Arg Ser Gly Trp Thr Lys Leu Ala Ala Gly Gly Ala Gln
            100                 105                 110

Arg Asp Leu Ser Thr Ser Thr Ala Leu Thr Asn Ala Gly Asp Leu Gly
        115                 120                 125

Ser Leu Ser Ala Lys Thr Leu Asp Ala Ile Ile Lys Ala Arg Gln Leu
    130                 135                 140

Gly Lys Gln Ile Ser Phe Glu Tyr Arg Arg Ala Pro Lys Asp Ala Pro
145                 150                 155                 160

Ser Leu Arg His Met Asp Pro Trp Gly Leu Val Pro Glu Arg Asp Arg
                165                 170                 175

Ile Tyr Leu Val Gly Phe Asp Leu Asp Arg Gln Glu Ala Arg Thr Phe
            180                 185                 190

Arg Ile Thr Arg Val Arg Asn Ile Lys Leu
        195                 200


<210> 1307
<211> 606
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(606)
<223> FRXA02818

<400> 1307
tcc tat tcc cgg aag ttt ttg acc cag gtg tgg att cga gac aat gtc   48
Ser Tyr Ser Arg Lys Phe Leu Thr Gln Val Trp Ile Arg Asp Asn Val
  1               5                  10                  15

ggc gat tat aaa ggc ctt acc gat acg gcg ttc cgt aag aag ctg cag   96
Gly Asp Tyr Lys Gly Leu Thr Asp Thr Ala Phe Arg Lys Lys Leu Gln
             20                  25                  30

cgc gat ctt gcc tac ctg cgc aga gtt ggc gtt ccg att gag cag ttc   144
Arg Asp Leu Ala Tyr Leu Arg Arg Val Gly Val Pro Ile Glu Gln Phe
         35                  40                  45

acg gtc acc tca ggc ata gct gaa ggc cag cag gcg tac cgt ctg gcc   192
Thr Val Thr Ser Gly Ile Ala Glu Gly Gln Gln Ala Tyr Arg Leu Ala
```

```
     50                  55                  60

cag gat tct tat aag ctc ccc gag gtc gaa ttc acc cca gat gag gcc   240
Gln Asp Ser Tyr Lys Leu Pro Glu Val Glu Phe Thr Pro Asp Glu Ala
 65                  70                  75                  80

gcc gtg ctg ggc atg gca ggg gag atg ggc cat aat cag gaa ctc ggc   288
Ala Val Leu Gly Met Ala Gly Glu Met Gly His Asn Gln Glu Leu Gly
                85                  90                  95

gcc ttc gcg cgt tcg ggg tgg acc aaa ttg gcg gcc ggc ggc gcg cag   336
Ala Phe Ala Arg Ser Gly Trp Thr Lys Leu Ala Ala Gly Gly Ala Gln
            100                 105                 110

cgt gat ctg tcc acg tcc aca gcc ttg acc aat gcg ggc gat tta ggt   384
Arg Asp Leu Ser Thr Ser Thr Ala Leu Thr Asn Ala Gly Asp Leu Gly
        115                 120                 125

tcc ttg tct gca aaa acc ctc gat gcg atc atc aaa gcc cgc caa ttg   432
Ser Leu Ser Ala Lys Thr Leu Asp Ala Ile Ile Lys Ala Arg Gln Leu
    130                 135                 140

ggc aag caa atc agc ttc gaa tac cgg cgc gcc ccc aaa gac gcc ccc   480
Gly Lys Gln Ile Ser Phe Glu Tyr Arg Arg Ala Pro Lys Asp Ala Pro
145                 150                 155                 160

tcg ctt cga cac atg gat cct tgg ggt ctg gtc cct gag cgc gac cgc   528
Ser Leu Arg His Met Asp Pro Trp Gly Leu Val Pro Glu Arg Asp Arg
                165                 170                 175

atc tac ctg gtc gga ttc gac ctc gac cgc caa gaa gca cgc acc ttc   576
Ile Tyr Leu Val Gly Phe Asp Leu Asp Arg Gln Glu Ala Arg Thr Phe
            180                 185                 190

cgc atc acc cgc gtc cgc aac atc aaa ctc                          606
Arg Ile Thr Arg Val Arg Asn Ile Lys Leu
        195                 200
```

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<210> 1308
<211> 202
<212> PRT
<213> Corynebacterium glutamicum

<400> 1308

```
Ser Tyr Ser Arg Lys Phe Leu Thr Gln Val Trp Ile Arg Asp Asn Val
  1               5                  10                  15

Gly Asp Tyr Lys Gly Leu Thr Asp Thr Ala Phe Arg Lys Lys Leu Gln
             20                  25                  30

Arg Asp Leu Ala Tyr Leu Arg Arg Val Gly Val Pro Ile Glu Gln Phe
         35                  40                  45

Thr Val Thr Ser Gly Ile Ala Glu Gly Gln Gln Ala Tyr Arg Leu Ala
     50                  55                  60

Gln Asp Ser Tyr Lys Leu Pro Glu Val Glu Phe Thr Pro Asp Glu Ala
 65                  70                  75                  80

Ala Val Leu Gly Met Ala Gly Glu Met Gly His Asn Gln Glu Leu Gly
```

```
                85                  90                  95

Ala Phe Ala Arg Ser Gly Trp Thr Lys Leu Ala Ala Gly Gly Ala Gln
            100                 105                 110

Arg Asp Leu Ser Thr Ser Thr Ala Leu Thr Asn Ala Gly Asp Leu Gly
        115                 120                 125

Ser Leu Ser Ala Lys Thr Leu Asp Ala Ile Ile Lys Ala Arg Gln Leu
    130                 135                 140

Gly Lys Gln Ile Ser Phe Glu Tyr Arg Arg Ala Pro Lys Asp Ala Pro
145                 150                 155                 160

Ser Leu Arg His Met Asp Pro Trp Gly Leu Val Pro Glu Arg Asp Arg
                165                 170                 175

Ile Tyr Leu Val Gly Phe Asp Leu Asp Arg Gln Glu Ala Arg Thr Phe
            180                 185                 190

Arg Ile Thr Arg Val Arg Asn Ile Lys Leu
        195                 200
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Application Filed 2005-05-27 09:05:05 ACST

<210> 1309
<211> 1962
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1939)
<223> RXN02825

<400> 1309

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tggcctgccc ctgaaacttt tacggctttc agagcgcagg gcatcatttt cttgtgtcgc 60

caacacttga gaaaaattgc ggaaaaggac actgctgttc atg aaa ctt gca cct   115
                                            Met Lys Leu Ala Pro
                                              1               5

cgt atg cgg atg agg agc ccc aaa act ttc gcg gcc ctc gcc tca ctt   163
Arg Met Arg Met Arg Ser Pro Lys Thr Phe Ala Ala Leu Ala Ser Leu
                10                  15                  20

gct tta gtc ata ggt ctc ggc cag gta ccg atc gcc caa gct caa acc   211
Ala Leu Val Ile Gly Leu Gly Gln Val Pro Ile Ala Gln Ala Gln Thr
            25                  30                  35

gag tat cga acc gcc tcc gac ggt tcc ctg aac tgg gga ttt agg caa   259
Glu Tyr Arg Thr Ala Ser Asp Gly Ser Leu Asn Trp Gly Phe Arg Gln
        40                  45                  50

tcg ttc cgc aat tac atc caa acc ggc gtg gcc aaa ggt tcc atc acg   307
Ser Phe Arg Asn Tyr Ile Gln Thr Gly Val Ala Lys Gly Ser Ile Thr
    55                  60                  65

ctt ggc gac ggc gca tcc gac aac ggt ggc aac ttc gca ttc acc cca   355
Leu Gly Asp Gly Ala Ser Asp Asn Gly Gly Asn Phe Ala Phe Thr Pro
70                  75                  80                  85
```

```
cgc acc aac ggc acc acc gtg acc agc gat tcc caa ggc acc gtg gaa   403
Arg Thr Asn Gly Thr Thr Val Thr Ser Asp Ser Gln Gly Thr Val Glu
                 90                  95                 100

ttc aac ggc tcc gtg cac ttc ctc gga cac cag gca gag gac aaa tgg   451
Phe Asn Gly Ser Val His Phe Leu Gly His Gln Ala Glu Asp Lys Trp
            105                 110                 115

atc ctg gac acc acc atg tct gac atc aaa atg gtg ttc aac gga tcc   499
Ile Leu Asp Thr Thr Met Ser Asp Ile Lys Met Val Phe Asn Gly Ser
        120                 125                 130

tcc gcg cag cta gtt gtg gat ttg gtt gcc cgc gaa ttc aag ggc acc   547
Ser Ala Gln Leu Val Val Asp Leu Val Ala Arg Glu Phe Lys Gly Thr
    135                 140                 145

acc tac gat gac atc ggc gaa tac atc atc tcc gac gac atc gtg ctt   595
Thr Tyr Asp Asp Ile Gly Glu Tyr Ile Ile Ser Asp Asp Ile Val Leu
150                 155                 160                 165

gcc gac gtc tcc ctc aac tcc gcc gcc gac ttc tcc caa gat tcc atc   643
Ala Asp Val Ser Leu Asn Ser Ala Ala Asp Phe Ser Gln Asp Ser Ile
                170                 175                 180

gac ctg tcc ggc acc acc gac ctc acc gca gct ggc gcc caa gct ttc   691
Asp Leu Ser Gly Thr Thr Asp Leu Thr Ala Ala Gly Ala Gln Ala Phe
            185                 190                 195

gga gga ttc tac gaa acc ggc gaa gcc ctc gac ccg acc ggc ggc agc   739
Gly Gly Phe Tyr Glu Thr Gly Glu Ala Leu Asp Pro Thr Gly Gly Ser
        200                 205                 210

ctg acc att tcc tcc acc acc acc gcg cca tcg acc agc acg acc tcc   787
Leu Thr Ile Ser Ser Thr Thr Thr Ala Pro Ser Thr Ser Thr Thr Ser
    215                 220                 225

acc tct gcc tca act tcc ggt gga acc gcc gac tgt tcc tcc ggc gca   835
Thr Ser Ala Ser Thr Ser Gly Gly Thr Ala Asp Cys Ser Ser Gly Ala
230                 235                 240                 245

ttg ggt gtt gtc acc acc gga acc aac gac ggc atg ctg ggc acc atc   883
Leu Gly Val Val Thr Thr Gly Thr Asn Asp Gly Met Leu Gly Thr Ile
                250                 255                 260

cag gaa gta aac aac acc ttc gcg att tgg aac aac ctc atc gtc aac   931
Gln Glu Val Asn Asn Thr Phe Ala Ile Trp Asn Asn Leu Ile Val Asn
            265                 270                 275

acc gag cgc atg ttc tgc aac att gat acc ctc aag gcg cgc ttc gac   979
Thr Glu Arg Met Phe Cys Asn Ile Asp Thr Leu Lys Ala Arg Phe Asp
        280                 285                 290

acg gat gat tcc agc gat tca gcg acc tct gcg act tct ggg act act   1027
Thr Asp Asp Ser Ser Asp Ser Ala Thr Ser Ala Thr Ser Gly Thr Thr
    295                 300                 305

gcg tcc acc ggc acc acc gct gca act acc gcg gga acc acg ggt acc   1075
Ala Ser Thr Gly Thr Thr Ala Ala Thr Thr Ala Gly Thr Thr Gly Thr
310                 315                 320                 325

act gga act gcc agc acc gct tcc gga act tcc gga act tcc gga acc   1123
```

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Thr Gly Thr Ala Ser Thr Ala Ser Gly Thr Ser Gly Thr Ser Gly Thr
                330                 335                 340

tcc ggc acc gca gca act gtc gct ggc acc acc cca act gac aat ggc   1171
Ser Gly Thr Ala Ala Thr Val Ala Gly Thr Thr Pro Thr Asp Asn Gly
            345                 350                 355

gtt tgc acc gct tcc gga tct ttg ggc gtg acc caa gca tct gcg cag   1219
Val Cys Thr Ala Ser Gly Ser Leu Gly Val Thr Gln Ala Ser Ala Gln
        360                 365                 370

tgg ggt gtg aag gcg tcc ttc cag aac tac att cgc gga tcg atc gcc   1267
Trp Gly Val Lys Ala Ser Phe Gln Asn Tyr Ile Arg Gly Ser Ile Ala
    375                 380                 385

aac ggt agc tgg act ctc aac ggc gtt ggt ttt gat aat cag cag ttc   1315
Asn Gly Ser Trp Thr Leu Asn Gly Val Gly Phe Asp Asn Gln Gln Phe
390                 395                 400                 405

caa ttc tct gga aat tcc gga gca gtc gac gcg gaa aac aag acc ggc   1363
Gln Phe Ser Gly Asn Ser Gly Ala Val Asp Ala Glu Asn Lys Thr Gly
                410                 415                 420

agc atc aat ttc cct ggt tcc atc cac ttc acg ggt cac ggc gga atc   1411
Ser Ile Asn Phe Pro Gly Ser Ile His Phe Thr Gly His Gly Gly Ile
            425                 430                 435

ttg gac atg cag atc gca aac att gag atc agc ttc aac ggc aac tcc   1459
Leu Asp Met Gln Ile Ala Asn Ile Glu Ile Ser Phe Asn Gly Asn Ser
        440                 445                 450

ggc gag ctg att gcg gat gtc gtt tcc tct gac atg gat gga aat tcc   1507
Gly Glu Leu Ile Ala Asp Val Val Ser Ser Asp Met Asp Gly Asn Ser
    455                 460                 465

acc aac tac ggt cgc act gtc gtg ggc acc ctg aac ttc tct gcg ttg   1555
Thr Asn Tyr Gly Arg Thr Val Val Gly Thr Leu Asn Phe Ser Ala Leu
470                 475                 480                 485

aat gtt tct gca acg gaa gct tcc ggt tcc gct tcg gtg tcc ctg tca   1603
Asn Val Ser Ala Thr Glu Ala Ser Gly Ser Ala Ser Val Ser Leu Ser
                490                 495                 500

cag tcg ggt tcg cag gcg ttc gct gat ttc tac acc cca ggc acc cag   1651
Gln Ser Gly Ser Gln Ala Phe Ala Asp Phe Tyr Thr Pro Gly Thr Gln
            505                 510                 515

ttg gat ccg atc agt ttc agc gca act ttg ggc ggc gac gcc agc tgc   1699
Leu Asp Pro Ile Ser Phe Ser Ala Thr Leu Gly Gly Asp Ala Ser Cys
        520                 525                 530

gcc acc gga tcc acc tcg acc aca ggc gct gct gcc acc gcg aac act   1747
Ala Thr Gly Ser Thr Ser Thr Thr Gly Ala Ala Ala Thr Ala Asn Thr
    535                 540                 545

gac aac acc gaa ggt gtt gcc ggc gag gaa tcc acc acc ccc gct aac   1795
Asp Asn Thr Glu Gly Val Ala Gly Glu Glu Ser Thr Thr Pro Ala Asn
550                 555                 560                 565

caa aac agc cag ttc caa atc cgc cag gcc gct gca gat tcc acc gga   1843
Gln Asn Ser Gln Phe Gln Ile Arg Gln Ala Ala Ala Asp Ser Thr Gly
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                570                 575                 580

ctg gat acc acc acc aca atg ttg ctc atc ctc gcg gcg ttc gtt gtc   1891
Leu Asp Thr Thr Thr Thr Met Leu Leu Ile Leu Ala Ala Phe Val Val
            585                 590                 595

gca ggt ggc tcc atg act cgc ttc acc gtc ggc aac ccg act gga aaa   1939
Ala Gly Gly Ser Met Thr Arg Phe Thr Val Gly Asn Pro Thr Gly Lys
        600                 605                 610

taaggcttca catgaataac gct                                         1962


<210> 1310
<211> 613
<212> PRT
<213> Corynebacterium glutamicum

<400> 1310
Met Lys Leu Ala Pro Arg Met Arg Met Arg Ser Pro Lys Thr Phe Ala
  1               5                  10                  15

Ala Leu Ala Ser Leu Ala Leu Val Ile Gly Leu Gly Gln Val Pro Ile
             20                  25                  30

Ala Gln Ala Gln Thr Glu Tyr Arg Thr Ala Ser Asp Gly Ser Leu Asn
         35                  40                  45

Trp Gly Phe Arg Gln Ser Phe Arg Asn Tyr Ile Gln Thr Gly Val Ala
     50                  55                  60

Lys Gly Ser Ile Thr Leu Gly Asp Gly Ala Ser Asp Asn Gly Gly Asn
 65                  70                  75                  80

Phe Ala Phe Thr Pro Arg Thr Asn Gly Thr Thr Val Thr Ser Asp Ser
                 85                  90                  95

Gln Gly Thr Val Glu Phe Asn Gly Ser Val His Phe Leu Gly His Gln
            100                 105                 110

Ala Glu Asp Lys Trp Ile Leu Asp Thr Thr Met Ser Asp Ile Lys Met
        115                 120                 125

Val Phe Asn Gly Ser Ser Ala Gln Leu Val Val Asp Leu Val Ala Arg
    130                 135                 140

Glu Phe Lys Gly Thr Thr Tyr Asp Asp Ile Gly Glu Tyr Ile Ile Ser
145                 150                 155                 160

Asp Asp Ile Val Leu Ala Asp Val Ser Leu Asn Ser Ala Ala Asp Phe
                165                 170                 175

Ser Gln Asp Ser Ile Asp Leu Ser Gly Thr Thr Asp Leu Thr Ala Ala
            180                 185                 190

Gly Ala Gln Ala Phe Gly Gly Phe Tyr Glu Thr Gly Glu Ala Leu Asp
        195                 200                 205

Pro Thr Gly Gly Ser Leu Thr Ile Ser Ser Thr Thr Thr Ala Pro Ser
    210                 215                 220
```

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Thr Ser Thr Thr Ser Thr Ser Ala Ser Thr Ser Gly Gly Thr Ala Asp
225                 230                 235                 240

Cys Ser Ser Gly Ala Leu Gly Val Val Thr Thr Gly Thr Asn Asp Gly
                245                 250                 255

Met Leu Gly Thr Ile Gln Glu Val Asn Asn Thr Phe Ala Ile Trp Asn
            260                 265                 270

Asn Leu Ile Val Asn Thr Glu Arg Met Phe Cys Asn Ile Asp Thr Leu
        275                 280                 285

Lys Ala Arg Phe Asp Thr Asp Asp Ser Ser Asp Ser Ala Thr Ser Ala
    290                 295                 300

Thr Ser Gly Thr Thr Ala Ser Thr Gly Thr Thr Ala Ala Thr Thr Ala
305                 310                 315                 320

Gly Thr Thr Gly Thr Thr Gly Thr Ala Ser Thr Ala Ser Gly Thr Ser
                325                 330                 335

Gly Thr Ser Gly Thr Ser Gly Thr Ala Ala Thr Val Ala Gly Thr Thr
            340                 345                 350

Pro Thr Asp Asn Gly Val Cys Thr Ala Ser Gly Ser Leu Gly Val Thr
        355                 360                 365

Gln Ala Ser Ala Gln Trp Gly Val Lys Ala Ser Phe Gln Asn Tyr Ile
    370                 375                 380

Arg Gly Ser Ile Ala Asn Gly Ser Trp Thr Leu Asn Gly Val Gly Phe
385                 390                 395                 400

Asp Asn Gln Gln Phe Gln Phe Ser Gly Asn Ser Gly Ala Val Asp Ala
                405                 410                 415

Glu Asn Lys Thr Gly Ser Ile Asn Phe Pro Gly Ser Ile His Phe Thr
            420                 425                 430

Gly His Gly Gly Ile Leu Asp Met Gln Ile Ala Asn Ile Glu Ile Ser
        435                 440                 445

Phe Asn Gly Asn Ser Gly Glu Leu Ile Ala Asp Val Val Ser Ser Asp
    450                 455                 460

Met Asp Gly Asn Ser Thr Asn Tyr Gly Arg Thr Val Val Gly Thr Leu
465                 470                 475                 480

Asn Phe Ser Ala Leu Asn Val Ser Ala Thr Glu Ala Ser Gly Ser Ala
                485                 490                 495

Ser Val Ser Leu Ser Gln Ser Gly Ser Gln Ala Phe Ala Asp Phe Tyr
            500                 505                 510

Thr Pro Gly Thr Gln Leu Asp Pro Ile Ser Phe Ser Ala Thr Leu Gly
        515                 520                 525

Gly Asp Ala Ser Cys Ala Thr Gly Ser Thr Ser Thr Thr Gly Ala Ala
    530                 535                 540

Ala Thr Ala Asn Thr Asp Asn Thr Glu Gly Val Ala Gly Glu Glu Ser
```

```
545                 550                 555                 560

Thr Thr Pro Ala Asn Gln Asn Ser Gln Phe Gln Ile Arg Gln Ala Ala
                565                 570                 575

Ala Asp Ser Thr Gly Leu Asp Thr Thr Thr Thr Met Leu Leu Ile Leu
            580                 585                 590

Ala Ala Phe Val Val Ala Gly Gly Ser Met Thr Arg Phe Thr Val Gly
        595                 600                 605

Asn Pro Thr Gly Lys
    610
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<210> 1311
<211> 538
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(538)
<223> FRXA01322

<400> 1311

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tggcctgccc ctgaaacttt tacggctttc agagcgcagg gcatcatttt cttgtgtcgc 60

caacacttga gaaaaattgc ggaaaaggac actgctgttc atg aaa ctt gca cct   115
                                            Met Lys Leu Ala Pro
                                              1               5

cgt atg cgg atg agg agc ccc aaa act ttc gcg gcc ctc gcc tca ctt   163
Arg Met Arg Met Arg Ser Pro Lys Thr Phe Ala Ala Leu Ala Ser Leu
                10                  15                  20

gct tta gtc ata ggt ctc ggc cag gta ccg atc gcc caa gct caa acc   211
Ala Leu Val Ile Gly Leu Gly Gln Val Pro Ile Ala Gln Ala Gln Thr
            25                  30                  35

gag tat cga acc gcc tcc gac ggt tcc ctg aac tgg gga ttt agg caa   259
Glu Tyr Arg Thr Ala Ser Asp Gly Ser Leu Asn Trp Gly Phe Arg Gln
        40                  45                  50

tcg ttc cgc aat tac atc caa acc ggc gtg gcc aaa ggt tcc atc acg   307
Ser Phe Arg Asn Tyr Ile Gln Thr Gly Val Ala Lys Gly Ser Ile Thr
    55                  60                  65

ctt ggc gac ggc gca tcc gac aac ggt ggc aac ttc gca ttc acc cca   355
Leu Gly Asp Gly Ala Ser Asp Asn Gly Gly Asn Phe Ala Phe Thr Pro
70                  75                  80                  85

cgc acc aac ggc acc acc gtg acc agc gat tcc caa ggc acc gtg gaa   403
Arg Thr Asn Gly Thr Thr Val Thr Ser Asp Ser Gln Gly Thr Val Glu
                90                  95                  100

ttc aac ggc tcc gtg cac ttc ctc gga cac cag gca gag gac aaa tgg   451
Phe Asn Gly Ser Val His Phe Leu Gly His Gln Ala Glu Asp Lys Trp
            105                 110                 115

atc ctg gac acc acc atg tct gac atc aaa atg gtg ttc aac gga tcc   499
```

```
Ile Leu Asp Thr Thr Met Ser Asp Ile Lys Met Val Phe Asn Gly Ser
        120                 125                 130

tcc gcg cag cta gtt gtg gat ttg gtt gcc cgc gaa ttc              538
Ser Ala Gln Leu Val Val Asp Leu Val Ala Arg Glu Phe
    135                 140                 145


<210> 1312
<211> 146
<212> PRT
<213> Corynebacterium glutamicum

<400> 1312
Met Lys Leu Ala Pro Arg Met Arg Met Arg Ser Pro Lys Thr Phe Ala
  1               5                  10                  15

Ala Leu Ala Ser Leu Ala Leu Val Ile Gly Leu Gly Gln Val Pro Ile
             20                  25                  30

Ala Gln Ala Gln Thr Glu Tyr Arg Thr Ala Ser Asp Gly Ser Leu Asn
         35                  40                  45

Trp Gly Phe Arg Gln Ser Phe Arg Asn Tyr Ile Gln Thr Gly Val Ala
     50                  55                  60

Lys Gly Ser Ile Thr Leu Gly Asp Gly Ala Ser Asp Asn Gly Gly Asn
 65                  70                  75                  80

Phe Ala Phe Thr Pro Arg Thr Asn Gly Thr Thr Val Thr Ser Asp Ser
                 85                  90                  95

Gln Gly Thr Val Glu Phe Asn Gly Ser Val His Phe Leu Gly His Gln
            100                 105                 110

Ala Glu Asp Lys Trp Ile Leu Asp Thr Thr Met Ser Asp Ile Lys Met
        115                 120                 125

Val Phe Asn Gly Ser Ser Ala Gln Leu Val Val Asp Leu Val Ala Arg
    130                 135                 140

Glu Phe
145


<210> 1313
<211> 528
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(528)
<223> FRXA02824

<400> 1313
ttc tac gaa acc ggc gaa gcc ctc gac ccg acc ggc gac agc ctg acc   48
Phe Tyr Glu Thr Gly Glu Ala Leu Asp Pro Thr Gly Asp Ser Leu Thr
  1               5                  10                  15

att tcc tcc acc acc acc gcg cca tcg acc agc acg acc tcc acc tct   96
```

```
Ile Ser Ser Thr Thr Thr Ala Pro Ser Thr Ser Thr Thr Ser Thr Ser
            20                  25                  30

gcc tca act tcc ggt gga acc gcc gac tgt tcc tcc ggc gca ttg ggt   144
Ala Ser Thr Ser Gly Gly Thr Ala Asp Cys Ser Ser Gly Ala Leu Gly
         35                  40                  45

gtt gtc acc acc gga acc aac gac ggc atg ctg ggc acc atc cag gaa   192
Val Val Thr Thr Gly Thr Asn Asp Gly Met Leu Gly Thr Ile Gln Glu
     50                  55                  60

gta aac aac acc ttc gcg att tgg aac aac ctc atc gtc aac acc gag   240
Val Asn Asn Thr Phe Ala Ile Trp Asn Asn Leu Ile Val Asn Thr Glu
 65                  70                  75                  80

cgc atg ttc tgc aac att gat acc ctc aag gcg cgc ttc gac acg gat   288
Arg Met Phe Cys Asn Ile Asp Thr Leu Lys Ala Arg Phe Asp Thr Asp
                 85                  90                  95

gat tcc agc gat tca gcg acc tct gcg act tct ggg act act gcg tcc   336
Asp Ser Ser Asp Ser Ala Thr Ser Ala Thr Ser Gly Thr Thr Ala Ser
            100                 105                 110

acc ggc acc acc gct gca act acc gcg gga acc acg ggt acc act gga   384
Thr Gly Thr Thr Ala Ala Thr Thr Ala Gly Thr Thr Gly Thr Thr Gly
        115                 120                 125

act gcc agc acc gct tcc gga act tcc gga act tcc gga acc tcc ggc   432
Thr Ala Ser Thr Ala Ser Gly Thr Ser Gly Thr Ser Gly Thr Ser Gly
    130                 135                 140

acc gca gca act gtc gct ggc acc acc cca act gac aat ggc gtt tgc   480
Thr Ala Ala Thr Val Ala Gly Thr Thr Pro Thr Asp Asn Gly Val Cys
145                 150                 155                 160

acc gct tcc gga tct ttg ggc gtg acc caa gca tct gcg cag tgg ggt   528
Thr Ala Ser Gly Ser Leu Gly Val Thr Gln Ala Ser Ala Gln Trp Gly
                165                 170                 175
```

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<210> 1314
<211> 176
<212> PRT
<213> Corynebacterium glutamicum

<400> 1314

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Phe Tyr Glu Thr Gly Glu Ala Leu Asp Pro Thr Gly Asp Ser Leu Thr
  1               5                  10                  15

Ile Ser Ser Thr Thr Thr Ala Pro Ser Thr Ser Thr Thr Ser Thr Ser
            20                  25                  30

Ala Ser Thr Ser Gly Gly Thr Ala Asp Cys Ser Ser Gly Ala Leu Gly
         35                  40                  45

Val Val Thr Thr Gly Thr Asn Asp Gly Met Leu Gly Thr Ile Gln Glu
     50                  55                  60

Val Asn Asn Thr Phe Ala Ile Trp Asn Asn Leu Ile Val Asn Thr Glu
 65                  70                  75                  80
```

```
Arg Met Phe Cys Asn Ile Asp Thr Leu Lys Ala Arg Phe Asp Thr Asp
                85                  90                  95

Asp Ser Ser Asp Ser Ala Thr Ser Ala Thr Ser Gly Thr Thr Ala Ser
            100                 105                 110

Thr Gly Thr Thr Ala Ala Thr Thr Ala Gly Thr Thr Gly Thr Thr Gly
        115                 120                 125

Thr Ala Ser Thr Ala Ser Gly Thr Ser Gly Thr Ser Gly Thr Ser Gly
    130                 135                 140

Thr Ala Ala Thr Val Ala Gly Thr Thr Pro Thr Asp Asn Gly Val Cys
145                 150                 155                 160

Thr Ala Ser Gly Ser Leu Gly Val Thr Gln Ala Ser Ala Gln Trp Gly
                165                 170                 175
```

<210> 1315
<211> 407
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(384)
<223> FRXA02825

<400> 1315

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aat gtt tct gca acg gaa gct tcc ggt tcc gct tcg gtg tcc ctg tca   48
Asn Val Ser Ala Thr Glu Ala Ser Gly Ser Ala Ser Val Ser Leu Ser
  1               5                  10                  15

cag tcg ggt tcg cag gcg ttc gct gat ttc tac acc cca ggc acc cag   96
Gln Ser Gly Ser Gln Ala Phe Ala Asp Phe Tyr Thr Pro Gly Thr Gln
            20                  25                  30

ttg gat ccg atc agt ttc agc gca act ttg ggc ggc gac gcc agc tgc   144
Leu Asp Pro Ile Ser Phe Ser Ala Thr Leu Gly Gly Asp Ala Ser Cys
        35                  40                  45

gcc acc gga tcc acc tcg acc aca ggc gct gct gcc acc gcg aac act   192
Ala Thr Gly Ser Thr Ser Thr Thr Gly Ala Ala Ala Thr Ala Asn Thr
    50                  55                  60

gac aac acc gaa ggt gtt gcc ggc gag gaa tcc acc acc ccc gct aac   240
Asp Asn Thr Glu Gly Val Ala Gly Glu Glu Ser Thr Thr Pro Ala Asn
65                  70                  75                  80

caa aac agc cag ttc caa atc cgc cag gcc gct gca gat tcc acc gga   288
Gln Asn Ser Gln Phe Gln Ile Arg Gln Ala Ala Ala Asp Ser Thr Gly
                85                  90                  95

ctg gat acc acc acc aca atg ttg ctc atc ctc gcg gcg ttc gtt gtc   336
Leu Asp Thr Thr Thr Thr Met Leu Leu Ile Leu Ala Ala Phe Val Val
            100                 105                 110
```

```
gca ggt ggc tcc atg act cgc ttc acc gtc ggc aac ccg act gga aaa   384
Ala Gly Gly Ser Met Thr Arg Phe Thr Val Gly Asn Pro Thr Gly Lys
        115                 120                 125

taaggcttca catgaataac gct                                       407
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<210> 1316
<211> 128
<212> PRT
<213> Corynebacterium glutamicum

<400> 1316

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Asn Val Ser Ala Thr Glu Ala Ser Gly Ser Ala Ser Val Ser Leu Ser
  1               5                  10                  15

Gln Ser Gly Ser Gln Ala Phe Ala Asp Phe Tyr Thr Pro Gly Thr Gln
             20                  25                  30

Leu Asp Pro Ile Ser Phe Ser Ala Thr Leu Gly Gly Asp Ala Ser Cys
         35                  40                  45

Ala Thr Gly Ser Thr Ser Thr Thr Gly Ala Ala Ala Thr Ala Asn Thr
     50                  55                  60

Asp Asn Thr Glu Gly Val Ala Gly Glu Glu Ser Thr Thr Pro Ala Asn
 65                  70                  75                  80

Gln Asn Ser Gln Phe Gln Ile Arg Gln Ala Ala Ala Asp Ser Thr Gly
                 85                  90                  95

Leu Asp Thr Thr Thr Thr Met Leu Leu Ile Leu Ala Ala Phe Val Val
            100                 105                 110

Ala Gly Gly Ser Met Thr Arg Phe Thr Val Gly Asn Pro Thr Gly Lys
        115                 120                 125
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<210> 1317
<211> 528
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(528)
<223> RXN02838

<400> 1317

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aac acg ggc aag ggc ggg ggg ctg acg gtg ccg ctg ggc gac ggg cag   48
Asn Thr Gly Lys Gly Gly Gly Leu Thr Val Pro Leu Gly Asp Gly Gln
  1               5                  10                  15

ggg cgg tat atc gcg aag ttc ccc tcg acc gcg ttt gtg ggg gtg tcg   96
Gly Arg Tyr Ile Ala Lys Phe Pro Ser Thr Ala Phe Val Gly Val Ser
             20                  25                  30

gag aac gaa ttt gcc aat ctg gct ttg gcc gag gcg atc ggg atg gag   144
```

```
Glu Asn Glu Phe Ala Asn Leu Ala Leu Ala Glu Ala Ile Gly Met Glu
         35                  40                  45

gtg ccc gcg cgc gag ttg gtg ggg cgt gcg cag ttt gaa ggc gtg ccc   192
Val Pro Ala Arg Glu Leu Val Gly Arg Ala Gln Phe Glu Gly Val Pro
     50                  55                  60

ccc gag ttt gag gcc atg acc gac ggg ttg gtt ttg ctg gtg cgg cgg   240
Pro Glu Phe Glu Ala Met Thr Asp Gly Leu Val Leu Leu Val Arg Arg
 65                  70                  75                  80

ttt gat cgc gcg ggc gat ggc gtg cgc gtg cat atg gag gat ttc gca   288
Phe Asp Arg Ala Gly Asp Gly Val Arg Val His Met Glu Asp Phe Ala
                 85                  90                  95

cag gtg ttc ggc cta tac ccc gcg cgc aag tat gat ggg gcg gcc agt   336
Gln Val Phe Gly Leu Tyr Pro Ala Arg Lys Tyr Asp Gly Ala Ala Ser
            100                 105                 110

cac gat att gcg gcg gtg ctg ggc agt gcg gtg tcg atc gcg gcg ggg   384
His Asp Ile Ala Ala Val Leu Gly Ser Ala Val Ser Ile Ala Ala Gly
        115                 120                 125

ttg gag ttc gtg cgg cgg ctg gcg ctc tcg gtt gtg atg ggc aac ggc   432
Leu Glu Phe Val Arg Arg Leu Ala Leu Ser Val Val Met Gly Asn Gly
    130                 135                 140

gat atg cat ttg aag aac tgg tcg ctg atc tat cgc ggg cgg ggc gat   480
Asp Met His Leu Lys Asn Trp Ser Leu Ile Tyr Arg Gly Arg Gly Asp
145                 150                 155                 160

gtg ccg gcg ttg gcg cct gtg tat tat atg atg tcg acc gtg acc tat   528
Val Pro Ala Leu Ala Pro Val Tyr Tyr Met Met Ser Thr Val Thr Tyr
                165                 170                 175


<210> 1318
<211> 176
<212> PRT
<213> Corynebacterium glutamicum

<400> 1318
Asn Thr Gly Lys Gly Gly Gly Leu Thr Val Pro Leu Gly Asp Gly Gln
  1               5                  10                  15

Gly Arg Tyr Ile Ala Lys Phe Pro Ser Thr Ala Phe Val Gly Val Ser
            20                  25                  30

Glu Asn Glu Phe Ala Asn Leu Ala Leu Ala Glu Ala Ile Gly Met Glu
         35                  40                  45

Val Pro Ala Arg Glu Leu Val Gly Arg Ala Gln Phe Glu Gly Val Pro
     50                  55                  60

Pro Glu Phe Glu Ala Met Thr Asp Gly Leu Val Leu Leu Val Arg Arg
 65                  70                  75                  80

Phe Asp Arg Ala Gly Asp Gly Val Arg Val His Met Glu Asp Phe Ala
                 85                  90                  95

Gln Val Phe Gly Leu Tyr Pro Ala Arg Lys Tyr Asp Gly Ala Ala Ser
```

```
            100                 105                 110

His Asp Ile Ala Ala Val Leu Gly Ser Ala Val Ser Ile Ala Ala Gly
        115                 120                 125

Leu Glu Phe Val Arg Arg Leu Ala Leu Ser Val Val Met Gly Asn Gly
    130                 135                 140

Asp Met His Leu Lys Asn Trp Ser Leu Ile Tyr Arg Gly Arg Gly Asp
145                 150                 155                 160

Val Pro Ala Leu Ala Pro Val Tyr Tyr Met Met Ser Thr Val Thr Tyr
                165                 170                 175
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<210> 1319
<211> 462
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(462)
<223> FRXA02838

<400> 1319

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acc gtg ccg ctg ggc gac ggg cag ggg cgg tat atc gcg aag atc ccc   48
Thr Val Pro Leu Gly Asp Gly Gln Gly Arg Tyr Ile Ala Lys Ile Pro
  1               5                  10                  15

tcg acc gcg ttt gtg ggg gtg tcg gag aac aaa ttt gcc aat ctg gct   96
Ser Thr Ala Phe Val Gly Val Ser Glu Asn Lys Phe Ala Asn Leu Ala
             20                  25                  30

ttg gcc gag gcg atc ggg atg gag gtg ccc gcg cgc gag ttg gtg ggg   144
Leu Ala Glu Ala Ile Gly Met Glu Val Pro Ala Arg Glu Leu Val Gly
         35                  40                  45

cgt gcg cag ttt gaa ggc gtg ccc ccc gag ttt gag gcc atg acc gac   192
Arg Ala Gln Phe Glu Gly Val Pro Pro Glu Phe Glu Ala Met Thr Asp
     50                  55                  60

ggg ttg gtt ttg ctg gtg cgg cgg ttt gat cgc gcg ggc gat ggc gtg   240
Gly Leu Val Leu Leu Val Arg Arg Phe Asp Arg Ala Gly Asp Gly Val
 65                  70                  75                  80

cgc gtg cat atg gag gat ttc gca cag gtg ttc ggc cta tac ccc gcg   288
Arg Val His Met Glu Asp Phe Ala Gln Val Phe Gly Leu Tyr Pro Ala
                85                  90                  95

cgc aag tat gat ggg gcg gcc agt cac gat att gcg gcg gtg ctg ggc   336
Arg Lys Tyr Asp Gly Ala Ala Ser His Asp Ile Ala Ala Val Leu Gly
            100                 105                 110

agt gcg gtg tcg atc gcg gcg ggg ttg gag ttc gtg cgg cgg ctg gcg   384
Ser Ala Val Ser Ile Ala Ala Gly Leu Glu Phe Val Arg Arg Leu Ala
        115                 120                 125
```

ctc tct gtt gtg atg ggc aac ggc gat atg cat ttg aag aac tgg tcg 432
Leu Ser Val Val Met Gly Asn Gly Asp Met His Leu Lys Asn Trp Ser
130 135 140

ctg atc tat cac ggg cgg ggc gat gtg ccg 462
Leu Ile Tyr His Gly Arg Gly Asp Val Pro
145 150

<210> 1320
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 1320
Thr Val Pro Leu Gly Asp Gly Gln Gly Arg Tyr Ile Ala Lys Ile Pro
1 5 10 15

Ser Thr Ala Phe Val Gly Val Ser Glu Asn Lys Phe Ala Asn Leu Ala
20 25 30

Leu Ala Glu Ala Ile Gly Met Glu Val Pro Ala Arg Glu Leu Val Gly
35 40 45

Arg Ala Gln Phe Glu Gly Val Pro Pro Glu Phe Glu Ala Met Thr Asp
50 55 60

Gly Leu Val Leu Leu Val Arg Arg Phe Asp Arg Ala Gly Asp Gly Val
65 70 75 80

Arg Val His Met Glu Asp Phe Ala Gln Val Phe Gly Leu Tyr Pro Ala
85 90 95

Arg Lys Tyr Asp Gly Ala Ala Ser His Asp Ile Ala Ala Val Leu Gly
100 105 110

Ser Ala Val Ser Ile Ala Ala Gly Leu Glu Phe Val Arg Arg Leu Ala
115 120 125

Leu Ser Val Val Met Gly Asn Gly Asp Met His Leu Lys Asn Trp Ser
130 135 140

Leu Ile Tyr His Gly Arg Gly Asp Val Pro
145 150

<210> 1321
<211> 273
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(250)
<223> RXN02840

<400> 1321
aagtgaaatc aatcggcttt tccagcagca gcactggtcg cgccagcgtg ggtgttatgg 60

tgaaggcgaa tacaccttca gcaccgctga gccggaagag atg acg gta atc agt 115
Met Thr Val Ile Ser

```
                                                    1               5

ggc gcg ctg aat gtg tta ctg cct gac gcg acc gac tgg cag gtg tat   163
Gly Ala Leu Asn Val Leu Leu Pro Asp Ala Thr Asp Trp Gln Val Tyr
                10                  15                  20

gaa gcc ggt tcg gtg ttt aat gtt ccc ggt cac agt gag ttt cat ctg   211
Glu Ala Gly Ser Val Phe Asn Val Pro Gly His Ser Glu Phe His Leu
            25                  30                  35

caa gtt gcc gaa ccc acc tct tat ctg tgc cgc tat ctg taattcctcg    260
Gln Val Ala Glu Pro Thr Ser Tyr Leu Cys Arg Tyr Leu
        40                  45                  50

ccttcccctt gaa                                                   273


<210> 1322
<211> 50
<212> PRT
<213> Corynebacterium glutamicum

<400> 1322
Met Thr Val Ile Ser Gly Ala Leu Asn Val Leu Leu Pro Asp Ala Thr
  1               5                  10                  15

Asp Trp Gln Val Tyr Glu Ala Gly Ser Val Phe Asn Val Pro Gly His
            20                  25                  30

Ser Glu Phe His Leu Gln Val Ala Glu Pro Thr Ser Tyr Leu Cys Arg
        35                  40                  45

Tyr Leu
     50


<210> 1323
<211> 273
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(250)
<223> FRXA02840

<400> 1323
aagtgaaatc aatcggcttt tccagcagca gcactggtcg cgccagcgtg ggtgttatgg 60

tgaaggcgaa tacaccttca gcaccgctga gccggaagag atg acg gta atc agt   115
                                              Met Thr Val Ile Ser
                                                1               5

ggc gcg ctg aat gtg tta ctg cct gac gcg acc gac tgg cag gtg tat   163
Gly Ala Leu Asn Val Leu Leu Pro Asp Ala Thr Asp Trp Gln Val Tyr
                10                  15                  20

gaa gcc ggt tcg gtg ttt aat gtt ccc ggt cac agt gag ttt cat ctg   211
Glu Ala Gly Ser Val Phe Asn Val Pro Gly His Ser Glu Phe His Leu
            25                  30                  35
```

caa gtt gcc gaa ccc acc tct tat ctg tgc cgc tat ctg taattcctcg 260
Gln Val Ala Glu Pro Thr Ser Tyr Leu Cys Arg Tyr Leu
40 45 50

ccttcccctt gaa 273

<210> 1324
<211> 50
<212> PRT
<213> Corynebacterium glutamicum

<400> 1324
Met Thr Val Ile Ser Gly Ala Leu Asn Val Leu Leu Pro Asp Ala Thr
1 5 10 15

Asp Trp Gln Val Tyr Glu Ala Gly Ser Val Phe Asn Val Pro Gly His
20 25 30

Ser Glu Phe His Leu Gln Val Ala Glu Pro Thr Ser Tyr Leu Cys Arg
35 40 45

Tyr Leu
50

<210> 1325
<211> 558
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(535)
<223> RXN02841

<400> 1325
ctcacataac tttacgccac cccataccct ttaacccctg cactgctcat ccacaagcac 60

tgtgcagggg ttgtgttttc taacaagaaa agagaccacc atg ttc aca gct ttt 115
Met Phe Thr Ala Phe
1 5

aaa agc aat cct acg acc att aaa aag ctg gtt tct gag ctc att aat 163
Lys Ser Asn Pro Thr Thr Ile Lys Lys Leu Val Ser Glu Leu Ile Asn
10 15 20

ggc gac gat gca gcg ctc aac gaa cta gag cga cac gtc act aat gaa 211
Gly Asp Asp Ala Ala Leu Asn Glu Leu Glu Arg His Val Thr Asn Glu
25 30 35

tca gtc cgt gct cgc gaa ctc cct aat gtc cag tac aaa gcc act gcg 259
Ser Val Arg Ala Arg Glu Leu Pro Asn Val Gln Tyr Lys Ala Thr Ala
40 45 50

ggg cgc aac ttc gcc ata tcc aag ctg gtc caa aat ttg cgt cgc atc 307
Gly Arg Asn Phe Ala Ile Ser Lys Leu Val Gln Asn Leu Arg Arg Ile
55 60 65

aac aag gca caa aac aat cca cgt ggt gtg ccc act cat gcc acc gtg 355
Asn Lys Ala Gln Asn Asn Pro Arg Gly Val Pro Thr His Ala Thr Val

```
 70                  75                  80                  85

att ctg ctt aag gaa gac ggc agc tac gac ggt gaa gaa cag tgg cgc   403
Ile Leu Leu Lys Glu Asp Gly Ser Tyr Asp Gly Glu Glu Gln Trp Arg
                90                  95                  100

att cca gaa aag gcg atc act ccg ttc gac atg cta cgt tcg cct gac   451
Ile Pro Glu Lys Ala Ile Thr Pro Phe Asp Met Leu Arg Ser Pro Asp
            105                 110                 115

ttc aac cac aac agg ctg aag aac cgg ccg ctc atg gtc gag tcc caa   499
Phe Asn His Asn Arg Leu Lys Asn Arg Pro Leu Met Val Glu Ser Gln
        120                 125                 130

tac ccc tgg ggc gtc ccc gga ctc att aaa atg aac tgatcaatcc        545
Tyr Pro Trp Gly Val Pro Gly Leu Ile Lys Met Asn
    135                 140                 145

ctgacacagc cat                                                   558


<210> 1326
<211> 145
<212> PRT
<213> Corynebacterium glutamicum

<400> 1326
Met Phe Thr Ala Phe Lys Ser Asn Pro Thr Thr Ile Lys Lys Leu Val
  1               5                  10                  15

Ser Glu Leu Ile Asn Gly Asp Asp Ala Ala Leu Asn Glu Leu Glu Arg
             20                  25                  30

His Val Thr Asn Glu Ser Val Arg Ala Arg Glu Leu Pro Asn Val Gln
         35                  40                  45

Tyr Lys Ala Thr Ala Gly Arg Asn Phe Ala Ile Ser Lys Leu Val Gln
     50                  55                  60

Asn Leu Arg Arg Ile Asn Lys Ala Gln Asn Asn Pro Arg Gly Val Pro
 65                  70                  75                  80

Thr His Ala Thr Val Ile Leu Leu Lys Glu Asp Gly Ser Tyr Asp Gly
                85                  90                  95

Glu Glu Gln Trp Arg Ile Pro Glu Lys Ala Ile Thr Pro Phe Asp Met
            100                 105                 110

Leu Arg Ser Pro Asp Phe Asn His Asn Arg Leu Lys Asn Arg Pro Leu
        115                 120                 125

Met Val Glu Ser Gln Tyr Pro Trp Gly Val Pro Gly Leu Ile Lys Met
    130                 135                 140

Asn
145


<210> 1327
<211> 285
<212> DNA
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<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (7)..(285)
<223> FRXA02841

<400> 1327
accaccatg ttc gca gct ttt aaa agc aat ctt ccg acc att aaa aag ctg 51
Met Phe Ala Ala Phe Lys Ser Asn Leu Pro Thr Ile Lys Lys Leu
1 5 10 15

gtt tat gag gtc att aat ggc gtc gat gca gcg ctc aac gaa cta gag 99
Val Tyr Glu Val Ile Asn Gly Val Asp Ala Ala Leu Asn Glu Leu Glu
20 25 30

cga cac gtc act aat gaa tca gtc cgt gct cgc gaa ctc cct aat gtc 147
Arg His Val Thr Asn Glu Ser Val Arg Ala Arg Glu Leu Pro Asn Val
35 40 45

cag tac aaa gcc act gcg ggg cgc aac ttc gcc ata tcc aag ctg gtc 195
Gln Tyr Lys Ala Thr Ala Gly Arg Asn Phe Ala Ile Ser Lys Leu Val
50 55 60

caa aat ttg cgt cgc atc aac aag gca caa aac aat cca cgt ggt gtg 243
Gln Asn Leu Arg Arg Ile Asn Lys Ala Gln Asn Asn Pro Arg Gly Val
65 70 75

ccc act cat gcc acc gtg att ctg ctt aag gga gac ggc agc 285
Pro Thr His Ala Thr Val Ile Leu Leu Lys Gly Asp Gly Ser
80 85 90

<210> 1328
<211> 93
<212> PRT
<213> Corynebacterium glutamicum

<400> 1328
Met Phe Ala Ala Phe Lys Ser Asn Leu Pro Thr Ile Lys Lys Leu Val
1 5 10 15

Tyr Glu Val Ile Asn Gly Val Asp Ala Ala Leu Asn Glu Leu Glu Arg
20 25 30

His Val Thr Asn Glu Ser Val Arg Ala Arg Glu Leu Pro Asn Val Gln
35 40 45

Tyr Lys Ala Thr Ala Gly Arg Asn Phe Ala Ile Ser Lys Leu Val Gln
50 55 60

Asn Leu Arg Arg Ile Asn Lys Ala Gln Asn Asn Pro Arg Gly Val Pro
65 70 75 80

Thr His Ala Thr Val Ile Leu Leu Lys Gly Asp Gly Ser
85 90

<210> 1329
<211> 873
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(850)
<223> RXN02846

<400> 1329
tacaagcgct gaacgttgag tttgagtttg gtccattgag gggtaaaggc ttacctctcg 60

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actaggtggg gtgggcgtag agcgcctatt ctgattgatc gtg tta acc atc gct   115
                                             Val Leu Thr Ile Ala
                                               1               5

att gta ctt ctc gcg tca gtc ctc atc ggt gct ctt ctc caa cgc atg   163
Ile Val Leu Leu Ala Ser Val Leu Ile Gly Ala Leu Leu Gln Arg Met
                10                  15                  20

aca gga ttg ggc gtc ggt cta gtt acc ggc cca gtc ctg act tct ttg   211
Thr Gly Leu Gly Val Gly Leu Val Thr Gly Pro Val Leu Thr Ser Leu
            25                  30                  35

tta ggg ccg cta gca ggc gtg acc atg gtg aat ggt ctg tcc atc atc   259
Leu Gly Pro Leu Ala Gly Val Thr Met Val Asn Gly Leu Ser Ile Ile
        40                  45                  50

aac gcg gtg aat aat gcg tgg tcg gtg cgc aaa cgc act gac tgg gcc   307
Asn Ala Val Asn Asn Ala Trp Ser Val Arg Lys Arg Thr Asp Trp Ala
    55                  60                  65

aaa ttc cga att ctt gcc ggc gct ttg gtg ctt ggt tct gtt cct gct   355
Lys Phe Arg Ile Leu Ala Gly Ala Leu Val Leu Gly Ser Val Pro Ala
70                  75                  80                  85

gtt gca gtg gtg tat ttc ctt aac gga cca tgg ctg ttg att ttc gtt   403
Val Ala Val Val Tyr Phe Leu Asn Gly Pro Trp Leu Leu Ile Phe Val
                90                  95                 100

ggt gcg atg gtg ctg ctc gcg ttg ggt gtt tcc ctg ttc cca aca gag   451
Gly Ala Met Val Leu Leu Ala Leu Gly Val Ser Leu Phe Pro Thr Glu
            105                 110                 115

aaa ttc gca ctc aag caa gaa gct aaa ctg cct atg gtc atc ttc ggc   499
Lys Phe Ala Leu Lys Gln Glu Ala Lys Leu Pro Met Val Ile Phe Gly
        120                 125                 130

atg att ggt gga ttc atg tcc act gtt gca ggc atc gca ggg cca tcc   547
Met Ile Gly Gly Phe Met Ser Thr Val Ala Gly Ile Ala Gly Pro Ser
    135                 140                 145

ctg act gtt tat gcg cgc ctg agc cgc tgg gat tac cgc gac ttt gtg   595
Leu Thr Val Tyr Ala Arg Leu Ser Arg Trp Asp Tyr Arg Asp Phe Val
150                 155                 160                 165

gcc acc ttg cac cca gtt cta ctc gtg gcc aac acc gta tcg ttc ctg   643
Ala Thr Leu His Pro Val Leu Leu Val Ala Asn Thr Val Ser Phe Leu
                170                 175                 180

ctc aag gtt atc ttg atc ggt gga ctc gat ttc ggt ggc gca ccc gca   691
Leu Lys Val Ile Leu Ile Gly Gly Leu Asp Phe Gly Gly Ala Pro Ala
            185                 190                 195
```

```
tgg ctc tgg atc ggt gcc gta gcg atg atc ttt gtc ggt gct tgg ttg   739
Trp Leu Trp Ile Gly Ala Val Ala Met Ile Phe Val Gly Ala Trp Leu
        200                 205                 210

ggt gaa atc gtc aac gct aag gtg tcc acc cca atg gcc aag cgc atc   787
Gly Glu Ile Val Asn Ala Lys Val Ser Thr Pro Met Ala Lys Arg Ile
    215                 220                 225

gct acg ctc ctg gca gca gct ggt gcc gca gtg gtg ttg ttc cga ggc   835
Ala Thr Leu Leu Ala Ala Ala Gly Ala Ala Val Val Leu Phe Arg Gly
230                 235                 240                 245

atc atg gaa ttg gtt tagcggtctt aattggtggg aag                    873
Ile Met Glu Leu Val
                250
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<210> 1330
<211> 250
<212> PRT
<213> Corynebacterium glutamicum

<400> 1330

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Val Leu Thr Ile Ala Ile Val Leu Leu Ala Ser Val Leu Ile Gly Ala
  1               5                  10                  15

Leu Leu Gln Arg Met Thr Gly Leu Gly Val Gly Leu Val Thr Gly Pro
            20                  25                  30

Val Leu Thr Ser Leu Leu Gly Pro Leu Ala Gly Val Thr Met Val Asn
        35                  40                  45

Gly Leu Ser Ile Ile Asn Ala Val Asn Asn Ala Trp Ser Val Arg Lys
    50                  55                  60

Arg Thr Asp Trp Ala Lys Phe Arg Ile Leu Ala Gly Ala Leu Val Leu
65                  70                  75                  80

Gly Ser Val Pro Ala Val Ala Val Val Tyr Phe Leu Asn Gly Pro Trp
                85                  90                  95

Leu Leu Ile Phe Val Gly Ala Met Val Leu Leu Ala Leu Gly Val Ser
            100                 105                 110

Leu Phe Pro Thr Glu Lys Phe Ala Leu Lys Gln Glu Ala Lys Leu Pro
        115                 120                 125

Met Val Ile Phe Gly Met Ile Gly Gly Phe Met Ser Thr Val Ala Gly
    130                 135                 140

Ile Ala Gly Pro Ser Leu Thr Val Tyr Ala Arg Leu Ser Arg Trp Asp
145                 150                 155                 160

Tyr Arg Asp Phe Val Ala Thr Leu His Pro Val Leu Leu Val Ala Asn
                165                 170                 175

Thr Val Ser Phe Leu Leu Lys Val Ile Leu Ile Gly Gly Leu Asp Phe
            180                 185                 190

Gly Gly Ala Pro Ala Trp Leu Trp Ile Gly Ala Val Ala Met Ile Phe
```

```
        195                 200                 205

Val Gly Ala Trp Leu Gly Glu Ile Val Asn Ala Lys Val Ser Thr Pro
    210                 215                 220

Met Ala Lys Arg Ile Ala Thr Leu Leu Ala Ala Ala Gly Ala Ala Val
225                 230                 235                 240

Val Leu Phe Arg Gly Ile Met Glu Leu Val
                245                 250


<210> 1331
<211> 573
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(573)
<223> FRXA02846

<400> 1331
gtg aat ggt ctg tcc atc atc aac gcg gtg aat aat gcg tgg tcg gtg   48
Val Asn Gly Leu Ser Ile Ile Asn Ala Val Asn Asn Ala Trp Ser Val
  1               5                  10                  15

cgc aaa cgc act gac tgg gcc aaa ttc cga att ctt gcc ggc gct ttg   96
Arg Lys Arg Thr Asp Trp Ala Lys Phe Arg Ile Leu Ala Gly Ala Leu
             20                  25                  30

gtg ctt ggt tct gtt cct gct gtt gca gtg gtg tat ttc ctt aac gga   144
Val Leu Gly Ser Val Pro Ala Val Ala Val Val Tyr Phe Leu Asn Gly
         35                  40                  45

cca tgg ctg ttg att ttc gtt ggt gcg atg gtg ctg ctc gcg ttg ggt   192
Pro Trp Leu Leu Ile Phe Val Gly Ala Met Val Leu Leu Ala Leu Gly
     50                  55                  60

gtt tcc ctg ttc cca aca gag aaa ttc gca ctc aag caa gaa gct aaa   240
Val Ser Leu Phe Pro Thr Glu Lys Phe Ala Leu Lys Gln Glu Ala Lys
 65                  70                  75                  80

ctg cct atg gtc atc ttc ggc atg att ggt gga ttc atg tcc act gtt   288
Leu Pro Met Val Ile Phe Gly Met Ile Gly Gly Phe Met Ser Thr Val
                 85                  90                  95

gca ggc atc gca ggg cca tcc ctg act gtt tat gcg cgc ctg agc cgc   336
Ala Gly Ile Ala Gly Pro Ser Leu Thr Val Tyr Ala Arg Leu Ser Arg
            100                 105                 110

tgg gat tac cga gac ttt gtg gcc acc ttg cac cca gtt cta ctc gtg   384
Trp Asp Tyr Arg Asp Phe Val Ala Thr Leu His Pro Val Leu Leu Val
        115                 120                 125

gcc aac acc gta tcg ttc ctg ctc aag gtt atc ttg atc ggt gga ctc   432
Ala Asn Thr Val Ser Phe Leu Leu Lys Val Ile Leu Ile Gly Gly Leu
    130                 135                 140

gat ttc ggt ggc gca ccc gca tgg ctc tgg atc ggt gcc gta gcg atg   480
Asp Phe Gly Gly Ala Pro Ala Trp Leu Trp Ile Gly Ala Val Ala Met
```

```
145                 150                 155                 160

atc ttt gtc ggt gct tgg ttg ggt gaa atc gtc aac gct aag gtg tcc   528
Ile Phe Val Gly Ala Trp Leu Gly Glu Ile Val Asn Ala Lys Val Ser
                165                 170                 175

acc cca atg gcc aag cgc atc gct acg ctc ctg gca gca gct ggt       573
Thr Pro Met Ala Lys Arg Ile Ala Thr Leu Leu Ala Ala Ala Gly
            180                 185                 190


<210> 1332
<211> 191
<212> PRT
<213> Corynebacterium glutamicum

<400> 1332
Val Asn Gly Leu Ser Ile Ile Asn Ala Val Asn Asn Ala Trp Ser Val
  1               5                  10                  15

Arg Lys Arg Thr Asp Trp Ala Lys Phe Arg Ile Leu Ala Gly Ala Leu
             20                  25                  30

Val Leu Gly Ser Val Pro Ala Val Ala Val Val Tyr Phe Leu Asn Gly
         35                  40                  45

Pro Trp Leu Leu Ile Phe Val Gly Ala Met Val Leu Leu Ala Leu Gly
     50                  55                  60

Val Ser Leu Phe Pro Thr Glu Lys Phe Ala Leu Lys Gln Glu Ala Lys
 65                  70                  75                  80

Leu Pro Met Val Ile Phe Gly Met Ile Gly Gly Phe Met Ser Thr Val
                85                  90                  95

Ala Gly Ile Ala Gly Pro Ser Leu Thr Val Tyr Ala Arg Leu Ser Arg
            100                 105                 110

Trp Asp Tyr Arg Asp Phe Val Ala Thr Leu His Pro Val Leu Leu Val
        115                 120                 125

Ala Asn Thr Val Ser Phe Leu Leu Lys Val Ile Leu Ile Gly Gly Leu
    130                 135                 140

Asp Phe Gly Gly Ala Pro Ala Trp Leu Trp Ile Gly Ala Val Ala Met
145                 150                 155                 160

Ile Phe Val Gly Ala Trp Leu Gly Glu Ile Val Asn Ala Lys Val Ser
                165                 170                 175

Thr Pro Met Ala Lys Arg Ile Ala Thr Leu Leu Ala Ala Ala Gly
            180                 185                 190


<210> 1333
<211> 1135
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
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<222> (47)..(1135)
<223> RXN02847

<400> 1333
atatcgcagc agcctcgatg gtcaacgccc atatgatggg aagttgttg gcg cta acc 58
                                                Leu Ala Leu Thr
                                                  1

gcc aga ggc ttt ctc aat tct gaa aga agc cag aca agg tgg aaa acc 106
Ala Arg Gly Phe Leu Asn Ser Glu Arg Ser Gln Thr Arg Trp Lys Thr
  5   10   15   20

cac ttc acc acc cag aaa gtt cca cgc tcc ggc tac aga tat gac ctc 154
His Phe Thr Thr Gln Lys Val Pro Arg Ser Gly Tyr Arg Tyr Asp Leu
                 25   30   35

gat ggg ctc cgc ggc atc gcg atc gcc ttc gta gtt ttg ttc cat gtt 202
Asp Gly Leu Arg Gly Ile Ala Ile Ala Phe Val Val Leu Phe His Val
             40   45   50

ttc gtc gga aaa gtc tcc ggc ggt gtg gat gtc ttc ctg ctg ctg tct 250
Phe Val Gly Lys Val Ser Gly Gly Val Asp Val Phe Leu Leu Leu Ser
         55   60   65

ggc tat ttc ttc tta ggg tcg caa ttg cgt tat gca gat cgt cca gat 298
Gly Tyr Phe Phe Leu Gly Ser Gln Leu Arg Tyr Ala Asp Arg Pro Asp
     70   75   80

tct tcc atc aac ccc tgg tgg ccg att tgg cgc acg cta cgc aga tta 346
Ser Ser Ile Asn Pro Trp Trp Pro Ile Trp Arg Thr Leu Arg Arg Leu
 85   90   95   100

ctt cct gcg tta gtg ctg gtg ttg ggc gtt tcc atg gtc ctc atc ttg 394
Leu Pro Ala Leu Val Leu Val Leu Gly Val Ser Met Val Leu Ile Leu
                105   110   115

gcg tgg gtg ccc aga ctg caa cca ata gaa ata gcc aac caa gca gta 442
Ala Trp Val Pro Arg Leu Gln Pro Ile Glu Ile Ala Asn Gln Ala Val
            120   125   130

gcc agc ctc ttc tat gtc caa aac tgg gag ctc gca tcc caa ggt gct 490
Ala Ser Leu Phe Tyr Val Gln Asn Trp Glu Leu Ala Ser Gln Gly Ala
        135   140   145

gcc tac gga gca gcc tct gca gaa gtc agt cct ttc cag cac ttg tgg 538
Ala Tyr Gly Ala Ala Ser Ala Glu Val Ser Pro Phe Gln His Leu Trp
    150   155   160

tcc atg gct gtg caa ggg cag ttc tac ctc ttt gcc atc ttg ttg agc 586
Ser Met Ala Val Gln Gly Gln Phe Tyr Leu Phe Ala Ile Leu Leu Ser
165   170   175   180

atg gcg atc atc ctg att cgt cga tac cgc ccc gaa tac tcc gca gtg 634
Met Ala Ile Ile Leu Ile Arg Arg Tyr Arg Pro Glu Tyr Ser Ala Val
                185   190   195

cga cta gcg act cct gtg ctg gca gtg ctc aca tcc gta tca ttt ttc 682
Arg Leu Ala Thr Pro Val Leu Ala Val Leu Thr Ser Val Ser Phe Phe
            200   205   210

agt gca atc ctg tgg cat ttc att gat caa tca gtc aac tac tat tcc 730

```
Ser Ala Ile Leu Trp His Phe Ile Asp Gln Ser Val Asn Tyr Tyr Ser
        215                 220                 225

acc ttc acc agg ttc tgg gag ctc ggc ctt ggt gca cta ttg gtg ctg   778
Thr Phe Thr Arg Phe Trp Glu Leu Gly Leu Gly Ala Leu Leu Val Leu
    230                 235                 240

cat gcg cct cga att ttg att tct gcg aag act aaa tca ata ctc gca   826
His Ala Pro Arg Ile Leu Ile Ser Ala Lys Thr Lys Ser Ile Leu Ala
245                 250                 255                 260

gcc gtc ggt ttg ttt atg gtg cta tcc act gga ttc ttc atg gat ggc   874
Ala Val Gly Leu Phe Met Val Leu Ser Thr Gly Phe Phe Met Asp Gly
                265                 270                 275

gca gag act ttc cct gga ttc ccc gcg ctg tat ccc atc ttg ggt gct   922
Ala Glu Thr Phe Pro Gly Phe Pro Ala Leu Tyr Pro Ile Leu Gly Ala
            280                 285                 290

tgc tta gtc atc ctt ggc gac ggt aaa atc tcg gtc ttt ctc tcc cga   970
Cys Leu Val Ile Leu Gly Asp Gly Lys Ile Ser Val Phe Leu Ser Arg
        295                 300                 305

aaa tgg atg ctt tgg ctc ggc gat atc gcc tac ccg ctc tac ttg tgg   1018
Lys Trp Met Leu Trp Leu Gly Asp Ile Ala Tyr Pro Leu Tyr Leu Trp
    310                 315                 320

cac tgg cct ctg ctg atc att ttc acc gct ttg ttc aac caa gaa gag   1066
His Trp Pro Leu Leu Ile Ile Phe Thr Ala Leu Phe Asn Gln Glu Glu
325                 330                 335                 340

cca tcc atc tgg ctg ggt atc gcc gtg att atg ctg tcc ctt ggc ttg   1114
Pro Ser Ile Trp Leu Gly Ile Ala Val Ile Met Leu Ser Leu Gly Leu
                345                 350                 355

gcg cag ctg act aac aaa tac                                      1135
Ala Gln Leu Thr Asn Lys Tyr
            360
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<210> 1334
<211> 363
<212> PRT
<213> Corynebacterium glutamicum

<400> 1334

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Leu Ala Leu Thr Ala Arg Gly Phe Leu Asn Ser Glu Arg Ser Gln Thr
  1               5                  10                  15

Arg Trp Lys Thr His Phe Thr Thr Gln Lys Val Pro Arg Ser Gly Tyr
             20                  25                  30

Arg Tyr Asp Leu Asp Gly Leu Arg Gly Ile Ala Ile Ala Phe Val Val
         35                  40                  45

Leu Phe His Val Phe Val Gly Lys Val Ser Gly Gly Val Asp Val Phe
     50                  55                  60

Leu Leu Leu Ser Gly Tyr Phe Phe Leu Gly Ser Gln Leu Arg Tyr Ala
 65                  70                  75                  80
```

```
Asp Arg Pro Asp Ser Ser Ile Asn Pro Trp Trp Pro Ile Trp Arg Thr
                85                  90                  95

Leu Arg Arg Leu Leu Pro Ala Leu Val Leu Val Leu Gly Val Ser Met
            100                 105                 110

Val Leu Ile Leu Ala Trp Val Pro Arg Leu Gln Pro Ile Glu Ile Ala
        115                 120                 125

Asn Gln Ala Val Ala Ser Leu Phe Tyr Val Gln Asn Trp Glu Leu Ala
    130                 135                 140

Ser Gln Gly Ala Ala Tyr Gly Ala Ala Ser Ala Glu Val Ser Pro Phe
145                 150                 155                 160

Gln His Leu Trp Ser Met Ala Val Gln Gly Gln Phe Tyr Leu Phe Ala
                165                 170                 175

Ile Leu Leu Ser Met Ala Ile Ile Leu Ile Arg Arg Tyr Arg Pro Glu
            180                 185                 190

Tyr Ser Ala Val Arg Leu Ala Thr Pro Val Leu Ala Val Leu Thr Ser
        195                 200                 205

Val Ser Phe Phe Ser Ala Ile Leu Trp His Phe Ile Asp Gln Ser Val
    210                 215                 220

Asn Tyr Tyr Ser Thr Phe Thr Arg Phe Trp Glu Leu Gly Leu Gly Ala
225                 230                 235                 240

Leu Leu Val Leu His Ala Pro Arg Ile Leu Ile Ser Ala Lys Thr Lys
                245                 250                 255

Ser Ile Leu Ala Ala Val Gly Leu Phe Met Val Leu Ser Thr Gly Phe
            260                 265                 270

Phe Met Asp Gly Ala Glu Thr Phe Pro Gly Phe Pro Ala Leu Tyr Pro
        275                 280                 285

Ile Leu Gly Ala Cys Leu Val Ile Leu Gly Asp Gly Lys Ile Ser Val
    290                 295                 300

Phe Leu Ser Arg Lys Trp Met Leu Trp Leu Gly Asp Ile Ala Tyr Pro
305                 310                 315                 320

Leu Tyr Leu Trp His Trp Pro Leu Leu Ile Ile Phe Thr Ala Leu Phe
                325                 330                 335

Asn Gln Glu Glu Pro Ser Ile Trp Leu Gly Ile Ala Val Ile Met Leu
            340                 345                 350

Ser Leu Gly Leu Ala Gln Leu Thr Asn Lys Tyr
        355                 360
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<210> 1335
<211> 694
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(694)
<223> FRXA02847

<400> 1335
ccagcctctt ctatgtccaa aaactgggag ctcgcatccc aagggtgctg cctacggagc 60

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agcctctgca gaagtcagtc ctttccagca cttgtggtcc atg gct gtg caa ggg   115
                                            Met Ala Val Gln Gly
                                              1               5

cag ttc tac ctc ttt gcc atc ttg ttg agc atg gcg atc atc ctg att   163
Gln Phe Tyr Leu Phe Ala Ile Leu Leu Ser Met Ala Ile Ile Leu Ile
                 10                  15                  20

cgt cga tac cgc ccc gaa tac tcc gca gtg cga cta gcg act cct gtg   211
Arg Arg Tyr Arg Pro Glu Tyr Ser Ala Val Arg Leu Ala Thr Pro Val
             25                  30                  35

ctg gca gtg ctc aca tcc gta tca ttt ttc agt gca atc ctg tgg cat   259
Leu Ala Val Leu Thr Ser Val Ser Phe Phe Ser Ala Ile Leu Trp His
         40                  45                  50

ttc att gat caa tca gtc aac tac tat tcc acc ttc acc agg ttc tgg   307
Phe Ile Asp Gln Ser Val Asn Tyr Tyr Ser Thr Phe Thr Arg Phe Trp
     55                  60                  65

gag ctc ggc ctt ggt gca cta ttg gtg ctg cat gcg cct cga att ttg   355
Glu Leu Gly Leu Gly Ala Leu Leu Val Leu His Ala Pro Arg Ile Leu
 70                  75                  80                  85

att tct gcg aag act aaa tca ata ctc gca gcc gtc ggt ttg ttt atg   403
Ile Ser Ala Lys Thr Lys Ser Ile Leu Ala Ala Val Gly Leu Phe Met
                 90                  95                 100

gtg cta tcc act gga ttc ttc atg gat ggc gca gag act ttc cct gga   451
Val Leu Ser Thr Gly Phe Phe Met Asp Gly Ala Glu Thr Phe Pro Gly
            105                 110                 115

ttc ccc gcg ctg tat ccc atc ttg ggt gct tgc tta gtc atc ctt ggc   499
Phe Pro Ala Leu Tyr Pro Ile Leu Gly Ala Cys Leu Val Ile Leu Gly
        120                 125                 130

gac ggt aaa atc tcg gtc ttt ctc tcc cga aaa tgg atg ctt tgg ctc   547
Asp Gly Lys Ile Ser Val Phe Leu Ser Arg Lys Trp Met Leu Trp Leu
    135                 140                 145

ggc gat atc gcc tac ccg ctc tac ttg tgg cac tgg cct ctg ctg atc   595
Gly Asp Ile Ala Tyr Pro Leu Tyr Leu Trp His Trp Pro Leu Leu Ile
150                 155                 160                 165

att ttc acc gct ttg ttc aac caa gaa gag cca tcc atc tgg ctg ggt   643
Ile Phe Thr Ala Leu Phe Asn Gln Glu Glu Pro Ser Ile Trp Leu Gly
                170                 175                 180

atc gcc gtg att atg ctg tcc ctt ggc ttg gcg cag ctg act aac aaa   691
Ile Ala Val Ile Met Leu Ser Leu Gly Leu Ala Gln Leu Thr Asn Lys
            185                 190                 195

tac                                                               694
Tyr
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<210> 1336
<211> 198
<212> PRT
<213> Corynebacterium glutamicum

<400> 1336
Met Ala Val Gln Gly Gln Phe Tyr Leu Phe Ala Ile Leu Leu Ser Met
1 5 10 15

Ala Ile Ile Leu Ile Arg Arg Tyr Arg Pro Glu Tyr Ser Ala Val Arg
20 25 30

Leu Ala Thr Pro Val Leu Ala Val Leu Thr Ser Val Ser Phe Phe Ser
35 40 45

Ala Ile Leu Trp His Phe Ile Asp Gln Ser Val Asn Tyr Tyr Ser Thr
50 55 60

Phe Thr Arg Phe Trp Glu Leu Gly Leu Gly Ala Leu Leu Val Leu His
65 70 75 80

Ala Pro Arg Ile Leu Ile Ser Ala Lys Thr Lys Ser Ile Leu Ala Ala
85 90 95

Val Gly Leu Phe Met Val Leu Ser Thr Gly Phe Phe Met Asp Gly Ala
100 105 110

Glu Thr Phe Pro Gly Phe Pro Ala Leu Tyr Pro Ile Leu Gly Ala Cys
115 120 125

Leu Val Ile Leu Gly Asp Gly Lys Ile Ser Val Phe Leu Ser Arg Lys
130 135 140

Trp Met Leu Trp Leu Gly Asp Ile Ala Tyr Pro Leu Tyr Leu Trp His
145 150 155 160

Trp Pro Leu Leu Ile Ile Phe Thr Ala Leu Phe Asn Gln Glu Glu Pro
165 170 175

Ser Ile Trp Leu Gly Ile Ala Val Ile Met Leu Ser Leu Gly Leu Ala
180 185 190

Gln Leu Thr Asn Lys Tyr
195

<210> 1337
<211> 305
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(282)
<223> RXN02849

<400> 1337
tcc cca tac ccc gtc atg atc agc acc tct gcc gac gcc tca aac gtg 48

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Ser Pro Tyr Pro Val Met Ile Ser Thr Ser Ala Asp Ala Ser Asn Val
  1               5                  10                  15

acc gtg cgc atc atg ggt gtg gac acc acc tcc gtg gaa tcc atc aac   96
Thr Val Arg Ile Met Gly Val Asp Thr Thr Ser Val Glu Ser Ile Asn
            20                  25                  30

aac gga cgt tgg tcc acc acc cag ccc aac aca gtt cga gta tcg ggt   144
Asn Gly Arg Trp Ser Thr Thr Gln Pro Asn Thr Val Arg Val Ser Gly
         35                  40                  45

tca gat tgt gtg cca tca acc ggt gca cca gga ttt acc acc tca gac   192
Ser Asp Cys Val Pro Ser Thr Gly Ala Pro Gly Phe Thr Thr Ser Asp
     50                  55                  60

acc cga atc atc agc gat ctt tct ggc aac gaa atc acc aga gaa acc   240
Thr Arg Ile Ile Ser Asp Leu Ser Gly Asn Glu Ile Thr Arg Glu Thr
 65                  70                  75                  80

gtc acc acg gtt tac gat cct tca cca aac gtg gtc tgc tcc           282
Val Thr Thr Val Tyr Asp Pro Ser Pro Asn Val Val Cys Ser
                85                  90

taaaacaaaa tgccccacca gat                                        305


<210> 1338
<211> 94
<212> PRT
<213> Corynebacterium glutamicum

<400> 1338
Ser Pro Tyr Pro Val Met Ile Ser Thr Ser Ala Asp Ala Ser Asn Val
  1               5                  10                  15

Thr Val Arg Ile Met Gly Val Asp Thr Thr Ser Val Glu Ser Ile Asn
            20                  25                  30

Asn Gly Arg Trp Ser Thr Thr Gln Pro Asn Thr Val Arg Val Ser Gly
         35                  40                  45

Ser Asp Cys Val Pro Ser Thr Gly Ala Pro Gly Phe Thr Thr Ser Asp
     50                  55                  60

Thr Arg Ile Ile Ser Asp Leu Ser Gly Asn Glu Ile Thr Arg Glu Thr
 65                  70                  75                  80

Val Thr Thr Val Tyr Asp Pro Ser Pro Asn Val Val Cys Ser
                85                  90


<210> 1339
<211> 305
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(282)
<223> FRXA02849
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<400> 1339
tcc cca tac ccc gtc atg atc agc acc tct gcc gac gcc tca aac gtg 48
Ser Pro Tyr Pro Val Met Ile Ser Thr Ser Ala Asp Ala Ser Asn Val
1 5 10 15

acc gtg cgc atc atg ggt gtg gac acc acc tcc gtg gaa tcc atc aac 96
Thr Val Arg Ile Met Gly Val Asp Thr Thr Ser Val Glu Ser Ile Asn
20 25 30

aac gga cgt tgg tcc acc acc cag ccc aac aca gtt cga gta tcg ggt 144
Asn Gly Arg Trp Ser Thr Thr Gln Pro Asn Thr Val Arg Val Ser Gly
35 40 45

tca gat tgt gtg cca tca acc ggt gca cca gga ttt acc acc tca gac 192
Ser Asp Cys Val Pro Ser Thr Gly Ala Pro Gly Phe Thr Thr Ser Asp
50 55 60

acc cga atc atc agc gat ctt tct ggc aac gaa atc acc aga gaa ccc 240
Thr Arg Ile Ile Ser Asp Leu Ser Gly Asn Glu Ile Thr Arg Glu Pro
65 70 75 80

gtc acc acg gtt tac gat cct tca cca aac gtg gtc tgc tcc 282
Val Thr Thr Val Tyr Asp Pro Ser Pro Asn Val Val Cys Ser
85 90

taaaacaaaa tgccccacca gat 305

<210> 1340
<211> 94
<212> PRT
<213> Corynebacterium glutamicum

<400> 1340
Ser Pro Tyr Pro Val Met Ile Ser Thr Ser Ala Asp Ala Ser Asn Val
1 5 10 15

Thr Val Arg Ile Met Gly Val Asp Thr Thr Ser Val Glu Ser Ile Asn
20 25 30

Asn Gly Arg Trp Ser Thr Thr Gln Pro Asn Thr Val Arg Val Ser Gly
35 40 45

Ser Asp Cys Val Pro Ser Thr Gly Ala Pro Gly Phe Thr Thr Ser Asp
50 55 60

Thr Arg Ile Ile Ser Asp Leu Ser Gly Asn Glu Ile Thr Arg Glu Pro
65 70 75 80

Val Thr Thr Val Tyr Asp Pro Ser Pro Asn Val Val Cys Ser
85 90

<210> 1341
<211> 582
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(559)

<223> RXN02911

<400> 1341
accgcataca ttaacgtgtt gatcattgcc ctagtatgcg cagtagcggc tgctctgatc 60

agcagttacc ttttccgcgg aaatccgaag ggagccaata atg cgc act agt aaa 115
Met Arg Thr Ser Lys
1 5

aaa gag atg att ctg cgc acg gcc atc gat tat atc ggc gag tac agc 163
Lys Glu Met Ile Leu Arg Thr Ala Ile Asp Tyr Ile Gly Glu Tyr Ser
10 15 20

ctc gag acg ctg agt tac gat tcg ctc gcc gag gcg acc ggt ctg tcc 211
Leu Glu Thr Leu Ser Tyr Asp Ser Leu Ala Glu Ala Thr Gly Leu Ser
25 30 35

aag tcg ggc ttg att tat cat ttc ccc agc cgc cat gcg ctg ctt tta 259
Lys Ser Gly Leu Ile Tyr His Phe Pro Ser Arg His Ala Leu Leu Leu
40 45 50

ggc atg cac gag ttg ctt gcc gac gac tgg gac aag gaa ttg cgc gac 307
Gly Met His Glu Leu Leu Ala Asp Asp Trp Asp Lys Glu Leu Arg Asp
55 60 65

ata acc cgc gac cca gag gat cca ctt gag cga ttg cgc gcc gtc gtg 355
Ile Thr Arg Asp Pro Glu Asp Pro Leu Glu Arg Leu Arg Ala Val Val
70 75 80 85

gtt acg ctt gct gaa aac gtt tcg cgc ccc gag ctg gtt ttg ctt atg 403
Val Thr Leu Ala Glu Asn Val Ser Arg Pro Glu Leu Val Leu Leu Met
90 95 100

gac gcc ccc tcc cac ccg gga ttt ctt aac gcc tgg cgc act gta aat 451
Asp Ala Pro Ser His Pro Gly Phe Leu Asn Ala Trp Arg Thr Val Asn
105 110 115

cat caa tgg atc ccc gac acc gat gat ctg gaa aac gat gcc cac aaa 499
His Gln Trp Ile Pro Asp Thr Asp Asp Leu Glu Asn Asp Ala His Lys
120 125 130

cgc gcc gtc tac tct ggt gca gct cgc agc cga tgg cct ctt cgt gca 547
Arg Ala Val Tyr Ser Gly Ala Ala Arg Ser Arg Trp Pro Leu Arg Ala
135 140 145

cga tta cat tca tgatgatgtc ctcagcaagt cca 582
Arg Leu His Ser
150

<210> 1342
<211> 153
<212> PRT
<213> Corynebacterium glutamicum

<400> 1342
Met Arg Thr Ser Lys Lys Glu Met Ile Leu Arg Thr Ala Ile Asp Tyr
1 5 10 15

Ile Gly Glu Tyr Ser Leu Glu Thr Leu Ser Tyr Asp Ser Leu Ala Glu
20 25 30

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Ala Thr Gly Leu Ser Lys Ser Gly Leu Ile Tyr His Phe Pro Ser Arg
         35                  40                  45

His Ala Leu Leu Leu Gly Met His Glu Leu Leu Ala Asp Asp Trp Asp
     50                  55                  60

Lys Glu Leu Arg Asp Ile Thr Arg Asp Pro Glu Asp Pro Leu Glu Arg
 65                  70                  75                  80

Leu Arg Ala Val Val Val Thr Leu Ala Glu Asn Val Ser Arg Pro Glu
                 85                  90                  95

Leu Val Leu Leu Met Asp Ala Pro Ser His Pro Gly Phe Leu Asn Ala
            100                 105                 110

Trp Arg Thr Val Asn His Gln Trp Ile Pro Asp Thr Asp Asp Leu Glu
        115                 120                 125

Asn Asp Ala His Lys Arg Ala Val Tyr Ser Gly Ala Ala Arg Ser Arg
    130                 135                 140

Trp Pro Leu Arg Ala Arg Leu His Ser
145                 150


<210> 1343
<211> 666
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(643)
<223> RXN02914

<400> 1343
tgtggatcgc agcaattgca tcccctgggc cagacctttt cagatcatca ggctaagtgc 60

caaaaaccgc cgtgatggcg tactgactgc cgtaggcatc atg gtg gga aac tcc   115
                                            Met Val Gly Asn Ser
                                              1               5

atc tgg atc ata gcc agc ctc ctt ggg ctc tcg gca ctg atc tcc acg   163
Ile Trp Ile Ile Ala Ser Leu Leu Gly Leu Ser Ala Leu Ile Ser Thr
                 10                  15                  20

tat cca gca att ttg aac ctg ttg cag ctc gtc ggt ggc ggt tat ttg   211
Tyr Pro Ala Ile Leu Asn Leu Leu Gln Leu Val Gly Gly Gly Tyr Leu
             25                  30                  35

acc tgg atg ggc atc ggg gcg gtg agg tca tgg tgg acg aaa cgc tcc   259
Thr Trp Met Gly Ile Gly Ala Val Arg Ser Trp Trp Thr Lys Arg Ser
         40                  45                  50

aca cag caa gct gca gcg gat tct caa gct gta gag aat acg ttg gtg   307
Thr Gln Gln Ala Ala Ala Asp Ser Gln Ala Val Glu Asn Thr Leu Val
     55                  60                  65

aca gcc acg gct gca tct gtc gga gtg tgg cca gct att cga tct ggc   355
Thr Ala Thr Ala Ala Ser Val Gly Val Trp Pro Ala Ile Arg Ser Gly
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```
 70                  75                  80                  85

att gct acc aac ttg tcc aac ccc aaa gct gtg ctg ttt ttt ggt tcc   403
Ile Ala Thr Asn Leu Ser Asn Pro Lys Ala Val Leu Phe Phe Gly Ser
                90                  95                 100

gtt ttc gcc caa ttt gtt aga cct gac atg gga atc ggg tgg agt att   451
Val Phe Ala Gln Phe Val Arg Pro Asp Met Gly Ile Gly Trp Ser Ile
            105                 110                 115

ttc att gga gtc ttc ctc acc ctc act ggc ctg ctg tgg ttt gtg ggg   499
Phe Ile Gly Val Phe Leu Thr Leu Thr Gly Leu Leu Trp Phe Val Gly
        120                 125                 130

ttc gcc gtc ttg gtc cgc aaa cta gcc gct ggc ctc acc cga aat gga   547
Phe Ala Val Leu Val Arg Lys Leu Ala Ala Gly Leu Thr Arg Asn Gly
    135                 140                 145

gcc atc atc gac ctg cta acg ggg gtg att ttc atc ggg ctg gga atg   595
Ala Ile Ile Asp Leu Leu Thr Gly Val Ile Phe Ile Gly Leu Gly Met
150                 155                 160                 165

ttc atg atc ttc gag ggg gtt gta gga atc ggt ggc agg gta gtg ggt   643
Phe Met Ile Phe Glu Gly Val Val Gly Ile Gly Gly Arg Val Val Gly
                170                 175                 180

tagccccgcc cccaggacgt cac                                        666


<210> 1344
<211> 181
<212> PRT
<213> Corynebacterium glutamicum

<400> 1344
Met Val Gly Asn Ser Ile Trp Ile Ile Ala Ser Leu Leu Gly Leu Ser
  1               5                  10                  15

Ala Leu Ile Ser Thr Tyr Pro Ala Ile Leu Asn Leu Leu Gln Leu Val
             20                  25                  30

Gly Gly Gly Tyr Leu Thr Trp Met Gly Ile Gly Ala Val Arg Ser Trp
         35                  40                  45

Trp Thr Lys Arg Ser Thr Gln Gln Ala Ala Ala Asp Ser Gln Ala Val
     50                  55                  60

Glu Asn Thr Leu Val Thr Ala Thr Ala Ala Ser Val Gly Val Trp Pro
 65                  70                  75                  80

Ala Ile Arg Ser Gly Ile Ala Thr Asn Leu Ser Asn Pro Lys Ala Val
                85                  90                  95

Leu Phe Phe Gly Ser Val Phe Ala Gln Phe Val Arg Pro Asp Met Gly
            100                 105                 110

Ile Gly Trp Ser Ile Phe Ile Gly Val Phe Leu Thr Leu Thr Gly Leu
        115                 120                 125

Leu Trp Phe Val Gly Phe Ala Val Leu Val Arg Lys Leu Ala Ala Gly
    130                 135                 140
```

```
Leu Thr Arg Asn Gly Ala Ile Ile Asp Leu Leu Thr Gly Val Ile Phe
145                 150                 155                 160

Ile Gly Leu Gly Met Phe Met Ile Phe Glu Gly Val Val Gly Ile Gly
                165                 170                 175

Gly Arg Val Val Gly
            180


<210> 1345
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(571)
<223> RXN02921

<400> 1345
tggaaaactg ggaagggttg acgttgcgga atctctccgc agcgtcggtt cggaccctaa 60

aaaagggtga ggaaccacat gagctgtttt aaggaatttt gtg tct gca ctt gaa   115
                                              Val Ser Ala Leu Glu
                                                1               5

gag tcg atc cgc atc gcg acc atc gcg gcg aaa gca gcg gat gaa aag   163
Glu Ser Ile Arg Ile Ala Thr Ile Ala Ala Lys Ala Ala Asp Glu Lys
                10                  15                  20

aag gcc gat gac atc gct gtc atc gat gtc tct gac atg atc gca atc   211
Lys Ala Asp Asp Ile Ala Val Ile Asp Val Ser Asp Met Ile Ala Ile
            25                  30                  35

acc gat tgc ttt gtt gtt gca tct gct gac aat gag cgc cag gtg ggc   259
Thr Asp Cys Phe Val Val Ala Ser Ala Asp Asn Glu Arg Gln Val Gly
        40                  45                  50

gcc att gtt gag gag atc gaa gat gag atg acc aag gct ggt ttc gag   307
Ala Ile Val Glu Glu Ile Glu Asp Glu Met Thr Lys Ala Gly Phe Glu
    55                  60                  65

cct aag cgc cgt gaa ggc aac cgc gaa aac cgt tgg gtt ctc ctt gac   355
Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg Trp Val Leu Leu Asp
70                  75                  80                  85

tac gga ttg gtt gtt atc cac gtt cag cga cag gca gag cgc gag ttc   403
Tyr Gly Leu Val Val Ile His Val Gln Arg Gln Ala Glu Arg Glu Phe
                90                  95                  100

tac gga ctg gat cgt ctg tac cgc gac tgc cca ctc att gaa att gaa   451
Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro Leu Ile Glu Ile Glu
            105                 110                 115

gga ctt gaa acc ttc aag cgt gaa tcc tcc tgg tct gat gag gcg gat   499
Gly Leu Glu Thr Phe Lys Arg Glu Ser Ser Trp Ser Asp Glu Ala Asp
        120                 125                 130

atc cgc aac atc gac agc att gat gaa ctc cca cct ttg cca gct gaa   547
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```
Ile Arg Asn Ile Asp Ser Ile Asp Glu Leu Pro Pro Leu Pro Ala Glu
    135                 140                 145

tac gag cct ggc tac gag gac gat taagaggtag tcctgtgact cgt        594
Tyr Glu Pro Gly Tyr Glu Asp Asp
150                 155


<210> 1346
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 1346
Val Ser Ala Leu Glu Glu Ser Ile Arg Ile Ala Thr Ile Ala Ala Lys
  1               5                  10                  15

Ala Ala Asp Glu Lys Lys Ala Asp Asp Ile Ala Val Ile Asp Val Ser
             20                  25                  30

Asp Met Ile Ala Ile Thr Asp Cys Phe Val Val Ala Ser Ala Asp Asn
         35                  40                  45

Glu Arg Gln Val Gly Ala Ile Val Glu Glu Ile Glu Asp Glu Met Thr
     50                  55                  60

Lys Ala Gly Phe Glu Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg
 65                  70                  75                  80

Trp Val Leu Leu Asp Tyr Gly Leu Val Val Ile His Val Gln Arg Gln
                 85                  90                  95

Ala Glu Arg Glu Phe Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro
            100                 105                 110

Leu Ile Glu Ile Glu Gly Leu Glu Thr Phe Lys Arg Glu Ser Ser Trp
        115                 120                 125

Ser Asp Glu Ala Asp Ile Arg Asn Ile Asp Ser Ile Asp Glu Leu Pro
    130                 135                 140

Pro Leu Pro Ala Glu Tyr Glu Pro Gly Tyr Glu Asp Asp
145                 150                 155


<210> 1347
<211> 672
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(649)
<223> RXN02924

<400> 1347
ctaggcaggt gtgcgatcaa accacactgt cagaatcaaa tctgctggac gctatgccag 60

cggattgttg atcacgaaaa agcatgtcac agacaccttt gtg cct tct gta gca   115
                                              Val Pro Ser Val Ala
                                                1               5
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tcc atc tca gag cgc gcc acg ttt att ctc acc gcc gat cac ttt ttg   163
Ser Ile Ser Glu Arg Ala Thr Phe Ile Leu Thr Ala Asp His Phe Leu
                10                  15                  20

cgc agc tgc tcg aaa gta att tat gtc cgg ggc gaa aat ttc acc gcc   211
Arg Ser Cys Ser Lys Val Ile Tyr Val Arg Gly Glu Asn Phe Thr Ala
            25                  30                  35

aca gca acc acc agc ctg tct gta ttt ggc aca gat ctg ggt ttg atc   259
Thr Ala Thr Thr Ser Leu Ser Val Phe Gly Thr Asp Leu Gly Leu Ile
        40                  45                  50

aaa tta gac ggc aaa gcc ccc acc atg cca ctt cca ctt ttc gca gat   307
Lys Leu Asp Gly Lys Ala Pro Thr Met Pro Leu Pro Leu Phe Ala Asp
    55                  60                  65

aag cca ctt cgc gtg ggc atg aaa acc acc acg ttc gga ttc ggc ggt   355
Lys Pro Leu Arg Val Gly Met Lys Thr Thr Thr Phe Gly Phe Gly Gly
70                  75                  80                  85

ctg cca tca gcc acc gtt gct aaa gaa atc cac ggg cgc gtt atc tct   403
Leu Pro Ser Ala Thr Val Ala Lys Glu Ile His Gly Arg Val Ile Ser
                90                  95                  100

gcc atc ccc cat ggc gta tca aga aac cgc atc acc cga gtc cat cac   451
Ala Ile Pro His Gly Val Ser Arg Asn Arg Ile Thr Arg Val His His
            105                 110                 115

ggt gcc ttg atc ttt aac tcc cca gaa aag gca gta aag gga gac tcc   499
Gly Ala Leu Ile Phe Asn Ser Pro Glu Lys Ala Val Lys Gly Asp Ser
        120                 125                 130

ggc gga cct gtg ctg gtt aat gga cga gta gcc gga atc caa tca atg   547
Gly Gly Pro Val Leu Val Asn Gly Arg Val Ala Gly Ile Gln Ser Met
    135                 140                 145

atc tct gac ccc ggt gga ttt aac acc ggg gtc gcc act gcc gca tcc   595
Ile Ser Asp Pro Gly Gly Phe Asn Thr Gly Val Ala Thr Ala Ala Ser
150                 155                 160                 165

ctt atc cag cac atg cct gcc cta gct caa gcg ctt gaa ctg ctc gaa   643
Leu Ile Gln His Met Pro Ala Leu Ala Gln Ala Leu Glu Leu Leu Glu
                170                 175                 180

cat agc tagctcgcta ggaaccgatc gcc                                672
His Ser
```

Sequence Listing

<210> 1348
<211> 183
<212> PRT
<213> Corynebacterium glutamicum

<400> 1348

```
Val Pro Ser Val Ala Ser Ile Ser Glu Arg Ala Thr Phe Ile Leu Thr
  1               5                  10                  15

Ala Asp His Phe Leu Arg Ser Cys Ser Lys Val Ile Tyr Val Arg Gly
            20                  25                  30
```

```
Glu Asn Phe Thr Ala Thr Ala Thr Thr Ser Leu Ser Val Phe Gly Thr
         35                  40                  45

Asp Leu Gly Leu Ile Lys Leu Asp Gly Lys Ala Pro Thr Met Pro Leu
     50                  55                  60

Pro Leu Phe Ala Asp Lys Pro Leu Arg Val Gly Met Lys Thr Thr Thr
 65                  70                  75                  80

Phe Gly Phe Gly Gly Leu Pro Ser Ala Thr Val Ala Lys Glu Ile His
                 85                  90                  95

Gly Arg Val Ile Ser Ala Ile Pro His Gly Val Ser Arg Asn Arg Ile
            100                 105                 110

Thr Arg Val His His Gly Ala Leu Ile Phe Asn Ser Pro Glu Lys Ala
        115                 120                 125

Val Lys Gly Asp Ser Gly Gly Pro Val Leu Val Asn Gly Arg Val Ala
    130                 135                 140

Gly Ile Gln Ser Met Ile Ser Asp Pro Gly Gly Phe Asn Thr Gly Val
145                 150                 155                 160

Ala Thr Ala Ala Ser Leu Ile Gln His Met Pro Ala Leu Ala Gln Ala
                165                 170                 175

Leu Glu Leu Leu Glu His Ser
            180


<210> 1349
<211> 591
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(568)
<223> RXN02927

<400> 1349
tccgcagttg ggcctgcttg acgccagatc tcaagtgtaa gtttcattac ttgtagttcc 60

ttgtctgcag tgggacagat tcgaagaaca gtggttctgc gtg gca gac gaa ggt   115
                                            Val Ala Asp Glu Gly
                                              1               5

tcc att ctc gcc tgg ttc cca tgc gga gac gaa gca cca gtt ttg gtc   163
Ser Ile Leu Ala Trp Phe Pro Cys Gly Asp Glu Ala Pro Val Leu Val
                10                  15                  20

gtc acg ttg tgc ttc gcc atc ttc gga gag gtg gtc gtc gcg gaa gtg   211
Val Thr Leu Cys Phe Ala Ile Phe Gly Glu Val Val Val Ala Glu Val
            25                  30                  35

agc gcc aca gga ctc gtc gcg gtc gag ggc gtc gac aca cat gag ttc   259
Ser Ala Thr Gly Leu Val Ala Val Glu Gly Val Asp Thr His Glu Phe
        40                  45                  50
```

```
gcc gag gtc gat gta gtc ggc tac gcg tgc tgc gta ttc gag aac ctg   307
Ala Glu Val Asp Val Val Gly Tyr Ala Cys Cys Val Phe Glu Asn Leu
     55                  60                  65

gtt cat ctc atc ggt gct gcc ggt gat gcg cat gtt ctt cca gaa gtc   355
Val His Leu Ile Gly Ala Ala Gly Asp Ala His Val Leu Pro Glu Val
 70                  75                  80                  85

atc gcg gag ggc acg gat ctt gtt gat gcc atc ctg gag gtc ttc tac   403
Ile Ala Glu Gly Thr Asp Leu Val Asp Ala Ile Leu Glu Val Phe Tyr
                90                  95                 100

gtt tcg gga aac gcc aca gga gaa gta cag gat atc gcc aag ctg gcg   451
Val Ser Gly Asn Ala Thr Gly Glu Val Gln Asp Ile Ala Lys Leu Ala
            105                 110                 115

gtg gta gta ctc agg tcc gtg aac gtt gtc acc gac cca ctc tgg gcg   499
Val Val Val Leu Arg Ser Val Asn Val Val Thr Asp Pro Leu Trp Ala
        120                 125                 130

gtt gcc cat gag gcg gtc aat gcg agc ctg tgc acg cgc aat cgc tgc   547
Val Ala His Glu Ala Val Asn Ala Ser Leu Cys Thr Arg Asn Arg Cys
    135                 140                 145

ctg tgc ttc tgg tgc atc ctc tgacagacgc tcggagccaa gca            591
Leu Cys Phe Trp Cys Ile Leu
150                 155
```

<210> 1350
<211> 156
<212> PRT
<213> Corynebacterium glutamicum

<400> 1350

```
Val Ala Asp Glu Gly Ser Ile Leu Ala Trp Phe Pro Cys Gly Asp Glu
  1               5                  10                  15

Ala Pro Val Leu Val Val Thr Leu Cys Phe Ala Ile Phe Gly Glu Val
             20                  25                  30

Val Val Ala Glu Val Ser Ala Thr Gly Leu Val Ala Val Glu Gly Val
         35                  40                  45

Asp Thr His Glu Phe Ala Glu Val Asp Val Val Gly Tyr Ala Cys Cys
     50                  55                  60

Val Phe Glu Asn Leu Val His Leu Ile Gly Ala Ala Gly Asp Ala His
 65                  70                  75                  80

Val Leu Pro Glu Val Ile Ala Glu Gly Thr Asp Leu Val Asp Ala Ile
                 85                  90                  95

Leu Glu Val Phe Tyr Val Ser Gly Asn Ala Thr Gly Glu Val Gln Asp
            100                 105                 110

Ile Ala Lys Leu Ala Val Val Val Leu Arg Ser Val Asn Val Val Thr
        115                 120                 125

Asp Pro Leu Trp Ala Val Ala His Glu Ala Val Asn Ala Ser Leu Cys
    130                 135                 140
```

```
Thr Arg Asn Arg Cys Leu Cys Phe Trp Cys Ile Leu
145                 150                 155


<210> 1351
<211> 816
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(793)
<223> RXN02928

<400> 1351
ggtttgcacc gtggtaggtc caggatgctt cgcctgcgca gaacagacct gggagtgacg 60

tcatttcgtt gaagtcagtc cagaggccac ccatggtgaa gtg gca ggt cgg tgc   115
                                              Val Ala Gly Arg Cys
                                                1               5

aat acg cat tgg gct gga gta tgg gtc ctc gcc aat tgc ctc ttc gta   163
Asn Thr His Trp Ala Gly Val Trp Val Leu Ala Asn Cys Leu Phe Val
                10                  15                  20

cat ggt gaa gag gtt gga gta acg ctc gcg gat ggt gtc ctg tcc gag   211
His Gly Glu Glu Val Gly Val Thr Leu Ala Asp Gly Val Leu Ser Glu
            25                  30                  35

gcg ctc ggt ggc gtc gcg gaa gtc cag gta tgc agc gtt gtt cag agg   259
Ala Leu Gly Gly Val Ala Glu Val Gln Val Cys Ser Val Val Gln Arg
        40                  45                  50

tcc aac acc gag acc agc att gat ctg ctg gga gat cgc acg gga agc   307
Ser Asn Thr Glu Thr Ser Ile Asp Leu Leu Gly Asp Arg Thr Gly Ser
    55                  60                  65

aac gtc acg tgg gac gag gtt acc gaa tgc tgg gta gcg gcg ctc cag   355
Asn Val Thr Trp Asp Glu Val Thr Glu Cys Trp Val Ala Ala Leu Gln
70                  75                  80                  85

gaa gta gtc gcg ctc atc ctc agg gat ggt gtt tgg atc gcg gtt atc   403
Glu Val Val Ala Leu Ile Leu Arg Asp Gly Val Trp Ile Ala Val Ile
                90                  95                  100

gtt cgg ttc ctt agg gga cca gat gcg gcc gtc gtt acg cag cga ctc   451
Val Arg Phe Leu Arg Gly Pro Asp Ala Ala Val Val Thr Gln Arg Leu
            105                 110                 115

gga cat cag aat ggt ctt gga ctg cca ggt gga gtt cac agg cag gcc   499
Gly His Gln Asn Gly Leu Gly Leu Pro Gly Gly Val His Arg Gln Ala
        120                 125                 130

ggt tgg gtg gaa ctg gat gaa cga tgg gga cgc gaa gta tgc gcc ggc   547
Gly Trp Val Glu Leu Asp Glu Arg Trp Gly Arg Glu Val Cys Ala Gly
    135                 140                 145

ttc gta tgc acg cat gat ggc cga ggc gtt gga gtt ctt ggc cag ggt   595
Phe Val Cys Thr His Asp Gly Arg Gly Val Gly Val Leu Gly Gln Gly
150                 155                 160                 165
```

```
gga cat gtg gta cac gtt gcc gta gcc acc ggt tgc cag gat aac ggc   643
Gly His Val Val His Val Ala Val Ala Thr Gly Cys Gln Asp Asn Gly
               170                 175                 180

atg gcc ggt gtg tgc ggt gag ctc gcc ggt gat cag gtt gcg cat gat   691
Met Ala Gly Val Cys Gly Glu Leu Ala Gly Asp Gln Val Ala His Asp
           185                 190                 195

cag gcc ttc gca gcg ctt ttc acc gtt acg ttc ggt gac aat gac gtc   739
Gln Ala Phe Ala Ala Leu Phe Thr Val Thr Phe Gly Asp Asn Asp Val
       200                 205                 210

aac cat ttc gtt atg ggt gaa gat ttc tac gga gcc gag gtg gat ctg   787
Asn His Phe Val Met Gly Glu Asp Phe Tyr Gly Ala Glu Val Asp Leu
   215                 220                 225

gcg ctg tagtgcggat gcggtggaga act                                816
Ala Leu
230
```

<210> 1352
<211> 231
<212> PRT
<213> Corynebacterium glutamicum

<400> 1352

```
Val Ala Gly Arg Cys Asn Thr His Trp Ala Gly Val Trp Val Leu Ala
  1               5                  10                  15

Asn Cys Leu Phe Val His Gly Glu Glu Val Gly Val Thr Leu Ala Asp
             20                  25                  30

Gly Val Leu Ser Glu Ala Leu Gly Gly Val Ala Glu Val Gln Val Cys
         35                  40                  45

Ser Val Val Gln Arg Ser Asn Thr Glu Thr Ser Ile Asp Leu Leu Gly
     50                  55                  60

Asp Arg Thr Gly Ser Asn Val Thr Trp Asp Glu Val Thr Glu Cys Trp
 65                  70                  75                  80

Val Ala Ala Leu Gln Glu Val Val Ala Leu Ile Leu Arg Asp Gly Val
                 85                  90                  95

Trp Ile Ala Val Ile Val Arg Phe Leu Arg Gly Pro Asp Ala Ala Val
            100                 105                 110

Val Thr Gln Arg Leu Gly His Gln Asn Gly Leu Gly Leu Pro Gly Gly
        115                 120                 125

Val His Arg Gln Ala Gly Trp Val Glu Leu Asp Glu Arg Trp Gly Arg
    130                 135                 140

Glu Val Cys Ala Gly Phe Val Cys Thr His Asp Gly Arg Gly Val Gly
145                 150                 155                 160

Val Leu Gly Gln Gly Gly His Val Val His Val Ala Val Ala Thr Gly
                165                 170                 175
```

```
Cys Gln Asp Asn Gly Met Ala Gly Val Cys Gly Glu Leu Ala Gly Asp
            180                 185                 190

Gln Val Ala His Asp Gln Ala Phe Ala Ala Leu Phe Thr Val Thr Phe
        195                 200                 205

Gly Asp Asn Asp Val Asn His Phe Val Met Gly Glu Asp Phe Tyr Gly
    210                 215                 220

Ala Glu Val Asp Leu Ala Leu
225                 230
```

<210> 1353
<211> 348
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(325)
<223> RXN02931

<400> 1353

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gatgggtgca gaaattgaat tgaaagaatc cgggcacatg tgggtggaat ccccgagtga 60

ctagtgcggt gtaagagcac tagactgttc aactatgagc atg caa cca tac ccc   115
                                            Met Gln Pro Tyr Pro
                                              1               5

cgc aac cca atc gaa aaa cgt aag caa gaa gta cgc aag aac tcc cgc   163
Arg Asn Pro Ile Glu Lys Arg Lys Gln Glu Val Arg Lys Asn Ser Arg
                 10                  15                  20

aac gca gtt gtc agt gtt ggc ggt ggc atc gta ggc ggt gcg gct ctg   211
Asn Ala Val Val Ser Val Gly Gly Gly Ile Val Gly Gly Ala Ala Leu
             25                  30                  35

tgg cta gtg ttc ggc tct gca ttc ttt atg gga ctt gga ttg atc atc   259
Trp Leu Val Phe Gly Ser Ala Phe Phe Met Gly Leu Gly Leu Ile Ile
         40                  45                  50

gcc gtg gtc ggc ggt ttt tat tac tac aac aag gtc caa aag atc att   307
Ala Val Val Gly Gly Phe Tyr Tyr Tyr Asn Lys Val Gln Lys Ile Ile
     55                  60                  65

aac gaa aaa gac cgt tac tagttagaaa tctatgtcag aca                 348
Asn Glu Lys Asp Arg Tyr
 70                  75
```

<210> 1354
<211> 75
<212> PRT
<213> Corynebacterium glutamicum

<400> 1354

```
Met Gln Pro Tyr Pro Arg Asn Pro Ile Glu Lys Arg Lys Gln Glu Val
  1               5                  10                  15

Arg Lys Asn Ser Arg Asn Ala Val Val Ser Val Gly Gly Gly Ile Val
```

```
            20                  25                  30

Gly Gly Ala Ala Leu Trp Leu Val Phe Gly Ser Ala Phe Phe Met Gly
         35                  40                  45

Leu Gly Leu Ile Ile Ala Val Val Gly Gly Phe Tyr Tyr Tyr Asn Lys
     50                  55                  60

Val Gln Lys Ile Ile Asn Glu Lys Asp Arg Tyr
 65                  70                  75


<210> 1355
<211> 1095
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1072)
<223> RXN02932

<400> 1355
cactactgcg ttaaggtatg aaagttcgca caccagcgat ttaattctgt gcccaccact 60

agcacgacca tttcagtttt aactttcttg gagttttcta gtg tcc aaa aca gaa   115
                                            Val Ser Lys Thr Glu
                                              1               5

gaa ggc cgt tca gcg gcc ata att att tac gcg ttt cca act ttc att   163
Glu Gly Arg Ser Ala Ala Ile Ile Ile Tyr Ala Phe Pro Thr Phe Ile
                10                  15                  20

ctg ctg ggc gcg atc att gcg ttt atc ttc ccg gaa cca ttc att ccg   211
Leu Leu Gly Ala Ile Ile Ala Phe Ile Phe Pro Glu Pro Phe Ile Pro
            25                  30                  35

ctg aca aac tac att aat atc ttc ctc acg atc atc atg ttc acc atg   259
Leu Thr Asn Tyr Ile Asn Ile Phe Leu Thr Ile Ile Met Phe Thr Met
         40                  45                  50

ggt ttg acc ttg acg gtg ccc gat ttt cag atg gtg ctt aaa cgt cca   307
Gly Leu Thr Leu Thr Val Pro Asp Phe Gln Met Val Leu Lys Arg Pro
     55                  60                  65

ctg cct atc ttg atc ggt gta gta gcg cag ttt gtc atc atg cca ttc   355
Leu Pro Ile Leu Ile Gly Val Val Ala Gln Phe Val Ile Met Pro Phe
 70                  75                  80                  85

ctg gcg atc gtg gtt gcg aaa atg ttc aac ctc aac cca gca ctc gcc   403
Leu Ala Ile Val Val Ala Lys Met Phe Asn Leu Asn Pro Ala Leu Ala
                90                  95                 100

gtt ggc ctt ctc atg ctg gga tcc gtt ccg ggt ggc acc tcc tcc aat   451
Val Gly Leu Leu Met Leu Gly Ser Val Pro Gly Gly Thr Ser Ser Asn
            105                 110                 115

gtg att gcg ttt ctc gcc cga gga gat gtc gcg cta tcg gtc acc atg   499
Val Ile Ala Phe Leu Ala Arg Gly Asp Val Ala Leu Ser Val Thr Met
        120                 125                 130
```

```
acc tct gtg tcc acc att gtt tcc cca atc atg acg cct ttc ctc atg   547
Thr Ser Val Ser Thr Ile Val Ser Pro Ile Met Thr Pro Phe Leu Met
    135                 140                 145

ctc atg ctg gca ggt act gaa acc gcc gtc gat ggt gga ggc atg gcg   595
Leu Met Leu Ala Gly Thr Glu Thr Ala Val Asp Gly Gly Gly Met Ala
150                 155                 160                 165

tgg act ttg gta caa aca gtg ctg ctg cct gtg atc atc ggc cta gtt   643
Trp Thr Leu Val Gln Thr Val Leu Leu Pro Val Ile Ile Gly Leu Val
                170                 175                 180

ctg cgt gtc ttc ttg aac aag tgg atc gac aag att ttg ccg atc ctt   691
Leu Arg Val Phe Leu Asn Lys Trp Ile Asp Lys Ile Leu Pro Ile Leu
            185                 190                 195

cct tat ctc tcc atc ctc ggt atc ggt ggc gtg gtg ttc ggc gca gtc   739
Pro Tyr Leu Ser Ile Leu Gly Ile Gly Gly Val Val Phe Gly Ala Val
        200                 205                 210

gca gcc aac gcg gaa cga ctc gtg tct gtc gga ctc atc gtg ttc gtt   787
Ala Ala Asn Ala Glu Arg Leu Val Ser Val Gly Leu Ile Val Phe Val
    215                 220                 225

gca gtt atc gtg cac aac gta ctt gga tac gtt gtg gga tac ctc acc   835
Ala Val Ile Val His Asn Val Leu Gly Tyr Val Val Gly Tyr Leu Thr
230                 235                 240                 245

ggc cgt gta ttc aaa ttc cca gaa gca gca aac cgc acc atg gcg att   883
Gly Arg Val Phe Lys Phe Pro Glu Ala Ala Asn Arg Thr Met Ala Ile
                250                 255                 260

gaa atc gga acc caa tcc gca ggc ctc gca tcg gga atg gca gga cga   931
Glu Ile Gly Thr Gln Ser Ala Gly Leu Ala Ser Gly Met Ala Gly Arg
            265                 270                 275

ttc ttc acc cca gaa gca gcc ctt cca ggt gct gtc gct gcc ttg gtc   979
Phe Phe Thr Pro Glu Ala Ala Leu Pro Gly Ala Val Ala Ala Leu Val
        280                 285                 290

cac aac atc acc ggc gca gtt tat gtt ggg ctg gta cga aac agg cct   1027
His Asn Ile Thr Gly Ala Val Tyr Val Gly Leu Val Arg Asn Arg Pro
    295                 300                 305

ttg act aag gca tca agg aag aag gaa tcc gtc gcg gtt tcc agc       1072
Leu Thr Lys Ala Ser Arg Lys Lys Glu Ser Val Ala Val Ser Ser
310                 315                 320

taacttattt gctgcccgtt aga                                        1095


<210> 1356
<211> 324
<212> PRT
<213> Corynebacterium glutamicum

<400> 1356
Val Ser Lys Thr Glu Glu Gly Arg Ser Ala Ala Ile Ile Ile Tyr Ala
  1               5                  10                  15

Phe Pro Thr Phe Ile Leu Leu Gly Ala Ile Ile Ala Phe Ile Phe Pro
```

```
            20                  25                  30

Glu Pro Phe Ile Pro Leu Thr Asn Tyr Ile Asn Ile Phe Leu Thr Ile
         35                  40                  45

Ile Met Phe Thr Met Gly Leu Thr Leu Thr Val Pro Asp Phe Gln Met
     50                  55                  60

Val Leu Lys Arg Pro Leu Pro Ile Leu Ile Gly Val Val Ala Gln Phe
 65                  70                  75                  80

Val Ile Met Pro Phe Leu Ala Ile Val Val Ala Lys Met Phe Asn Leu
                85                  90                  95

Asn Pro Ala Leu Ala Val Gly Leu Leu Met Leu Gly Ser Val Pro Gly
            100                 105                 110

Gly Thr Ser Ser Asn Val Ile Ala Phe Leu Ala Arg Gly Asp Val Ala
        115                 120                 125

Leu Ser Val Thr Met Thr Ser Val Ser Thr Ile Val Ser Pro Ile Met
    130                 135                 140

Thr Pro Phe Leu Met Leu Met Leu Ala Gly Thr Glu Thr Ala Val Asp
145                 150                 155                 160

Gly Gly Gly Met Ala Trp Thr Leu Val Gln Thr Val Leu Leu Pro Val
                165                 170                 175

Ile Ile Gly Leu Val Leu Arg Val Phe Leu Asn Lys Trp Ile Asp Lys
            180                 185                 190

Ile Leu Pro Ile Leu Pro Tyr Leu Ser Ile Leu Gly Ile Gly Gly Val
        195                 200                 205

Val Phe Gly Ala Val Ala Ala Asn Ala Glu Arg Leu Val Ser Val Gly
    210                 215                 220

Leu Ile Val Phe Val Ala Val Ile Val His Asn Val Leu Gly Tyr Val
225                 230                 235                 240

Val Gly Tyr Leu Thr Gly Arg Val Phe Lys Phe Pro Glu Ala Ala Asn
                245                 250                 255

Arg Thr Met Ala Ile Glu Ile Gly Thr Gln Ser Ala Gly Leu Ala Ser
            260                 265                 270

Gly Met Ala Gly Arg Phe Phe Thr Pro Glu Ala Ala Leu Pro Gly Ala
        275                 280                 285

Val Ala Ala Leu Val His Asn Ile Thr Gly Ala Val Tyr Val Gly Leu
    290                 295                 300

Val Arg Asn Arg Pro Leu Thr Lys Ala Ser Arg Lys Lys Glu Ser Val
305                 310                 315                 320

Ala Val Ser Ser
```

<210> 1357

<211> 429
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(406)
<223> RXN02934

<400> 1357
tggatgggcc ggtggcggtg accatggtag atgcggattc aagctgccag gcgcgctcat 60

tgagtggctg gccgtagtag atttctacaa ctccgccggc gtg ggt gca gac gaa 115
Val Gly Ala Asp Glu
1 5

ttc gat ttc atc ttt gag att gat gcg cca gaa gcc gga ttc gcg ctg 163
Phe Asp Phe Ile Phe Glu Ile Asp Ala Pro Glu Ala Gly Phe Ala Leu
10 15 20

gtc gac gcc ggt ggg gtt tcc ttc ttc gtc gag ttt cca cat gcg gga 211
Val Asp Ala Gly Gly Val Ser Phe Phe Val Glu Phe Pro His Ala Gly
25 30 35

ttc gaa gga gag gta gtt ttc acc gtc gtg ggc gaa ggt gat ttg ctg 259
Phe Glu Gly Glu Val Val Phe Thr Val Val Gly Glu Gly Asp Leu Leu
40 45 50

gcc gaa tgc gta ttg tcc gtc ttc tgc ggt gtc ggc ttg gcc ttc gcc 307
Ala Glu Cys Val Leu Ser Val Phe Cys Gly Val Gly Leu Ala Phe Ala
55 60 65

gcg cca gac gcc gac gag agg gag gag cgc gag gag tcc gtc gtg gag 355
Ala Pro Asp Ala Asp Glu Arg Glu Glu Arg Glu Glu Ser Val Val Glu
70 75 80 85

gtt ggg gcc ttc gcg gag gtt agc ggt gtc gtc agg gat agg aag gtc 403
Val Gly Ala Phe Ala Glu Val Ser Gly Val Val Arg Asp Arg Lys Val
90 95 100

acc taggcctggg atgttgcggt gag 429
Thr

<210> 1358
<211> 102
<212> PRT
<213> Corynebacterium glutamicum

<400> 1358
Val Gly Ala Asp Glu Phe Asp Phe Ile Phe Glu Ile Asp Ala Pro Glu
1 5 10 15

Ala Gly Phe Ala Leu Val Asp Ala Gly Gly Val Ser Phe Phe Val Glu
20 25 30

Phe Pro His Ala Gly Phe Glu Gly Glu Val Val Phe Thr Val Val Gly
35 40 45

Glu Gly Asp Leu Leu Ala Glu Cys Val Leu Ser Val Phe Cys Gly Val

```
     50                  55                  60

Gly Leu Ala Phe Ala Ala Pro Asp Ala Asp Glu Arg Glu Glu Arg Glu
 65                  70                  75                  80

Glu Ser Val Val Glu Val Gly Ala Phe Ala Glu Val Ser Gly Val Val
                 85                  90                  95

Arg Asp Arg Lys Val Thr
            100


<210> 1359
<211> 321
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(298)
<223> RXN02936

<400> 1359
accaagttca gacagctctg ggttggacct accggagtaa aggcgtgcca ctgacatagc 60

agtttggccg tggcgaagca acaagaaacg agtgggatct gtg gtt gcg ccg ttc   115
                                              Val Val Ala Pro Phe
                                                1               5

cag ttg gtg ggt ttg gtt tcg gtg cag ttg agg tct tct ttc tct gag   163
Gln Leu Val Gly Leu Val Ser Val Gln Leu Arg Ser Ser Phe Ser Glu
                10                  15                  20

ccc gca acc gaa gaa gca gaa gat aca gaa gca gaa tcc cct aca aca   211
Pro Ala Thr Glu Glu Ala Glu Asp Thr Glu Ala Glu Ser Pro Thr Thr
            25                  30                  35

cct acc ggc tta cct gcc gct gca gca tcc atc gcc acg ttg gac aat   259
Pro Thr Gly Leu Pro Ala Ala Ala Ala Ser Ile Ala Thr Leu Asp Asn
        40                  45                  50

gcg tca gct cgt ttg ttt ttc tca cgc gga atc cac gta taagaaacgg    308
Ala Ser Ala Arg Leu Phe Phe Ser Arg Gly Ile His Val
    55                  60                  65

acccgatttc gga                                                   321


<210> 1360
<211> 66
<212> PRT
<213> Corynebacterium glutamicum

<400> 1360
Val Val Ala Pro Phe Gln Leu Val Gly Leu Val Ser Val Gln Leu Arg
  1               5                  10                  15

Ser Ser Phe Ser Glu Pro Ala Thr Glu Glu Ala Glu Asp Thr Glu Ala
            20                  25                  30

Glu Ser Pro Thr Thr Pro Thr Gly Leu Pro Ala Ala Ala Ala Ser Ile
```

```
         35                  40                  45

Ala Thr Leu Asp Asn Ala Ser Ala Arg Leu Phe Phe Ser Arg Gly Ile
     50                  55                  60

His Val
 65


<210> 1361
<211> 1725
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1702)
<223> RXN02939

<400> 1361
cttcgaagaa gacgatatcc cctacgaagt cgacgtggat gacttattta tcctcggtgg 60

cttagacaac ttcataaatc cccttggagt gattgagata atg aat ctc cac tcc   115
                                            Met Asn Leu His Ser
                                              1               5

tta gag att cgc caa att tca tcc ggc aca att tca gaa cga aaa act   163
Leu Glu Ile Arg Gln Ile Ser Ser Gly Thr Ile Ser Glu Arg Lys Thr
                 10                  15                  20

tgg atc ttt ccc act gct gct cgc tca ttc aat caa aat cta gta cac   211
Trp Ile Phe Pro Thr Ala Ala Arg Ser Phe Asn Gln Asn Leu Val His
             25                  30                  35

ccg caa agc att gaa atc gat gca caa acc ggc gtt att ttg gct atg   259
Pro Gln Ser Ile Glu Ile Asp Ala Gln Thr Gly Val Ile Leu Ala Met
         40                  45                  50

gaa aac cga cta caa cgt acc gaa gtt gaa tca gta gag tac cca acg   307
Glu Asn Arg Leu Gln Arg Thr Glu Val Glu Ser Val Glu Tyr Pro Thr
     55                  60                  65

gat ctt cct aat cct gca tgg aca ggt cca gcc att tct tgg cca cta   355
Asp Leu Pro Asn Pro Ala Trp Thr Gly Pro Ala Ile Ser Trp Pro Leu
 70                  75                  80                  85

aaa gac cca tca atc gat ttc cct gac ccg ctc ccc cac agc att tcc   403
Lys Asp Pro Ser Ile Asp Phe Pro Asp Pro Leu Pro His Ser Ile Ser
                 90                  95                 100

gaa tta cca cct caa tcc gat aat cct cgg cat ttg cga gta tcc atc   451
Glu Leu Pro Pro Gln Ser Asp Asn Pro Arg His Leu Arg Val Ser Ile
            105                 110                 115

agc tta gat gca gtg gaa ggt gct ttt ccg cgc tac cgg atc gga gat   499
Ser Leu Asp Ala Val Glu Gly Ala Phe Pro Arg Tyr Arg Ile Gly Asp
        120                 125                 130

tca ata cgt att ccg ctt gtc ttt gcc cgg gac acg ccc ttc atg tcc   547
Ser Ile Arg Ile Pro Leu Val Phe Ala Arg Asp Thr Pro Phe Met Ser
    135                 140                 145
```

```
ggc tta gaa aca aca cgt cgc gcc tgg att gag gcg gcc acg gaa atg   595
Gly Leu Glu Thr Thr Arg Arg Ala Trp Ile Glu Ala Ala Thr Glu Met
150                 155                 160                 165

gac atc cat aac aca tgg ccc ata atc ctc acc ggt gac ggc tgg act   643
Asp Ile His Asn Thr Trp Pro Ile Ile Leu Thr Gly Asp Gly Trp Thr
                170                 175                 180

gca ctc tct cat tca gac aaa cca ata cgc cac gaa gcc gag tta aag   691
Ala Leu Ser His Ser Asp Lys Pro Ile Arg His Glu Ala Glu Leu Lys
            185                 190                 195

gga tgg ttt ttc cac agt ttg ttc ggc agt gaa atg ccc ttg act gat   739
Gly Trp Phe Phe His Ser Leu Phe Gly Ser Glu Met Pro Leu Thr Asp
        200                 205                 210

ctg aag att gaa cga atc tac gga ggc ctg ggt act ttc gac agc gga   787
Leu Lys Ile Glu Arg Ile Tyr Gly Gly Leu Gly Thr Phe Asp Ser Gly
    215                 220                 225

gcc acc cgg tgg caa gaa ctc aca gac aca gat gat gcc tac aca gaa   835
Ala Thr Arg Trp Gln Glu Leu Thr Asp Thr Asp Asp Ala Tyr Thr Glu
230                 235                 240                 245

aat ggc agc tgg ctg ttg gaa gtt atc gtc gat gcc acc ctt gac ggt   883
Asn Gly Ser Trp Leu Leu Glu Val Ile Val Asp Ala Thr Leu Asp Gly
                250                 255                 260

gca att cca cca cca ctt cag cca caa cag ttt gaa gca tcc atc act   931
Ala Ile Pro Pro Pro Leu Gln Pro Gln Gln Phe Glu Ala Ser Ile Thr
            265                 270                 275

cac atc gtc gat gag caa cta tgg gtc ctt ggg cag atg ctt cca gtt   979
His Ile Val Asp Glu Gln Leu Trp Val Leu Gly Gln Met Leu Pro Val
        280                 285                 290

cta cga tgc tgg gat ctt gaa acc gga aaa tac ctg ggg caa acc tat  1027
Leu Arg Cys Trp Asp Leu Glu Thr Gly Lys Tyr Leu Gly Gln Thr Tyr
    295                 300                 305

gta cct att tcg gtt tct cat agt tct cgg ctt cag ttt tcg gaa ggg  1075
Val Pro Ile Ser Val Ser His Ser Ser Arg Leu Gln Phe Ser Glu Gly
310                 315                 320                 325

ttg att cac gat tat gaa aat gcc tgg tcg ctg aat cct ggg gtg cgc  1123
Leu Ile His Asp Tyr Glu Asn Ala Trp Ser Leu Asn Pro Gly Val Arg
                330                 335                 340

atg ctt gcg gag cca cag ccg tgg ata gag cct gtc att gaa ctc gac  1171
Met Leu Ala Glu Pro Gln Pro Trp Ile Glu Pro Val Ile Glu Leu Asp
            345                 350                 355

gtt cca gcg cca tgg gaa tta caa gaa agc ttc ccc gat ggg ctt tac  1219
Val Pro Ala Pro Trp Glu Leu Gln Glu Ser Phe Pro Asp Gly Leu Tyr
        360                 365                 370

tcc cta act gat gga gag caa aca gca ctg ggt cga agc act cca gca  1267
Ser Leu Thr Asp Gly Glu Gln Thr Ala Leu Gly Arg Ser Thr Pro Ala
    375                 380                 385
```

```
gga caa ttg gaa atc tgt gta atc agc aat gac gga tcc agg atc tta   1315
Gly Gln Leu Glu Ile Cys Val Ile Ser Asn Asp Gly Ser Arg Ile Leu
390                 395                 400                 405

aac gca ggc cga gta gaa gac ctg tac ttt gtg caa ttc tgg ggc atg   1363
Asn Ala Gly Arg Val Glu Asp Leu Tyr Phe Val Gln Phe Trp Gly Met
                410                 415                 420

acc gtc ttt ttg aat tcc aac ttt caa gtg caa agt gcc gaa gaa cat   1411
Thr Val Phe Leu Asn Ser Asn Phe Gln Val Gln Ser Ala Glu Glu His
            425                 430                 435

cag ctt ggt gcg aaa cgt gaa cgc tgg att aca caa gaa ggc gta gct   1459
Gln Leu Gly Ala Lys Arg Glu Arg Trp Ile Thr Gln Glu Gly Val Ala
        440                 445                 450

gcc aag ttc acc gaa gaa gat gaa atc gta ttc ctc gat cag ata tct   1507
Ala Lys Phe Thr Glu Glu Asp Glu Ile Val Phe Leu Asp Gln Ile Ser
    455                 460                 465

gaa agc gaa ata acc agg tgg aaa aca cca gaa gga tac ttc act gag   1555
Glu Ser Glu Ile Thr Arg Trp Lys Thr Pro Glu Gly Tyr Phe Thr Glu
470                 475                 480                 485

gtc aga att ctg tca cca aac cac ttc aac ata ctg gtt act ccg cct   1603
Val Arg Ile Leu Ser Pro Asn His Phe Asn Ile Leu Val Thr Pro Pro
                490                 495                 500

act ggt tct gac tat ctc aaa cca gta cct tcc tct gtc tca gtg ttt   1651
Thr Gly Ser Asp Tyr Leu Lys Pro Val Pro Ser Ser Val Ser Val Phe
            505                 510                 515

aga gac ggt caa tgg agc aac att aaa ttc gag gac gtc tct gta gaa   1699
Arg Asp Gly Gln Trp Ser Asn Ile Lys Phe Glu Asp Val Ser Val Glu
        520                 525                 530

atc tagggctttc gacgcttgag ccc                                    1725
Ile
```

<210> 1362
<211> 534
<212> PRT
<213> Corynebacterium glutamicum

<400> 1362

```
Met Asn Leu His Ser Leu Glu Ile Arg Gln Ile Ser Ser Gly Thr Ile
  1               5                  10                  15

Ser Glu Arg Lys Thr Trp Ile Phe Pro Thr Ala Ala Arg Ser Phe Asn
             20                  25                  30

Gln Asn Leu Val His Pro Gln Ser Ile Glu Ile Asp Ala Gln Thr Gly
         35                  40                  45

Val Ile Leu Ala Met Glu Asn Arg Leu Gln Arg Thr Glu Val Glu Ser
     50                  55                  60

Val Glu Tyr Pro Thr Asp Leu Pro Asn Pro Ala Trp Thr Gly Pro Ala
 65                  70                  75                  80
```

```
Ile Ser Trp Pro Leu Lys Asp Pro Ser Ile Asp Phe Pro Asp Pro Leu
                 85                  90                  95

Pro His Ser Ile Ser Glu Leu Pro Pro Gln Ser Asp Asn Pro Arg His
            100                 105                 110

Leu Arg Val Ser Ile Ser Leu Asp Ala Val Glu Gly Ala Phe Pro Arg
        115                 120                 125

Tyr Arg Ile Gly Asp Ser Ile Arg Ile Pro Leu Val Phe Ala Arg Asp
    130                 135                 140

Thr Pro Phe Met Ser Gly Leu Glu Thr Thr Arg Arg Ala Trp Ile Glu
145                 150                 155                 160

Ala Ala Thr Glu Met Asp Ile His Asn Thr Trp Pro Ile Ile Leu Thr
                165                 170                 175

Gly Asp Gly Trp Thr Ala Leu Ser His Ser Asp Lys Pro Ile Arg His
            180                 185                 190

Glu Ala Glu Leu Lys Gly Trp Phe Phe His Ser Leu Phe Gly Ser Glu
        195                 200                 205

Met Pro Leu Thr Asp Leu Lys Ile Glu Arg Ile Tyr Gly Gly Leu Gly
    210                 215                 220

Thr Phe Asp Ser Gly Ala Thr Arg Trp Gln Glu Leu Thr Asp Thr Asp
225                 230                 235                 240

Asp Ala Tyr Thr Glu Asn Gly Ser Trp Leu Leu Glu Val Ile Val Asp
                245                 250                 255

Ala Thr Leu Asp Gly Ala Ile Pro Pro Pro Leu Gln Pro Gln Gln Phe
            260                 265                 270

Glu Ala Ser Ile Thr His Ile Val Asp Glu Gln Leu Trp Val Leu Gly
        275                 280                 285

Gln Met Leu Pro Val Leu Arg Cys Trp Asp Leu Glu Thr Gly Lys Tyr
    290                 295                 300

Leu Gly Gln Thr Tyr Val Pro Ile Ser Val Ser His Ser Ser Arg Leu
305                 310                 315                 320

Gln Phe Ser Glu Gly Leu Ile His Asp Tyr Glu Asn Ala Trp Ser Leu
                325                 330                 335

Asn Pro Gly Val Arg Met Leu Ala Glu Pro Gln Pro Trp Ile Glu Pro
            340                 345                 350

Val Ile Glu Leu Asp Val Pro Ala Pro Trp Glu Leu Gln Glu Ser Phe
        355                 360                 365

Pro Asp Gly Leu Tyr Ser Leu Thr Asp Gly Glu Gln Thr Ala Leu Gly
    370                 375                 380

Arg Ser Thr Pro Ala Gly Gln Leu Glu Ile Cys Val Ile Ser Asn Asp
385                 390                 395                 400
```

```
Gly Ser Arg Ile Leu Asn Ala Gly Arg Val Glu Asp Leu Tyr Phe Val
                405                 410                 415

Gln Phe Trp Gly Met Thr Val Phe Leu Asn Ser Asn Phe Gln Val Gln
            420                 425                 430

Ser Ala Glu Glu His Gln Leu Gly Ala Lys Arg Glu Arg Trp Ile Thr
        435                 440                 445

Gln Glu Gly Val Ala Ala Lys Phe Thr Glu Glu Asp Glu Ile Val Phe
    450                 455                 460

Leu Asp Gln Ile Ser Glu Ser Glu Ile Thr Arg Trp Lys Thr Pro Glu
465                 470                 475                 480

Gly Tyr Phe Thr Glu Val Arg Ile Leu Ser Pro Asn His Phe Asn Ile
                485                 490                 495

Leu Val Thr Pro Pro Thr Gly Ser Asp Tyr Leu Lys Pro Val Pro Ser
            500                 505                 510

Ser Val Ser Val Phe Arg Asp Gly Gln Trp Ser Asn Ile Lys Phe Glu
        515                 520                 525

Asp Val Ser Val Glu Ile
    530


<210> 1363
<211> 1243
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1243)
<223> FRXA01383

<400> 1363
cttcgaagaa gacgatatcc cctacgaagt cgacgtggat gacttattta tcctcggtgg 60

cttagacaac ttcataaatc cccttggagt gattgagata atg aat ctc cac tcc   115
                                              Met Asn Leu His Ser
                                                1               5

tta gag att cgc caa att tca tcc ggc aca att tca gaa cga aaa act   163
Leu Glu Ile Arg Gln Ile Ser Ser Gly Thr Ile Ser Glu Arg Lys Thr
                10                  15                  20

tgg atc ttt ccc act gct gct cgc tca ttc aat caa aat cta gta cac   211
Trp Ile Phe Pro Thr Ala Ala Arg Ser Phe Asn Gln Asn Leu Val His
            25                  30                  35

ccg caa agc att gaa atc gat gca caa acc ggc gtt att ttg gct atg   259
Pro Gln Ser Ile Glu Ile Asp Ala Gln Thr Gly Val Ile Leu Ala Met
        40                  45                  50

gaa aac cga cta caa cgt acc gaa gtt gaa tca gta gag tac cca acg   307
Glu Asn Arg Leu Gln Arg Thr Glu Val Glu Ser Val Glu Tyr Pro Thr
    55                  60                  65
```

```
gat ctt cct aat cct gca tgg aca ggt cca gcc att tct tgg cca cta   355
Asp Leu Pro Asn Pro Ala Trp Thr Gly Pro Ala Ile Ser Trp Pro Leu
 70                  75                  80                  85

aaa gac cca tca atc gat ttc cct gac ccg ctc ccc cac agc att tcc   403
Lys Asp Pro Ser Ile Asp Phe Pro Asp Pro Leu Pro His Ser Ile Ser
                90                  95                 100

gaa tta cca cct caa tcc gat aat cct cgg cat ttg cga gta tcc atc   451
Glu Leu Pro Pro Gln Ser Asp Asn Pro Arg His Leu Arg Val Ser Ile
            105                 110                 115

agc tta gat gca gtg gaa ggt gct ttt ccg cgc tac cgg atc gga gat   499
Ser Leu Asp Ala Val Glu Gly Ala Phe Pro Arg Tyr Arg Ile Gly Asp
        120                 125                 130

tca ata cgt att ccg ctt gtc ttt gcc cgg gac acg ccc ttc atg tcc   547
Ser Ile Arg Ile Pro Leu Val Phe Ala Arg Asp Thr Pro Phe Met Ser
    135                 140                 145

ggc tta gaa aca aca cgt cgc gcc tgg att gag gcg gcc acg gaa atg   595
Gly Leu Glu Thr Thr Arg Arg Ala Trp Ile Glu Ala Ala Thr Glu Met
150                 155                 160                 165

gac atc cat aac aca tgg ccc ata atc ctc acc ggt gac ggc tgg act   643
Asp Ile His Asn Thr Trp Pro Ile Ile Leu Thr Gly Asp Gly Trp Thr
                170                 175                 180

gca ctc tct cat tca gac aaa cca ata cgc cac gaa gcc gag tta aag   691
Ala Leu Ser His Ser Asp Lys Pro Ile Arg His Glu Ala Glu Leu Lys
            185                 190                 195

gga tgg ttt ttc cac agt ttg ttc ggc agt gaa atg ccc ttg act gat   739
Gly Trp Phe Phe His Ser Leu Phe Gly Ser Glu Met Pro Leu Thr Asp
        200                 205                 210

ctg aag att gaa cga atc tac gga ggc ctg ggt act ttc gac agc gga   787
Leu Lys Ile Glu Arg Ile Tyr Gly Gly Leu Gly Thr Phe Asp Ser Gly
    215                 220                 225

gcc acc cgg tgg caa gaa ctc aca gac aca gat gat gcc tac aca gaa   835
Ala Thr Arg Trp Gln Glu Leu Thr Asp Thr Asp Asp Ala Tyr Thr Glu
230                 235                 240                 245

aat ggc agc tgg ctg ttg gaa gtt atc gtc gat gcc acc ctt gac ggt   883
Asn Gly Ser Trp Leu Leu Glu Val Ile Val Asp Ala Thr Leu Asp Gly
                250                 255                 260

gca att cca cca cca ctt cag cca caa cag ttt gaa gca tcc atc act   931
Ala Ile Pro Pro Pro Leu Gln Pro Gln Gln Phe Glu Ala Ser Ile Thr
            265                 270                 275

cac atc gtc gat gag caa cta tgg gtc ctt ggg cag atg ctt cca gtt   979
His Ile Val Asp Glu Gln Leu Trp Val Leu Gly Gln Met Leu Pro Val
        280                 285                 290

cta cga tgc tgg gat ctt gaa acc gga aaa tac ctg ggg caa acc tat   1027
Leu Arg Cys Trp Asp Leu Glu Thr Gly Lys Tyr Leu Gly Gln Thr Tyr
    295                 300                 305

gta cct att tcg gtt tct cat agt tct cgg ctt cag ttt tcg gaa ggg   1075
```

```
Val Pro Ile Ser Val Ser His Ser Ser Arg Leu Gln Phe Ser Glu Gly
310                 315                 320                 325

ttg att cac gat tat gaa aat gcc tgg tcg ctg aat cct ggg gtg cgc   1123
Leu Ile His Asp Tyr Glu Asn Ala Trp Ser Leu Asn Pro Gly Val Arg
                330                 335                 340

atg ctt gcg gag cca cag ccg tgg ata gag cct gtc att gaa ctc gac   1171
Met Leu Ala Glu Pro Gln Pro Trp Ile Glu Pro Val Ile Glu Leu Asp
            345                 350                 355

gtt cca gcg cca tgg gaa tta caa gaa agc ttc ccc gat ggg ctt tac   1219
Val Pro Ala Pro Trp Glu Leu Gln Glu Ser Phe Pro Asp Gly Leu Tyr
        360                 365                 370

ttc cta act gat ggc aag caa aca                                  1243
Phe Leu Thr Asp Gly Lys Gln Thr
    375                 380
```

<210> 1364
<211> 381
<212> PRT
<213> Corynebacterium glutamicum

<400> 1364

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Met Asn Leu His Ser Leu Glu Ile Arg Gln Ile Ser Ser Gly Thr Ile
  1               5                  10                  15

Ser Glu Arg Lys Thr Trp Ile Phe Pro Thr Ala Ala Arg Ser Phe Asn
             20                  25                  30

Gln Asn Leu Val His Pro Gln Ser Ile Glu Ile Asp Ala Gln Thr Gly
         35                  40                  45

Val Ile Leu Ala Met Glu Asn Arg Leu Gln Arg Thr Glu Val Glu Ser
     50                  55                  60

Val Glu Tyr Pro Thr Asp Leu Pro Asn Pro Ala Trp Thr Gly Pro Ala
 65                  70                  75                  80

Ile Ser Trp Pro Leu Lys Asp Pro Ser Ile Asp Phe Pro Asp Pro Leu
                 85                  90                  95

Pro His Ser Ile Ser Glu Leu Pro Pro Gln Ser Asp Asn Pro Arg His
            100                 105                 110

Leu Arg Val Ser Ile Ser Leu Asp Ala Val Glu Gly Ala Phe Pro Arg
        115                 120                 125

Tyr Arg Ile Gly Asp Ser Ile Arg Ile Pro Leu Val Phe Ala Arg Asp
    130                 135                 140

Thr Pro Phe Met Ser Gly Leu Glu Thr Thr Arg Arg Ala Trp Ile Glu
145                 150                 155                 160

Ala Ala Thr Glu Met Asp Ile His Asn Thr Trp Pro Ile Ile Leu Thr
                165                 170                 175

Gly Asp Gly Trp Thr Ala Leu Ser His Ser Asp Lys Pro Ile Arg His
            180                 185                 190
```

```
Glu Ala Glu Leu Lys Gly Trp Phe Phe His Ser Leu Phe Gly Ser Glu
        195                 200                 205

Met Pro Leu Thr Asp Leu Lys Ile Glu Arg Ile Tyr Gly Gly Leu Gly
    210                 215                 220

Thr Phe Asp Ser Gly Ala Thr Arg Trp Gln Glu Leu Thr Asp Thr Asp
225                 230                 235                 240

Asp Ala Tyr Thr Glu Asn Gly Ser Trp Leu Leu Glu Val Ile Val Asp
                245                 250                 255

Ala Thr Leu Asp Gly Ala Ile Pro Pro Pro Leu Gln Pro Gln Gln Phe
            260                 265                 270

Glu Ala Ser Ile Thr His Ile Val Asp Glu Gln Leu Trp Val Leu Gly
        275                 280                 285

Gln Met Leu Pro Val Leu Arg Cys Trp Asp Leu Glu Thr Gly Lys Tyr
    290                 295                 300

Leu Gly Gln Thr Tyr Val Pro Ile Ser Val Ser His Ser Ser Arg Leu
305                 310                 315                 320

Gln Phe Ser Glu Gly Leu Ile His Asp Tyr Glu Asn Ala Trp Ser Leu
                325                 330                 335

Asn Pro Gly Val Arg Met Leu Ala Glu Pro Gln Pro Trp Ile Glu Pro
            340                 345                 350

Val Ile Glu Leu Asp Val Pro Ala Pro Trp Glu Leu Gln Glu Ser Phe
        355                 360                 365

Pro Asp Gly Leu Tyr Phe Leu Thr Asp Gly Lys Gln Thr
    370                 375                 380


<210> 1365
<211> 447
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(424)
<223> RXN02950

<400> 1365
tccgccctat ttcagcaatg tttaataccg gtggaatcgt ttttattagg atgggtggat 60

acctatcttt agtgagccgt actagcgaga aagctgcccc atg act gtt ttc aat   115
                                              Met Thr Val Phe Asn
                                                1               5

gtt ctc cat gac gca ccc gca cca cag ccg gat aaa aac cgc ccc ggt   163
Val Leu His Asp Ala Pro Ala Pro Gln Pro Asp Lys Asn Arg Pro Gly
                10                  15                  20

gtc aaa cgt ctc ctc caa ggt gat ggc gca aac ctc atc gcc ttc act   211
Val Lys Arg Leu Leu Gln Gly Asp Gly Ala Asn Leu Ile Ala Phe Thr
```

```
            25                  30                  35

ttc agc cct gga cag tca ctt ccc gac cac cgc gcc gca cat ccc atc   259
Phe Ser Pro Gly Gln Ser Leu Pro Asp His Arg Ala Ala His Pro Ile
        40                  45                  50

acc gtg acc gca ttt tct ggc cag ctc acc ttc agc tat ggc gag gaa   307
Thr Val Thr Ala Phe Ser Gly Gln Leu Thr Phe Ser Tyr Gly Glu Glu
    55                  60                  65

acc ttt gag ctc tcc ccc ggt gtg aca gtg cac ttg gaa gca gga gtt   355
Thr Phe Glu Leu Ser Pro Gly Val Thr Val His Leu Glu Ala Gly Val
70                  75                  80                  85

acc cac cgc gtg gac tgc ccg cca gaa gca cca ggc gat gca agt aat   403
Thr His Arg Val Asp Cys Pro Pro Glu Ala Pro Gly Asp Ala Ser Asn
                90                  95                  100

gct gtt aac tat gct cac tgg tgaaaaacac tcagtcaacc agg             447
Ala Val Asn Tyr Ala His Trp
            105
```

<210> 1366
<211> 108
<212> PRT
<213> Corynebacterium glutamicum

<400> 1366

```
Met Thr Val Phe Asn Val Leu His Asp Ala Pro Ala Pro Gln Pro Asp
  1               5                  10                  15

Lys Asn Arg Pro Gly Val Lys Arg Leu Leu Gln Gly Asp Gly Ala Asn
            20                  25                  30

Leu Ile Ala Phe Thr Phe Ser Pro Gly Gln Ser Leu Pro Asp His Arg
        35                  40                  45

Ala Ala His Pro Ile Thr Val Thr Ala Phe Ser Gly Gln Leu Thr Phe
    50                  55                  60

Ser Tyr Gly Glu Glu Thr Phe Glu Leu Ser Pro Gly Val Thr Val His
65                  70                  75                  80

Leu Glu Ala Gly Val Thr His Arg Val Asp Cys Pro Pro Glu Ala Pro
                85                  90                  95

Gly Asp Ala Ser Asn Ala Val Asn Tyr Ala His Trp
            100                 105
```

<210> 1367
<211> 732
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(709)
<223> RXN02951

<400> 1367
gataatgagt cagaaaatga aggtagcact acttgctgga ttaattttca aggttttctt 60

tcagaaatta atccatagcc gatatttaag gtgagaacac atg agc tcc acg ctc 115
Met Ser Ser Thr Leu
1 5

gca cga aaa gct tca ggc gac ggt tcc gaa aag aag aag cct ggc ttg 163
Ala Arg Lys Ala Ser Gly Asp Gly Ser Glu Lys Lys Lys Pro Gly Leu
10 15 20

ttt aga cgt gcg ctt cgt ttc ctc acc cac cca cct cac aaa cag gta 211
Phe Arg Arg Ala Leu Arg Phe Leu Thr His Pro Pro His Lys Gln Val
25 30 35

gac aac agc ctt gcg gat atc cgt gaa gga tta ggc ctc ggg gtg gac 259
Asp Asn Ser Leu Ala Asp Ile Arg Glu Gly Leu Gly Leu Gly Val Asp
40 45 50

gat tcc cac gaa gga tcc aaa ccc agc aac gat cat tct ttg ctg cat 307
Asp Ser His Glu Gly Ser Lys Pro Ser Asn Asp His Ser Leu Leu His
55 60 65

gaa aag cct gaa att tcc gtc atg ccg acc gaa tca atg gca cgg ctg 355
Glu Lys Pro Glu Ile Ser Val Met Pro Thr Glu Ser Met Ala Arg Leu
70 75 80 85

atc ttt tat gcg cct gat atg gat ggg caa aca gac ccc ggt gaa gta 403
Ile Phe Tyr Ala Pro Asp Met Asp Gly Gln Thr Asp Pro Gly Glu Val
90 95 100

gtg tgg att tgg gca cca gcc gat ggc ccc cag caa cca ccc cgt aaa 451
Val Trp Ile Trp Ala Pro Ala Asp Gly Pro Gln Gln Pro Pro Arg Lys
105 110 115

cgt gcc atc gtt gtt gtt gga aga aac cga aac gcc att tta ggt ctg 499
Arg Ala Ile Val Val Val Gly Arg Asn Arg Asn Ala Ile Leu Gly Leu
120 125 130

ctc att tcc tgc aac ccc gag cac cgc act gat gaa gac tgg atc gac 547
Leu Ile Ser Cys Asn Pro Glu His Arg Thr Asp Glu Asp Trp Ile Asp
135 140 145

att gga tct ggc agc tgg gac cct cga ggt cgc caa agt tgg gta cga 595
Ile Gly Ser Gly Ser Trp Asp Pro Arg Gly Arg Gln Ser Trp Val Arg
150 155 160 165

ctc gac cgc gtt ctg gag gta ccc gaa ttg ggt atc cgg cgc caa gga 643
Leu Asp Arg Val Leu Glu Val Pro Glu Leu Gly Ile Arg Arg Gln Gly
170 175 180

aca gtc gtc ccc ccg ggg cgc ttt gag cgt atc gcc aac cgc ctc cgc 691
Thr Val Val Pro Pro Gly Arg Phe Glu Arg Ile Ala Asn Arg Leu Arg
185 190 195

aac gat ttc aac tgg gtc taacatttat ttggtaattg ggc 732
Asn Asp Phe Asn Trp Val
200

<210> 1368

<211> 203
<212> PRT
<213> Corynebacterium glutamicum

<400> 1368
Met Ser Ser Thr Leu Ala Arg Lys Ala Ser Gly Asp Gly Ser Glu Lys
1 5 10 15

Lys Lys Pro Gly Leu Phe Arg Arg Ala Leu Arg Phe Leu Thr His Pro
20 25 30

Pro His Lys Gln Val Asp Asn Ser Leu Ala Asp Ile Arg Glu Gly Leu
35 40 45

Gly Leu Gly Val Asp Asp Ser His Glu Gly Ser Lys Pro Ser Asn Asp
50 55 60

His Ser Leu Leu His Glu Lys Pro Glu Ile Ser Val Met Pro Thr Glu
65 70 75 80

Ser Met Ala Arg Leu Ile Phe Tyr Ala Pro Asp Met Asp Gly Gln Thr
85 90 95

Asp Pro Gly Glu Val Val Trp Ile Trp Ala Pro Ala Asp Gly Pro Gln
100 105 110

Gln Pro Pro Arg Lys Arg Ala Ile Val Val Val Gly Arg Asn Arg Asn
115 120 125

Ala Ile Leu Gly Leu Leu Ile Ser Cys Asn Pro Glu His Arg Thr Asp
130 135 140

Glu Asp Trp Ile Asp Ile Gly Ser Gly Ser Trp Asp Pro Arg Gly Arg
145 150 155 160

Gln Ser Trp Val Arg Leu Asp Arg Val Leu Glu Val Pro Glu Leu Gly
165 170 175

Ile Arg Arg Gln Gly Thr Val Val Pro Pro Gly Arg Phe Glu Arg Ile
180 185 190

Ala Asn Arg Leu Arg Asn Asp Phe Asn Trp Val
195 200

<210> 1369
<211> 414
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(391)
<223> RXN02957

<400> 1369
gcatgctatt gcgctccggg tgggagattc tgtcgtccat gccgcggttg tggtggcgca 60

atgactgcgc cccgggcacg gaatggctcc gggtcaccaa atg caa act gcc caa 115
Met Gln Thr Ala Gln
1 5

```
gga gga agg gtc tac acc tca ctg atg gac gag aag tcc ctt tcc ccg   163
Gly Gly Arg Val Tyr Thr Ser Leu Met Asp Glu Lys Ser Leu Ser Pro
                10                  15                  20

ttg atc ggt ctg ccg ggt cgg gag aac atc ggc ctg ggc cga cac tgg   211
Leu Ile Gly Leu Pro Gly Arg Glu Asn Ile Gly Leu Gly Arg His Trp
            25                  30                  35

cac ggt ctg tcg acg atg ttg cgg gtg ctc aac ggc atc gtc tac gtc   259
His Gly Leu Ser Thr Met Leu Arg Val Leu Asn Gly Ile Val Tyr Val
        40                  45                  50

gtt ctg ctg ttc gcc acc ggg ctg tgg caa ggc att atc ccc acc tcc   307
Val Leu Leu Phe Ala Thr Gly Leu Trp Gln Gly Ile Ile Pro Thr Ser
    55                  60                  65

tgg gac gtc ttc ccc gag gcg tgg gag aca ttg aag gtt tac ctg ggc   355
Trp Asp Val Phe Pro Glu Ala Trp Glu Thr Leu Lys Val Tyr Leu Gly
70                  75                  80                  85

ttt cgt gcc cca ggc atc gag cac ttc acc ccc cta tgacgccttg        401
Phe Arg Ala Pro Gly Ile Glu His Phe Thr Pro Leu
                90                  95

caaatgctgg gct                                                   414
```

<210> 1370
<211> 97
<212> PRT
<213> Corynebacterium glutamicum

<400> 1370

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Met Gln Thr Ala Gln Gly Gly Arg Val Tyr Thr Ser Leu Met Asp Glu
  1               5                  10                  15

Lys Ser Leu Ser Pro Leu Ile Gly Leu Pro Gly Arg Glu Asn Ile Gly
            20                  25                  30

Leu Gly Arg His Trp His Gly Leu Ser Thr Met Leu Arg Val Leu Asn
        35                  40                  45

Gly Ile Val Tyr Val Val Leu Leu Phe Ala Thr Gly Leu Trp Gln Gly
    50                  55                  60

Ile Ile Pro Thr Ser Trp Asp Val Phe Pro Glu Ala Trp Glu Thr Leu
65                  70                  75                  80

Lys Val Tyr Leu Gly Phe Arg Ala Pro Gly Ile Glu His Phe Thr Pro
                85                  90                  95

Leu
```

<210> 1371
<211> 441
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(418)
<223> RXN02967

<400> 1371
gggaatctag tcggccttca ccggtgatca acaagtcagt ttctggcagc gcatcctcga 60

ttccgttgga gcgggcaatc agtggcgcgc cggggaggat atg gat ctg ttg gtc 115
Met Asp Leu Leu Val
1 5

gtt gcc gtg cat gag ggt gga cag cca cgt cag tcc gat tgc aat gcc 163
Val Ala Val His Glu Gly Gly Gln Pro Arg Gln Ser Asp Cys Asn Ala
10 15 20

ccc ggc tgc gcc cat acc tgg ctt tgt gcc atc aac ttc cag ttg ggc 211
Pro Gly Cys Ala His Thr Trp Leu Cys Ala Ile Asn Phe Gln Leu Gly
25 30 35

gca ggc gtg gtg gag ggc ggc gtc gag aag cga aat gtc ttt ttc ggt 259
Ala Gly Val Val Glu Gly Gly Val Glu Lys Arg Asn Val Phe Phe Gly
40 45 50

ggc acc ttt ttg ggg ccc gaa tac ggt ggc cgc gcc ctg cgg gcc ggt 307
Gly Thr Phe Leu Gly Pro Glu Tyr Gly Gly Arg Ala Leu Arg Ala Gly
55 60 65

ggc ggg ggc gtc gac atc ggt gag cag gat cca ttc gac ggc ggc tgc 355
Gly Gly Gly Val Asp Ile Gly Glu Gln Asp Pro Phe Asp Gly Gly Cys
70 75 80 85

ggg gat gtt gag ttc ggc ggt atc gat gta atc gag gtt gat gag gtc 403
Gly Asp Val Glu Phe Gly Gly Ile Asp Val Ile Glu Val Asp Glu Val
90 95 100

ggc gcc acc ggt tcg tagtgcgtag ccctctttgt tgc 441
Gly Ala Thr Gly Ser
105

<210> 1372
<211> 106
<212> PRT
<213> Corynebacterium glutamicum

<400> 1372
Met Asp Leu Leu Val Val Ala Val His Glu Gly Gly Gln Pro Arg Gln
1 5 10 15

Ser Asp Cys Asn Ala Pro Gly Cys Ala His Thr Trp Leu Cys Ala Ile
20 25 30

Asn Phe Gln Leu Gly Ala Gly Val Val Glu Gly Gly Val Glu Lys Arg
35 40 45

Asn Val Phe Phe Gly Gly Thr Phe Leu Gly Pro Glu Tyr Gly Gly Arg
50 55 60

Ala Leu Arg Ala Gly Gly Gly Gly Val Asp Ile Gly Glu Gln Asp Pro
65 70 75 80

```
Phe Asp Gly Gly Cys Gly Asp Val Glu Phe Gly Gly Ile Asp Val Ile
                85                  90                  95

Glu Val Asp Glu Val Gly Ala Thr Gly Ser
            100                 105


<210> 1373
<211> 435
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(412)
<223> RXN02971

<400> 1373
ttctggtccg gattttcggg gaatacagcg agggagaaac gtggcacgcc attcaagtgg 60

gaattcaaac ttaaggttat ctaaatcgct aaccattgcg ttg att gcc atc gtc   115
                                        Leu Ile Ala Ile Val
                                          1               5

gct ctc atc gtg gca ctt gtg gtg tgg ctt ttt aac cgt tca gat gat   163
Ala Leu Ile Val Ala Leu Val Val Trp Leu Phe Asn Arg Ser Asp Asp
                10                  15                  20

tct ggc tcc acc acg acc acc tca caa gag tgc atc tcc gga aac ttg   211
Ser Gly Ser Thr Thr Thr Thr Ser Gln Glu Cys Ile Ser Gly Asn Leu
            25                  30                  35

agt ctg ccc gtt ggt ggc gat tcc acc gca gcc gaa gaa tta gtg aac   259
Ser Leu Pro Val Gly Gly Asp Ser Thr Ala Ala Glu Glu Leu Val Asn
        40                  45                  50

aaa ttt aat gac tca tca cct gtc agc cgt gat ttc tgt gtt gag gcg   307
Lys Phe Asn Asp Ser Ser Pro Val Ser Arg Asp Phe Cys Val Glu Ala
    55                  60                  65

gaa gct gtg gac ggt aac gtc ccc gct gcc acg tac ctg ttc gct ggt   355
Glu Ala Val Asp Gly Asn Val Pro Ala Ala Thr Tyr Leu Phe Ala Gly
70                  75                  80                  85

tct cgt tct gat gct gcc acc gca ctt gct gaa acc ggt gcc gta gca   403
Ser Arg Ser Asp Ala Ala Thr Ala Leu Ala Glu Thr Gly Ala Val Ala
                90                  95                  100

agc agc tct taaagctctt ggccctaggt tgg                            435
Ser Ser Ser


<210> 1374
<211> 104
<212> PRT
<213> Corynebacterium glutamicum

<400> 1374
Leu Ile Ala Ile Val Ala Leu Ile Val Ala Leu Val Val Trp Leu Phe
```

```
  1               5                  10                  15

Asn Arg Ser Asp Asp Ser Gly Ser Thr Thr Thr Thr Ser Gln Glu Cys
            20                  25                  30

Ile Ser Gly Asn Leu Ser Leu Pro Val Gly Gly Asp Ser Thr Ala Ala
        35                  40                  45

Glu Glu Leu Val Asn Lys Phe Asn Asp Ser Ser Pro Val Ser Arg Asp
    50                  55                  60

Phe Cys Val Glu Ala Glu Ala Val Asp Gly Asn Val Pro Ala Ala Thr
65                  70                  75                  80

Tyr Leu Phe Ala Gly Ser Arg Ser Asp Ala Ala Thr Ala Leu Ala Glu
                85                  90                  95

Thr Gly Ala Val Ala Ser Ser Ser
            100
```

<210> 1375
<211> 1632
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1609)
<223> RXN02978

<400> 1375

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gcctcttaaa atcagacaat ttcagtgttg gaatagctac aagggtctac tgtaaacgaa  60

gaacgctcga tagggctgtg tacctcaacg gaggtaaaac gtg att gat cga cct   115
                                        Val Ile Asp Arg Pro
                                          1               5

gta tgg ttg ttt gaa ctt tat aac acc gcg aaa gaa gta gta tat tcg   163
Val Trp Leu Phe Glu Leu Tyr Asn Thr Ala Lys Glu Val Val Tyr Ser
                10                  15                  20

cta ctc att gat caa gta act ggg gaa aat aca ata ctc aag aag gat   211
Leu Leu Ile Asp Gln Val Thr Gly Glu Asn Thr Ile Leu Lys Lys Asp
            25                  30                  35

gat ggt tgg cga gat caa ttc atg att gag tct ttc ttt gct tat gat   259
Asp Gly Trp Arg Asp Gln Phe Met Ile Glu Ser Phe Phe Ala Tyr Asp
        40                  45                  50

tca gaa gct gac gcg acc tcg tgg agc ggt aag aac atg aat agc tac   307
Ser Glu Ala Asp Ala Thr Ser Trp Ser Gly Lys Asn Met Asn Ser Tyr
    55                  60                  65

tgg ttc gtt agc gat cta atc agc aat ata tcc ttc gct gag cga tcc   355
Trp Phe Val Ser Asp Leu Ile Ser Asn Ile Ser Phe Ala Glu Arg Ser
70                  75                  80                  85

ttg gaa agc ttt tct tgg gct ctt cga gat ctt gag gat ctt tct tct   403
Leu Glu Ser Phe Ser Trp Ala Leu Arg Asp Leu Glu Asp Leu Ser Ser
                90                  95                  100
```

```
agt gaa act gaa ttt gaa ggg ctt gaa gag ctg aat cta aag ttt agt   451
Ser Glu Thr Glu Phe Glu Gly Leu Glu Glu Leu Asn Leu Lys Phe Ser
            105                 110                 115

gag ctc caa gaa tgg tat acg aac ctg gaa ctt cct ttt cag ccg tcg   499
Glu Leu Gln Glu Trp Tyr Thr Asn Leu Glu Leu Pro Phe Gln Pro Ser
        120                 125                 130

gct gct gat gtt gat gag gtg gag cag tat ctg caa gct gaa gtg aca   547
Ala Ala Asp Val Asp Glu Val Glu Gln Tyr Leu Gln Ala Glu Val Thr
    135                 140                 145

agg caa cgg ggt gac tat caa tgg tct cct gag ttt tgg ata cca aag   595
Arg Gln Arg Gly Asp Tyr Gln Trp Ser Pro Glu Phe Trp Ile Pro Lys
150                 155                 160                 165

ccg gat tca tac tat atc gac cat gca cta gcg gtt gtc aca gat gtt   643
Pro Asp Ser Tyr Tyr Ile Asp His Ala Leu Ala Val Val Thr Asp Val
                170                 175                 180

ttg gga gct att gaa caa ggg gag ctg cgt gaa gaa gta gag gtg cag   691
Leu Gly Ala Ile Glu Gln Gly Glu Leu Arg Glu Glu Val Glu Val Gln
            185                 190                 195

cag gct tta gac gag gta tct gaa aat tgg aat cct ttg gaa gat tct   739
Gln Ala Leu Asp Glu Val Ser Glu Asn Trp Asn Pro Leu Glu Asp Ser
        200                 205                 210

gat tac tac tta cag gat cac cgt ggg cgc cct gta caa gat ctt tcc   787
Asp Tyr Tyr Leu Gln Asp His Arg Gly Arg Pro Val Gln Asp Leu Ser
    215                 220                 225

cgg gaa atg gag gag ttg gtc aga tgt cta atg ctt gac caa gag tgg   835
Arg Glu Met Glu Glu Leu Val Arg Cys Leu Met Leu Asp Gln Glu Trp
230                 235                 240                 245

tgg ggt gca gag gca agg att aga aag ctt gtt gaa tca gtt gag tgg   883
Trp Gly Ala Glu Ala Arg Ile Arg Lys Leu Val Glu Ser Val Glu Trp
                250                 255                 260

gag gat act cag gcg atc agc tct tta att gaa cac gag caa tat tgg   931
Glu Asp Thr Gln Ala Ile Ser Ser Leu Ile Glu His Glu Gln Tyr Trp
            265                 270                 275

gag gat ggt cgt ttt cgc cca cct cta cat aag ttt tcg gaa gga cta   979
Glu Asp Gly Arg Phe Arg Pro Pro Leu His Lys Phe Ser Glu Gly Leu
        280                 285                 290

gac gag cca gag ccc ttg ccg atg acg aga aaa atg ata ctt gcg acg   1027
Asp Glu Pro Glu Pro Leu Pro Met Thr Arg Lys Met Ile Leu Ala Thr
    295                 300                 305

aat cac cct gat gtt tta cgc gta aac att gct gat tat tat cag cag   1075
Asn His Pro Asp Val Leu Arg Val Asn Ile Ala Asp Tyr Tyr Gln Gln
310                 315                 320                 325

cat agg cgc att gct act cag aag gtg gaa tgt tat aag gaa gtt ttg   1123
His Arg Arg Ile Ala Thr Gln Lys Val Glu Cys Tyr Lys Glu Val Leu
                330                 335                 340
```

```
gca ttg tat cca gag att ctt aag aaa ttt gat gat tca tct ttc gtc   1171
Ala Leu Tyr Pro Glu Ile Leu Lys Lys Phe Asp Asp Ser Ser Phe Val
            345                 350                 355

aat cga cat tgg atc tat agg gcg ttt gat cgc gaa ggt cag ctt ttg   1219
Asn Arg His Trp Ile Tyr Arg Ala Phe Asp Arg Glu Gly Gln Leu Leu
        360                 365                 370

tat atc ggg gag aca ata aac cct ctt gta cgg ttg agg gag cat gcc   1267
Tyr Ile Gly Glu Thr Ile Asn Pro Leu Val Arg Leu Arg Glu His Ala
    375                 380                 385

ggc tta ggg tct att aac cac gca cat cat agg cta gta tcg ccg tgg   1315
Gly Leu Gly Ser Ile Asn His Ala His His Arg Leu Val Ser Pro Trp
390                 395                 400                 405

ttt tct acg atg gct aca ttt cat ctt gaa tct tgc ttt acc cag gct   1363
Phe Ser Thr Met Ala Thr Phe His Leu Glu Ser Cys Phe Thr Gln Ala
                410                 415                 420

gag gca aaa gag aag gag gct tta tat att aag ctg gaa cag cca aga   1411
Glu Ala Lys Glu Lys Glu Ala Leu Tyr Ile Lys Leu Glu Gln Pro Arg
            425                 430                 435

tat aat aag acg cat aat tct gct aga ttg gcg gtt tct gaa gaa ggg   1459
Tyr Asn Lys Thr His Asn Ser Ala Arg Leu Ala Val Ser Glu Glu Gly
        440                 445                 450

gtg ccg gtg aac gag gtg ccg tca aga aat gat ccg agg aat gtc ggt   1507
Val Pro Val Asn Glu Val Pro Ser Arg Asn Asp Pro Arg Asn Val Gly
    455                 460                 465

tgg aag ggt cat agg cac gtg cca cca atg ttg ccg att gtt gca cgt   1555
Trp Lys Gly His Arg His Val Pro Pro Met Leu Pro Ile Val Ala Arg
470                 475                 480                 485

gtt gtc gat gaa tcg aca aca cgt gag gga tat gcg ttt tac gag gac   1603
Val Val Asp Glu Ser Thr Thr Arg Glu Gly Tyr Ala Phe Tyr Glu Asp
                490                 495                 500

aac cgg tagcgttgcg atctctcgtg gaa                                1632
Asn Arg
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<210> 1376
<211> 503
<212> PRT
<213> Corynebacterium glutamicum

<400> 1376

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Val Ile Asp Arg Pro Val Trp Leu Phe Glu Leu Tyr Asn Thr Ala Lys
  1               5                  10                  15

Glu Val Val Tyr Ser Leu Leu Ile Asp Gln Val Thr Gly Glu Asn Thr
            20                  25                  30

Ile Leu Lys Lys Asp Asp Gly Trp Arg Asp Gln Phe Met Ile Glu Ser
        35                  40                  45

Phe Phe Ala Tyr Asp Ser Glu Ala Asp Ala Thr Ser Trp Ser Gly Lys
```

```
     50                  55                  60

Asn Met Asn Ser Tyr Trp Phe Val Ser Asp Leu Ile Ser Asn Ile Ser
 65                  70                  75                  80

Phe Ala Glu Arg Ser Leu Glu Ser Phe Ser Trp Ala Leu Arg Asp Leu
                85                  90                  95

Glu Asp Leu Ser Ser Ser Glu Thr Glu Phe Glu Gly Leu Glu Glu Leu
            100                 105                 110

Asn Leu Lys Phe Ser Glu Leu Gln Glu Trp Tyr Thr Asn Leu Glu Leu
        115                 120                 125

Pro Phe Gln Pro Ser Ala Ala Asp Val Asp Glu Val Glu Gln Tyr Leu
    130                 135                 140

Gln Ala Glu Val Thr Arg Gln Arg Gly Asp Tyr Gln Trp Ser Pro Glu
145                 150                 155                 160

Phe Trp Ile Pro Lys Pro Asp Ser Tyr Tyr Ile Asp His Ala Leu Ala
                165                 170                 175

Val Val Thr Asp Val Leu Gly Ala Ile Glu Gln Gly Glu Leu Arg Glu
            180                 185                 190

Glu Val Glu Val Gln Gln Ala Leu Asp Glu Val Ser Glu Asn Trp Asn
        195                 200                 205

Pro Leu Glu Asp Ser Asp Tyr Tyr Leu Gln Asp His Arg Gly Arg Pro
    210                 215                 220

Val Gln Asp Leu Ser Arg Glu Met Glu Glu Leu Val Arg Cys Leu Met
225                 230                 235                 240

Leu Asp Gln Glu Trp Trp Gly Ala Glu Ala Arg Ile Arg Lys Leu Val
                245                 250                 255

Glu Ser Val Glu Trp Glu Asp Thr Gln Ala Ile Ser Ser Leu Ile Glu
            260                 265                 270

His Glu Gln Tyr Trp Glu Asp Gly Arg Phe Arg Pro Pro Leu His Lys
        275                 280                 285

Phe Ser Glu Gly Leu Asp Glu Pro Glu Pro Leu Pro Met Thr Arg Lys
    290                 295                 300

Met Ile Leu Ala Thr Asn His Pro Asp Val Leu Arg Val Asn Ile Ala
305                 310                 315                 320

Asp Tyr Tyr Gln Gln His Arg Arg Ile Ala Thr Gln Lys Val Glu Cys
                325                 330                 335

Tyr Lys Glu Val Leu Ala Leu Tyr Pro Glu Ile Leu Lys Lys Phe Asp
            340                 345                 350

Asp Ser Ser Phe Val Asn Arg His Trp Ile Tyr Arg Ala Phe Asp Arg
        355                 360                 365

Glu Gly Gln Leu Leu Tyr Ile Gly Glu Thr Ile Asn Pro Leu Val Arg
    370                 375                 380
```

```
Leu Arg Glu His Ala Gly Leu Gly Ser Ile Asn His Ala His His Arg
385                 390                 395                 400

Leu Val Ser Pro Trp Phe Ser Thr Met Ala Thr Phe His Leu Glu Ser
                405                 410                 415

Cys Phe Thr Gln Ala Glu Ala Lys Glu Lys Glu Ala Leu Tyr Ile Lys
            420                 425                 430

Leu Glu Gln Pro Arg Tyr Asn Lys Thr His Asn Ser Ala Arg Leu Ala
        435                 440                 445

Val Ser Glu Glu Gly Val Pro Val Asn Glu Val Pro Ser Arg Asn Asp
    450                 455                 460

Pro Arg Asn Val Gly Trp Lys Gly His Arg His Val Pro Pro Met Leu
465                 470                 475                 480

Pro Ile Val Ala Arg Val Val Asp Glu Ser Thr Thr Arg Glu Gly Tyr
                485                 490                 495

Ala Phe Tyr Glu Asp Asn Arg
            500


<210> 1377
<211> 1689
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1666)
<223> RXN02995

<400> 1377
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tcgcgcaaca gggatacaat gagcaaccgt gacgcagcaa ttg aac cac gca aag   115
                                        Leu Asn His Ala Lys
                                          1               5

gta aat caa cat ccc ggt caa gcc acc ctc cca gaa acc gca gag ggg   163
Val Asn Gln His Pro Gly Gln Ala Thr Leu Pro Glu Thr Ala Glu Gly
                 10                  15                  20

cag gtt cgc acc tac gag gta aaa acc tac ggc tgt cag atg aat gtg   211
Gln Val Arg Thr Tyr Glu Val Lys Thr Tyr Gly Cys Gln Met Asn Val
             25                  30                  35

cac gat tct gag cgc ctt tcg ggc ctg ctc gag gag gct gga tac gtt   259
His Asp Ser Glu Arg Leu Ser Gly Leu Leu Glu Glu Ala Gly Tyr Val
         40                  45                  50

gct gct ccg gag gac acc act ccg gat ctt gtc gta ttt aat acg tgc   307
Ala Ala Pro Glu Asp Thr Thr Pro Asp Leu Val Val Phe Asn Thr Cys
     55                  60                  65

gcc gtg cgt gaa aac gcc gat atg cgc ctc tat ggc act ttg ggc aac   355
Ala Val Arg Glu Asn Ala Asp Met Arg Leu Tyr Gly Thr Leu Gly Asn
```

```
 70                  75                  80                  85

ctg cgc agc gtg aaa gaa aag aac cca ggc atg caa atc gct gtc ggt   403
Leu Arg Ser Val Lys Glu Lys Asn Pro Gly Met Gln Ile Ala Val Gly
                90                  95                 100

ggt tgt ttg gct caa aaa gac aaa gat acc gtg gtg aaa aaa gca ccg   451
Gly Cys Leu Ala Gln Lys Asp Lys Asp Thr Val Val Lys Lys Ala Pro
            105                 110                 115

tgg gtg gac gtg gtg ttt ggt acc cac aac att ggt tcc ttg cca acc   499
Trp Val Asp Val Val Phe Gly Thr His Asn Ile Gly Ser Leu Pro Thr
        120                 125                 130

ttg ctt cag cgc gcg gag cac aat gcc caa gcg gaa gtc gaa att gtc   547
Leu Leu Gln Arg Ala Glu His Asn Ala Gln Ala Glu Val Glu Ile Val
    135                 140                 145

gat tcc ctc gag cag ttc ccg tca gta ctt cct gca aag cgc gag tct   595
Asp Ser Leu Glu Gln Phe Pro Ser Val Leu Pro Ala Lys Arg Glu Ser
150                 155                 160                 165

gct tac gct ggt tgg gtg tcc gta tca gtc gga tgt aac aac acc tgt   643
Ala Tyr Ala Gly Trp Val Ser Val Ser Val Gly Cys Asn Asn Thr Cys
                170                 175                 180

act ttc tgc atc gtt ccg tcg ctg cgc ggt aaa gag cag gac cgt cga   691
Thr Phe Cys Ile Val Pro Ser Leu Arg Gly Lys Glu Gln Asp Arg Arg
            185                 190                 195

cca gga gac atc ctc gca gag gta caa gca ctg gtg gat cag gga gtt   739
Pro Gly Asp Ile Leu Ala Glu Val Gln Ala Leu Val Asp Gln Gly Val
        200                 205                 210

acc gag gta act cta ctt ggc caa aac gta aat gct tac ggc gtg aac   787
Thr Glu Val Thr Leu Leu Gly Gln Asn Val Asn Ala Tyr Gly Val Asn
    215                 220                 225

ttt gtt gat cct gag cta gag cgc gat cgc agt gca ttt tcc aag ctg   835
Phe Val Asp Pro Glu Leu Glu Arg Asp Arg Ser Ala Phe Ser Lys Leu
230                 235                 240                 245

ctt cgt gcc tgt ggt gag atc gaa ggc ctc gag cgg gtt cgc ttc acc   883
Leu Arg Ala Cys Gly Glu Ile Glu Gly Leu Glu Arg Val Arg Phe Thr
                250                 255                 260

agc cct cac cct gca gaa ttc acc tct gat gtc att gac gcc atg gca   931
Ser Pro His Pro Ala Glu Phe Thr Ser Asp Val Ile Asp Ala Met Ala
            265                 270                 275

gag acc cca aac atc tgc ccg cag ctg cac atg cca ctg cag tcc gga   979
Glu Thr Pro Asn Ile Cys Pro Gln Leu His Met Pro Leu Gln Ser Gly
        280                 285                 290

tct gac aag gtg ctc aaa gag atg cgc cgt tcc tac cga tcc aag aag   1027
Ser Asp Lys Val Leu Lys Glu Met Arg Arg Ser Tyr Arg Ser Lys Lys
    295                 300                 305

ttc ctc tcc atc ttg gat gag gtc cgt gcg aag atc cct cac gcc tct   1075
Phe Leu Ser Ile Leu Asp Glu Val Arg Ala Lys Ile Pro His Ala Ser
310                 315                 320                 325
```

```
atc acc acc gat att att gtc gga ttc cct ggc gaa aca gag gag gat   1123
Ile Thr Thr Asp Ile Ile Val Gly Phe Pro Gly Glu Thr Glu Glu Asp
                330                 335                 340

ttc caa gca acc ctc gac gtt gtc aag aag gca cgc ttt act tct gct   1171
Phe Gln Ala Thr Leu Asp Val Val Lys Lys Ala Arg Phe Thr Ser Ala
            345                 350                 355

tac acc ttc caa tac agc cca cgc cct ggc acc cct gca gcg gaa tat   1219
Tyr Thr Phe Gln Tyr Ser Pro Arg Pro Gly Thr Pro Ala Ala Glu Tyr
        360                 365                 370

gaa aac cag ctt cca aaa gaa gtt gtg cag gaa cgc tac gag cgc ctc   1267
Glu Asn Gln Leu Pro Lys Glu Val Val Gln Glu Arg Tyr Glu Arg Leu
    375                 380                 385

atg gtc gtt cag gaa caa gtc tgc gaa gaa gaa aac caa aag ctc atc   1315
Met Val Val Gln Glu Gln Val Cys Glu Glu Glu Asn Gln Lys Leu Ile
390                 395                 400                 405

ggc acc acc gtc gaa ttg ctg gtc cag gct ggc gga ggc cgc aag aac   1363
Gly Thr Thr Val Glu Leu Leu Val Gln Ala Gly Gly Gly Arg Lys Asn
                410                 415                 420

gat gcc acc aag cgc atg agt ggt cgc gca cgc gat gga cgc ctc gtg   1411
Asp Ala Thr Lys Arg Met Ser Gly Arg Ala Arg Asp Gly Arg Leu Val
            425                 430                 435

cac ttt gcg cca gag ggc gac att gat ggt gag atc cgc ccc ggc gat   1459
His Phe Ala Pro Glu Gly Asp Ile Asp Gly Glu Ile Arg Pro Gly Asp
        440                 445                 450

ttt gtc act gtc acg gtg act gag gcc aag cct ttc ttc ctc atc gca   1507
Phe Val Thr Val Thr Val Thr Glu Ala Lys Pro Phe Phe Leu Ile Ala
    455                 460                 465

gac tcc ggt gtg cag acc cac cgc cgc acc aaa gct ggt gac aac tct   1555
Asp Ser Gly Val Gln Thr His Arg Arg Thr Lys Ala Gly Asp Asn Ser
470                 475                 480                 485

gca gtt ggt caa gtt cca acc aca gca ccg atc ggt gtg ggc ttg gga   1603
Ala Val Gly Gln Val Pro Thr Thr Ala Pro Ile Gly Val Gly Leu Gly
                490                 495                 500

ctg cca caa atc ggc gca cca aag gtg gct cct gcc aca gaa tct gcc   1651
Leu Pro Gln Ile Gly Ala Pro Lys Val Ala Pro Ala Thr Glu Ser Ala
            505                 510                 515

tgc tgc tcc att aac taaaaattgc aggctagaat aga                    1689
Cys Cys Ser Ile Asn
        520
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<210> 1378
<211> 522
<212> PRT
<213> Corynebacterium glutamicum

<400> 1378
Leu Asn His Ala Lys Val Asn Gln His Pro Gly Gln Ala Thr Leu Pro

```
  1               5                  10                  15
Glu Thr Ala Glu Gly Gln Val Arg Thr Tyr Glu Val Lys Thr Tyr Gly
            20                  25                  30
Cys Gln Met Asn Val His Asp Ser Glu Arg Leu Ser Gly Leu Leu Glu
        35                  40                  45
Glu Ala Gly Tyr Val Ala Ala Pro Glu Asp Thr Thr Pro Asp Leu Val
    50                  55                  60
Val Phe Asn Thr Cys Ala Val Arg Glu Asn Ala Asp Met Arg Leu Tyr
65                  70                  75                  80
Gly Thr Leu Gly Asn Leu Arg Ser Val Lys Glu Lys Asn Pro Gly Met
                85                  90                  95
Gln Ile Ala Val Gly Gly Cys Leu Ala Gln Lys Asp Lys Asp Thr Val
            100                 105                 110
Val Lys Lys Ala Pro Trp Val Asp Val Val Phe Gly Thr His Asn Ile
        115                 120                 125
Gly Ser Leu Pro Thr Leu Leu Gln Arg Ala Glu His Asn Ala Gln Ala
    130                 135                 140
Glu Val Glu Ile Val Asp Ser Leu Glu Gln Phe Pro Ser Val Leu Pro
145                 150                 155                 160
Ala Lys Arg Glu Ser Ala Tyr Ala Gly Trp Val Ser Val Ser Val Gly
                165                 170                 175
Cys Asn Asn Thr Cys Thr Phe Cys Ile Val Pro Ser Leu Arg Gly Lys
            180                 185                 190
Glu Gln Asp Arg Arg Pro Gly Asp Ile Leu Ala Glu Val Gln Ala Leu
        195                 200                 205
Val Asp Gln Gly Val Thr Glu Val Thr Leu Leu Gly Gln Asn Val Asn
    210                 215                 220
Ala Tyr Gly Val Asn Phe Val Asp Pro Glu Leu Glu Arg Asp Arg Ser
225                 230                 235                 240
Ala Phe Ser Lys Leu Leu Arg Ala Cys Gly Glu Ile Glu Gly Leu Glu
                245                 250                 255
Arg Val Arg Phe Thr Ser Pro His Pro Ala Glu Phe Thr Ser Asp Val
            260                 265                 270
Ile Asp Ala Met Ala Glu Thr Pro Asn Ile Cys Pro Gln Leu His Met
        275                 280                 285
Pro Leu Gln Ser Gly Ser Asp Lys Val Leu Lys Glu Met Arg Arg Ser
    290                 295                 300
Tyr Arg Ser Lys Lys Phe Leu Ser Ile Leu Asp Glu Val Arg Ala Lys
305                 310                 315                 320
Ile Pro His Ala Ser Ile Thr Thr Asp Ile Ile Val Gly Phe Pro Gly
                325                 330                 335
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Glu Thr Glu Glu Asp Phe Gln Ala Thr Leu Asp Val Val Lys Lys Ala
            340                 345                 350

Arg Phe Thr Ser Ala Tyr Thr Phe Gln Tyr Ser Pro Arg Pro Gly Thr
        355                 360                 365

Pro Ala Ala Glu Tyr Glu Asn Gln Leu Pro Lys Glu Val Val Gln Glu
    370                 375                 380

Arg Tyr Glu Arg Leu Met Val Val Gln Glu Gln Val Cys Glu Glu Glu
385                 390                 395                 400

Asn Gln Lys Leu Ile Gly Thr Thr Val Glu Leu Leu Val Gln Ala Gly
                405                 410                 415

Gly Gly Arg Lys Asn Asp Ala Thr Lys Arg Met Ser Gly Arg Ala Arg
            420                 425                 430

Asp Gly Arg Leu Val His Phe Ala Pro Glu Gly Asp Ile Asp Gly Glu
        435                 440                 445

Ile Arg Pro Gly Asp Phe Val Thr Val Thr Val Thr Glu Ala Lys Pro
    450                 455                 460

Phe Phe Leu Ile Ala Asp Ser Gly Val Gln Thr His Arg Arg Thr Lys
465                 470                 475                 480

Ala Gly Asp Asn Ser Ala Val Gly Gln Val Pro Thr Thr Ala Pro Ile
                485                 490                 495

Gly Val Gly Leu Gly Leu Pro Gln Ile Gly Ala Pro Lys Val Ala Pro
            500                 505                 510

Ala Thr Glu Ser Ala Cys Cys Ser Ile Asn
        515                 520
```

<210> 1379
<211> 752
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(729)
<223> RXN02997

<400> 1379

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ccc cta ccg ggc cag ccc ttt gag ggc gag gct tta acg ctt ata aac   48
Pro Leu Pro Gly Gln Pro Phe Glu Gly Glu Ala Leu Thr Leu Ile Asn
  1               5                  10                  15

gcc ctc ctc cac cac gcc gaa aac gtc gca gcc tcc aac ccc tgg aag   96
Ala Leu Leu His His Ala Glu Asn Val Ala Ala Ser Asn Pro Trp Lys
             20                  25                  30

cgc acc acc ttc cac acc gct cac atg cac cct cca ggg agt aat gcg   144
Arg Thr Thr Phe His Thr Ala His Met His Pro Pro Gly Ser Asn Ala
         35                  40                  45
```

```
gat tgt gac tac tgc ctg gtg ctg caa cgc cgc gga tac gtt aaa gcc   192
Asp Cys Asp Tyr Cys Leu Val Leu Gln Arg Arg Gly Tyr Val Lys Ala
     50                  55                  60

cac gaa gaa atc caa caa acc atc ccg ctt cct tca ggt gac tgg tcc   240
His Glu Glu Ile Gln Gln Thr Ile Pro Leu Pro Ser Gly Asp Trp Ser
 65                  70                  75                  80

gct gga gaa ttc acc gtg gtg gac gtt gaa ggc acc gcc ttc cca agc   288
Ala Gly Glu Phe Thr Val Val Asp Val Glu Gly Thr Ala Phe Pro Ser
                85                  90                  95

gcg ctg atc ccc agc atc gtg gaa ctc caa cac cgc gca gcc ctc gat   336
Ala Leu Ile Pro Ser Ile Val Glu Leu Gln His Arg Ala Ala Leu Asp
            100                 105                 110

gtg ccc cac gga aac tta agt gtt gcg cct gca cag tgg gat gaa cac   384
Val Pro His Gly Asn Leu Ser Val Ala Pro Ala Gln Trp Asp Glu His
        115                 120                 125

cgc ttg gcg cag caa tct gaa aga atc ctt aaa aca gga acg aaa ctg   432
Arg Leu Ala Gln Gln Ser Glu Arg Ile Leu Lys Thr Gly Thr Lys Leu
    130                 135                 140

ttc acc gta ctg ttt gcc gaa gga tcc aca gtc gct gcc atg tcc tcc   480
Phe Thr Val Leu Phe Ala Glu Gly Ser Thr Val Ala Ala Met Ser Ser
145                 150                 155                 160

atc gcg att ccc cca ggc tcc aac cct gac atc gcc gaa cag gga ctg   528
Ile Ala Ile Pro Pro Gly Ser Asn Pro Asp Ile Ala Glu Gln Gly Leu
                165                 170                 175

acc atc gtg cac cca gat ttc aga ggc cgt ggt ctt gga acc gct gtg   576
Thr Ile Val His Pro Asp Phe Arg Gly Arg Gly Leu Gly Thr Ala Val
            180                 185                 190

aaa tta gcg gga ctg tca cta ctt tcg agg tgc cac cca gaa att caa   624
Lys Leu Ala Gly Leu Ser Leu Leu Ser Arg Cys His Pro Glu Ile Gln
        195                 200                 205

cgc gta gcc acc tca aat gca gta gac aac cat gcg atg ctg gcg att   672
Arg Val Ala Thr Ser Asn Ala Val Asp Asn His Ala Met Leu Ala Ile
    210                 215                 220

aac cgc tcc ata ggg gca aca gag atc gcc cga acc acc ctg tgg gag   720
Asn Arg Ser Ile Gly Ala Thr Glu Ile Ala Arg Thr Thr Leu Trp Glu
225                 230                 235                 240

aag aaa ctc taggtgatgg aattcgagac caa                            752
Lys Lys Leu
```

Sequence Listing 20100222 ST25.txt

<210> 1380
<211> 243
<212> PRT
<213> Corynebacterium glutamicum

<400> 1380

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Pro Leu Pro Gly Gln Pro Phe Glu Gly Glu Ala Leu Thr Leu Ile Asn
  1               5                  10                  15
```

Ala Leu Leu His His Ala Glu Asn Val Ala Ala Ser Asn Pro Trp Lys
20 25 30

Arg Thr Thr Phe His Thr Ala His Met His Pro Pro Gly Ser Asn Ala
35 40 45

Asp Cys Asp Tyr Cys Leu Val Leu Gln Arg Arg Gly Tyr Val Lys Ala
50 55 60

His Glu Glu Ile Gln Gln Thr Ile Pro Leu Pro Ser Gly Asp Trp Ser
65 70 75 80

Ala Gly Glu Phe Thr Val Val Asp Val Glu Gly Thr Ala Phe Pro Ser
85 90 95

Ala Leu Ile Pro Ser Ile Val Glu Leu Gln His Arg Ala Ala Leu Asp
100 105 110

Val Pro His Gly Asn Leu Ser Val Ala Pro Ala Gln Trp Asp Glu His
115 120 125

Arg Leu Ala Gln Gln Ser Glu Arg Ile Leu Lys Thr Gly Thr Lys Leu
130 135 140

Phe Thr Val Leu Phe Ala Glu Gly Ser Thr Val Ala Ala Met Ser Ser
145 150 155 160

Ile Ala Ile Pro Pro Gly Ser Asn Pro Asp Ile Ala Glu Gln Gly Leu
165 170 175

Thr Ile Val His Pro Asp Phe Arg Gly Arg Gly Leu Gly Thr Ala Val
180 185 190

Lys Leu Ala Gly Leu Ser Leu Leu Ser Arg Cys His Pro Glu Ile Gln
195 200 205

Arg Val Ala Thr Ser Asn Ala Val Asp Asn His Ala Met Leu Ala Ile
210 215 220

Asn Arg Ser Ile Gly Ala Thr Glu Ile Ala Arg Thr Thr Leu Trp Glu
225 230 235 240

Lys Lys Leu

<210> 1381
<211> 553
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(553)
<223> RXN03001

<400> 1381
cccggttcac gtgatcaatg acttcacgag caccgatgaa atcgatgctg cgcttcgtga 60

acgctacgac atctaactac tttaaaagga cgaaaatatt atg gac tgg tta acc 115

```
                                                  Met Asp Trp Leu Thr
                                                    1               5

att cct ctt ttc ctc gtt aat gaa atc ctt gcg gtt ccg gct ttc ctc   163
Ile Pro Leu Phe Leu Val Asn Glu Ile Leu Ala Val Pro Ala Phe Leu
                10                  15                  20

atc ggt atc atc acc gcc gtg gga ttg ggt gcc atg ggg cgt tcc gtc   211
Ile Gly Ile Ile Thr Ala Val Gly Leu Gly Ala Met Gly Arg Ser Val
            25                  30                  35

ggt cag gtt atc ggt gga gca atc aaa gca acg ttg ggc ttt ttg ctc   259
Gly Gln Val Ile Gly Gly Ala Ile Lys Ala Thr Leu Gly Phe Leu Leu
        40                  45                  50

att ggt gcg ggt gcc acg ttg gtc act gcc tcc ctg gag cca ctg ggt   307
Ile Gly Ala Gly Ala Thr Leu Val Thr Ala Ser Leu Glu Pro Leu Gly
    55                  60                  65

gcg atg atc atg ggt gcc aca ggc atg cgt ggt gtt gtc cca acg aat   355
Ala Met Ile Met Gly Ala Thr Gly Met Arg Gly Val Val Pro Thr Asn
70                  75                  80                  85

gaa gcc atc gcc gga atc gca cag gct gaa tac ggc gcg cag gtg gcg   403
Glu Ala Ile Ala Gly Ile Ala Gln Ala Glu Tyr Gly Ala Gln Val Ala
                90                  95                  100

tgg ctg atg att ctg ggc ttc gcc atc tct ttg gtg ttg gct cgt ttc   451
Trp Leu Met Ile Leu Gly Phe Ala Ile Ser Leu Val Leu Ala Arg Phe
            105                 110                 115

acc aac ctg cgt tat gtc ttg ctc aac gga cac cac gtg ctg ttg atg   499
Thr Asn Leu Arg Tyr Val Leu Leu Asn Gly His His Val Leu Leu Met
        120                 125                 130

tgc acc atg ctc acc atg gtc ttg gcc acc gga aga gtt gat gcg tgg   547
Cys Thr Met Leu Thr Met Val Leu Ala Thr Gly Arg Val Asp Ala Trp
    135                 140                 145

atc ttc                                                           553
Ile Phe
150
```

<210> 1382
<211> 151
<212> PRT
<213> Corynebacterium glutamicum

<400> 1382

```
Met Asp Trp Leu Thr Ile Pro Leu Phe Leu Val Asn Glu Ile Leu Ala
  1               5                  10                  15

Val Pro Ala Phe Leu Ile Gly Ile Ile Thr Ala Val Gly Leu Gly Ala
            20                  25                  30

Met Gly Arg Ser Val Gly Gln Val Ile Gly Gly Ala Ile Lys Ala Thr
        35                  40                  45

Leu Gly Phe Leu Leu Ile Gly Ala Gly Ala Thr Leu Val Thr Ala Ser
    50                  55                  60
```

```
Leu Glu Pro Leu Gly Ala Met Ile Met Gly Ala Thr Gly Met Arg Gly
 65                  70                  75                  80

Val Val Pro Thr Asn Glu Ala Ile Ala Gly Ile Ala Gln Ala Glu Tyr
                85                  90                  95

Gly Ala Gln Val Ala Trp Leu Met Ile Leu Gly Phe Ala Ile Ser Leu
            100                 105                 110

Val Leu Ala Arg Phe Thr Asn Leu Arg Tyr Val Leu Leu Asn Gly His
        115                 120                 125

His Val Leu Leu Met Cys Thr Met Leu Thr Met Val Leu Ala Thr Gly
    130                 135                 140

Arg Val Asp Ala Trp Ile Phe
145                 150


<210> 1383
<211> 891
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(868)
<223> RXN03005

<400> 1383
taggtaaacc ttaaacagtc gccattgaag aattttaaaa acaaacaacc ttcaacgcgc 60

taacaagcat cttcccactc tcgttaccgg agtttctcac atg tct cac aag ttt   115
                                              Met Ser His Lys Phe
                                                1               5

tcc cgc cgt gct ttc gca gta ctg acc gct gcc gca att tcc act tcc   163
Ser Arg Arg Ala Phe Ala Val Leu Thr Ala Ala Ala Ile Ser Thr Ser
                10                  15                  20

gct ttc gca acc act gct ccg tct gcg att gca gag cca gtt cta atg   211
Ala Phe Ala Thr Thr Ala Pro Ser Ala Ile Ala Glu Pro Val Leu Met
            25                  30                  35

tcg cac tgc aga cga ttc cag cgt cgc aac ttc aga aaa ctc cct cga   259
Ser His Cys Arg Arg Phe Gln Arg Arg Asn Phe Arg Lys Leu Pro Arg
        40                  45                  50

ctg ggg ctt caa ggc ttc ctg gcg cac cta tgt cac cgg acc ttg gac   307
Leu Gly Leu Gln Gly Phe Leu Ala His Leu Cys His Arg Thr Leu Asp
    55                  60                  65

tgg tgg aac cgt gac gca act ggc ggt gca act gtc aac gaa gat gga   355
Trp Trp Asn Arg Asp Ala Thr Gly Gly Ala Thr Val Asn Glu Asp Gly
 70                  75                  80                  85

acc tac aac ttc acc ctc gga act ggc tcc aat tac gac gtc gac acc   403
Thr Tyr Asn Phe Thr Leu Gly Thr Gly Ser Asn Tyr Asp Val Asp Thr
                90                  95                  100
```

```
gag aag ggc cag ctg aac tac gaa gga act gtt gcc ttc gcc agt gac   451
Glu Lys Gly Gln Leu Asn Tyr Glu Gly Thr Val Ala Phe Ala Ser Asp
            105                 110                 115

gct cac ggc ttc aac atc acc ttg tcc aac ccg cag atc acc gtc gag   499
Ala His Gly Phe Asn Ile Thr Leu Ser Asn Pro Gln Ile Thr Val Glu
        120                 125                 130

ggc gac act gca act ttg agc gcc gag ctg tct gac aat gcc gct ccc   547
Gly Asp Thr Ala Thr Leu Ser Ala Glu Leu Ser Asp Asn Ala Ala Pro
    135                 140                 145

gaa gag acc tcc act act cgc gtt gat gtt gct gag ttc gaa ctg acc   595
Glu Glu Thr Ser Thr Thr Arg Val Asp Val Ala Glu Phe Glu Leu Thr
150                 155                 160                 165

gct cct gag gtt tca gaa acc gat gcg gac att acc tac acc tgg acc   643
Ala Pro Glu Val Ser Glu Thr Asp Ala Asp Ile Thr Tyr Thr Trp Thr
                170                 175                 180

gat gct tcc ggc act ttc ttg gag acc ctg cag cct gaa gaa ttg agc   691
Asp Ala Ser Gly Thr Phe Leu Glu Thr Leu Gln Pro Glu Glu Leu Ser
            185                 190                 195

cgt tac gca ggc cag gaa gcg gat gcg ctg agc ttc tcc atc acc gtg   739
Arg Tyr Ala Gly Gln Glu Ala Asp Ala Leu Ser Phe Ser Ile Thr Val
        200                 205                 210

gac aag gct tca gag aac cct tcc gat gat gtt gct acc gga tct tcc   787
Asp Lys Ala Ser Glu Asn Pro Ser Asp Asp Val Ala Thr Gly Ser Ser
    215                 220                 225

tcc agc ttc ctc tcc acc atc ttg aac ttc ctt cag cag ctg gcg agc   835
Ser Ser Phe Leu Ser Thr Ile Leu Asn Phe Leu Gln Gln Leu Ala Ser
230                 235                 240                 245

cca ctg ctc aag ctc ttc ggt tcg ctt tct tcc taaataatca gtaatgcccc 888
Pro Leu Leu Lys Leu Phe Gly Ser Leu Ser Ser
                250                 255

acc                                                               891
```

<210> 1384
<211> 256
<212> PRT
<213> Corynebacterium glutamicum

<400> 1384

```
Met Ser His Lys Phe Ser Arg Arg Ala Phe Ala Val Leu Thr Ala Ala
  1               5                  10                  15

Ala Ile Ser Thr Ser Ala Phe Ala Thr Thr Ala Pro Ser Ala Ile Ala
             20                  25                  30

Glu Pro Val Leu Met Ser His Cys Arg Arg Phe Gln Arg Arg Asn Phe
         35                  40                  45

Arg Lys Leu Pro Arg Leu Gly Leu Gln Gly Phe Leu Ala His Leu Cys
     50                  55                  60
```

```
His Arg Thr Leu Asp Trp Trp Asn Arg Asp Ala Thr Gly Gly Ala Thr
 65                  70                  75                  80

Val Asn Glu Asp Gly Thr Tyr Asn Phe Thr Leu Gly Thr Gly Ser Asn
                85                  90                  95

Tyr Asp Val Asp Thr Glu Lys Gly Gln Leu Asn Tyr Glu Gly Thr Val
            100                 105                 110

Ala Phe Ala Ser Asp Ala His Gly Phe Asn Ile Thr Leu Ser Asn Pro
        115                 120                 125

Gln Ile Thr Val Glu Gly Asp Thr Ala Thr Leu Ser Ala Glu Leu Ser
    130                 135                 140

Asp Asn Ala Ala Pro Glu Glu Thr Ser Thr Thr Arg Val Asp Val Ala
145                 150                 155                 160

Glu Phe Glu Leu Thr Ala Pro Glu Val Ser Glu Thr Asp Ala Asp Ile
                165                 170                 175

Thr Tyr Thr Trp Thr Asp Ala Ser Gly Thr Phe Leu Glu Thr Leu Gln
            180                 185                 190

Pro Glu Glu Leu Ser Arg Tyr Ala Gly Gln Glu Ala Asp Ala Leu Ser
        195                 200                 205

Phe Ser Ile Thr Val Asp Lys Ala Ser Glu Asn Pro Ser Asp Asp Val
    210                 215                 220

Ala Thr Gly Ser Ser Ser Ser Phe Leu Ser Thr Ile Leu Asn Phe Leu
225                 230                 235                 240

Gln Gln Leu Ala Ser Pro Leu Leu Lys Leu Phe Gly Ser Leu Ser Ser
                245                 250                 255
```

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<210> 1385
<211> 448
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(448)
<223> RXN03009

<400> 1385
atgtgaacct gatgctggca cctgaagata gccacagccc aggcaccgca acagtgacct 60

accgtcatgg tttcagcgat caccgtttac cctgcactgc gtg gct aat atc gcc 115
                                            Val Ala Asn Ile Ala
                                              1   5

agc ttg tac gga ctg tgg gaa ggc agc aca tcc aca cca atc gaa cag 163
Ser Leu Tyr Gly Leu Trp Glu Gly Ser Thr Ser Thr Pro Ile Glu Gln
                10   15   20

```
ctc gta cct gcg aaa ggt tcc agc ttt cgt ttg gtg agg tct ttt tac   211
Leu Val Pro Ala Lys Gly Ser Ser Phe Arg Leu Val Arg Ser Phe Tyr
            25                  30                  35

agg cga att gac ggc caa gca gtt cag gct cgt ctc aag gag aag att   259
Arg Arg Ile Asp Gly Gln Ala Val Gln Ala Arg Leu Lys Glu Lys Ile
        40                  45                  50

ctc aac acc gcg gaa aac ccg ctt cct cgc ttg gac att cca ggt aag   307
Leu Asn Thr Ala Glu Asn Pro Leu Pro Arg Leu Asp Ile Pro Gly Lys
    55                  60                  65

gag cgc act gcg cag tac cca gaa aat ccg gat acc ttc gcc caa aaa   355
Glu Arg Thr Ala Gln Tyr Pro Glu Asn Pro Asp Thr Phe Ala Gln Lys
70                  75                  80                  85

gca gct caa gaa att ctt gat gag ttc aga act cca ctg atc ggt gaa   403
Ala Ala Gln Glu Ile Leu Asp Glu Phe Arg Thr Pro Leu Ile Gly Glu
                90                  95                  100

gaa gct gca gct cat gtt gag aaa acg aag acg att ttc tgg aag       448
Glu Ala Ala Ala His Val Glu Lys Thr Lys Thr Ile Phe Trp Lys
            105                 110                 115
```

<210> 1386
<211> 116
<212> PRT
<213> Corynebacterium glutamicum

<400> 1386

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Val Ala Asn Ile Ala Ser Leu Tyr Gly Leu Trp Glu Gly Ser Thr Ser
  1               5                  10                  15

Thr Pro Ile Glu Gln Leu Val Pro Ala Lys Gly Ser Ser Phe Arg Leu
            20                  25                  30

Val Arg Ser Phe Tyr Arg Arg Ile Asp Gly Gln Ala Val Gln Ala Arg
        35                  40                  45

Leu Lys Glu Lys Ile Leu Asn Thr Ala Glu Asn Pro Leu Pro Arg Leu
    50                  55                  60

Asp Ile Pro Gly Lys Glu Arg Thr Ala Gln Tyr Pro Glu Asn Pro Asp
65                  70                  75                  80

Thr Phe Ala Gln Lys Ala Ala Gln Glu Ile Leu Asp Glu Phe Arg Thr
                85                  90                  95

Pro Leu Ile Gly Glu Glu Ala Ala Ala His Val Glu Lys Thr Lys Thr
            100                 105                 110

Ile Phe Trp Lys
        115
```

<210> 1387
<211> 360
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(337)
<223> RXN03010

<400> 1387
tgggcgcctt caatcggcac ccactgaatg gattcttccg ggcctagttt tagggctgat 60

cagcctggga ctcaatgcgt ggattacctt cggtgcgcca gtg ccc acc gat aat 115
Val Pro Thr Asp Asn
1 5

ctt ttt ctc atc gtt gct gga att gcg tgg gtg ttg gca gga att ttg 163
Leu Phe Leu Ile Val Ala Gly Ile Ala Trp Val Leu Ala Gly Ile Leu
10 15 20

agc gtg ctg tcc atc ggc aag tac atg tca gca gta aat gag cga aag 211
Ser Val Leu Ser Ile Gly Lys Tyr Met Ser Ala Val Asn Glu Arg Lys
25 30 35

tcg aca ggc ttt tat aca gaa gtg ccg tgg aag aaa gcg ctc ttt act 259
Ser Thr Gly Phe Tyr Thr Glu Val Pro Trp Lys Lys Ala Leu Phe Thr
40 45 50

gcg aca gcc gtc cta ttg gtg ttt gct gtt gtg tgg tcg gcc ttg gat 307
Ala Thr Ala Val Leu Leu Val Phe Ala Val Val Trp Ser Ala Leu Asp
55 60 65

att gcc ctg tgg gta gga aag cag tca tgg tgaacacgtt gaactctaaa 357
Ile Ala Leu Trp Val Gly Lys Gln Ser Trp
70 75

acc 360

<210> 1388
<211> 79
<212> PRT
<213> Corynebacterium glutamicum

<400> 1388
Val Pro Thr Asp Asn Leu Phe Leu Ile Val Ala Gly Ile Ala Trp Val
1 5 10 15

Leu Ala Gly Ile Leu Ser Val Leu Ser Ile Gly Lys Tyr Met Ser Ala
20 25 30

Val Asn Glu Arg Lys Ser Thr Gly Phe Tyr Thr Glu Val Pro Trp Lys
35 40 45

Lys Ala Leu Phe Thr Ala Thr Ala Val Leu Leu Val Phe Ala Val Val
50 55 60

Trp Ser Ala Leu Asp Ile Ala Leu Trp Val Gly Lys Gln Ser Trp
65 70 75

<210> 1389
<211> 324
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(301)
<223> RXN03011

<400> 1389
ccgacgtacc agtttttgtc gttccacccc tggactaaaa ccgagacgag aaccaagaag 60

atgaaaccaa ggggtaaaaa ctggtagtct cttccacgtc atg gca tac gaa act 115
Met Ala Tyr Glu Thr
1 5

gat tcc ctc aac cga cgc acc ctc ggg ccc gcg att gca agc gca gtc 163
Asp Ser Leu Asn Arg Arg Thr Leu Gly Pro Ala Ile Ala Ser Ala Val
10 15 20

gtg gga atc gcc gtc ggc gca gtc gca gta gtt ggg gtt tca atg atc 211
Val Gly Ile Ala Val Gly Ala Val Ala Val Val Gly Val Ser Met Ile
25 30 35

tca ggg cag gac act gtt ccc act ggt aac gcc gta act gca gac gat 259
Ser Gly Gln Asp Thr Val Pro Thr Gly Asn Ala Val Thr Ala Asp Asp
40 45 50

gcc ctg ctc ggt ggc cct gag tat ggt tca cgc gaa gca gac 301
Ala Leu Leu Gly Gly Pro Glu Tyr Gly Ser Arg Glu Ala Asp
55 60 65

taagaagcca cttccccgtt ttc 324

<210> 1390
<211> 67
<212> PRT
<213> Corynebacterium glutamicum

<400> 1390
Met Ala Tyr Glu Thr Asp Ser Leu Asn Arg Arg Thr Leu Gly Pro Ala
1 5 10 15

Ile Ala Ser Ala Val Val Gly Ile Ala Val Gly Ala Val Ala Val Val
20 25 30

Gly Val Ser Met Ile Ser Gly Gln Asp Thr Val Pro Thr Gly Asn Ala
35 40 45

Val Thr Ala Asp Asp Ala Leu Leu Gly Gly Pro Glu Tyr Gly Ser Arg
50 55 60

Glu Ala Asp
65

<210> 1391
<211> 593
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (1)..(570)
<223> RXN03012

<400> 1391

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acc act atc aac atc atc atc acc aat ggc gct gca cca cac cca act   48
Thr Thr Ile Asn Ile Ile Ile Thr Asn Gly Ala Ala Pro His Pro Thr
  1               5                  10                  15

aat ctc aat cgc gca gaa att cat gat cac cta ccc ctc act gcc tct   96
Asn Leu Asn Arg Ala Glu Ile His Asp His Leu Pro Leu Thr Ala Ser
             20                  25                  30

gat tcg gag cta acc cgc ccc tcc cag gaa tca gtt ctc tat gac cat  144
Asp Ser Glu Leu Thr Arg Pro Ser Gln Glu Ser Val Leu Tyr Asp His
         35                  40                  45

gaa tcc gaa act gtc ttg cgc acc atg gtc atc cct gca gac ctg cac  192
Glu Ser Glu Thr Val Leu Arg Thr Met Val Ile Pro Ala Asp Leu His
     50                  55                  60

gtc gct atg aag cat cta gct aaa aaa cac aac ctc acg gtc aca gag  240
Val Ala Met Lys His Leu Ala Lys Lys His Asn Leu Thr Val Thr Glu
 65                  70                  75                  80

atc tcg cgc atc ctt ctg cag cgc tac atc gac cgc aat att aac cat  288
Ile Ser Arg Ile Leu Leu Gln Arg Tyr Ile Asp Arg Asn Ile Asn His
                 85                  90                  95

gta gag caa aac cag gct gaa tcc gac atg gtg gaa gtc ttt gcc agc  336
Val Glu Gln Asn Gln Ala Glu Ser Asp Met Val Glu Val Phe Ala Ser
            100                 105                 110

caa cca acc aat gca acc gca atg atc cct gta cct gga acc agc ttc  384
Gln Pro Thr Asn Ala Thr Ala Met Ile Pro Val Pro Gly Thr Ser Phe
        115                 120                 125

agg caa ata ttt atc aag cac agc act ggt ttc tgg aaa aac att gat  432
Arg Gln Ile Phe Ile Lys His Ser Thr Gly Phe Trp Lys Asn Ile Asp
    130                 135                 140

cat gat ctt gtc gat ctc gac gcc tct aag acc ccg cgt gta cgc gac  480
His Asp Leu Val Asp Leu Asp Ala Ser Lys Thr Pro Arg Val Arg Asp
145                 150                 155                 160

cgc agt gtc tta cca caa cct caa ctc cac aga gcg ttg tta tca gat  528
Arg Ser Val Leu Pro Gln Pro Gln Leu His Arg Ala Leu Leu Ser Asp
                165                 170                 175

gct gat atg gct cgc ctt gca gca caa ctg acc gac aaa cac          570
Ala Asp Met Ala Arg Leu Ala Ala Gln Leu Thr Asp Lys His
            180                 185                 190

taaaacctcc acaacaagga cat                                       593
```

<210> 1392
<211> 190
<212> PRT
<213> Corynebacterium glutamicum

<400> 1392

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Thr Thr Ile Asn Ile Ile Ile Thr Asn Gly Ala Ala Pro His Pro Thr
  1               5                  10                  15

Asn Leu Asn Arg Ala Glu Ile His Asp His Leu Pro Leu Thr Ala Ser
             20                  25                  30

Asp Ser Glu Leu Thr Arg Pro Ser Gln Glu Ser Val Leu Tyr Asp His
         35                  40                  45

Glu Ser Glu Thr Val Leu Arg Thr Met Val Ile Pro Ala Asp Leu His
     50                  55                  60

Val Ala Met Lys His Leu Ala Lys Lys His Asn Leu Thr Val Thr Glu
 65                  70                  75                  80

Ile Ser Arg Ile Leu Leu Gln Arg Tyr Ile Asp Arg Asn Ile Asn His
                 85                  90                  95

Val Glu Gln Asn Gln Ala Glu Ser Asp Met Val Glu Val Phe Ala Ser
            100                 105                 110

Gln Pro Thr Asn Ala Thr Ala Met Ile Pro Val Pro Gly Thr Ser Phe
        115                 120                 125

Arg Gln Ile Phe Ile Lys His Ser Thr Gly Phe Trp Lys Asn Ile Asp
    130                 135                 140

His Asp Leu Val Asp Leu Asp Ala Ser Lys Thr Pro Arg Val Arg Asp
145                 150                 155                 160

Arg Ser Val Leu Pro Gln Pro Gln Leu His Arg Ala Leu Leu Ser Asp
                165                 170                 175

Ala Asp Met Ala Arg Leu Ala Ala Gln Leu Thr Asp Lys His
            180                 185                 190


<210> 1393
<211> 1662
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1639)
<223> RXN03017

<400> 1393
aactcaatat taaagtcgcg taattagtgt tatattaatt acgcgacttt aatagttttc 60

gaatacgtag attctcgaaa tacagcagaa agcaggggtt atg ctc gat tca ttg   115
                                                Met Leu Asp Ser Leu
                                                  1               5

aaa aat cgc ttc acc aaa gcg aaa ggt tct cat gga gtg ggg gag ggg   163
Lys Asn Arg Phe Thr Lys Ala Lys Gly Ser His Gly Val Gly Glu Gly
                10                  15                  20

gct gtt tct ggc gat gca gca gta aag cca ctg cgc aaa gaa gaa cga   211
Ala Val Ser Gly Asp Ala Ala Val Lys Pro Leu Arg Lys Glu Glu Arg
            25                  30                  35
```

```
ctc gcc tca gtc att cag gaa acc gaa cca ggt gct gca gtc gag gtc   259
Leu Ala Ser Val Ile Gln Glu Thr Glu Pro Gly Ala Ala Val Glu Val
         40                  45                  50

atg cgt cgc aat gac gca ttc gct ttg cca ggt gag acc ggt tgg gta   307
Met Arg Arg Asn Asp Ala Phe Ala Leu Pro Gly Glu Thr Gly Trp Val
     55                  60                  65

gtc atg ctg ttg cca act cac gat tca caa ttc ggt ggg ctc aac gct   355
Val Met Leu Leu Pro Thr His Asp Ser Gln Phe Gly Gly Leu Asn Ala
 70                  75                  80                  85

aag gaa aag aac cgc gag gat aaa ggc acg atc atc aac ctg gtg gtc   403
Lys Glu Lys Asn Arg Glu Asp Lys Gly Thr Ile Ile Asn Leu Val Val
                 90                  95                 100

aac gat gat att cat tcc gtt gtc act cca gaa ctt ctt gac agc gat   451
Asn Asp Asp Ile His Ser Val Val Thr Pro Glu Leu Leu Asp Ser Asp
            105                 110                 115

gtg ctt ggt gtc att cct gat gca gat tct ttc gat cgc atg gat gag   499
Val Leu Gly Val Ile Pro Asp Ala Asp Ser Phe Asp Arg Met Asp Glu
        120                 125                 130

ttt gat tta ctg cgt aac aaa gca cgc tgg cac tac gga gtg gct gca   547
Phe Asp Leu Leu Arg Asn Lys Ala Arg Trp His Tyr Gly Val Ala Ala
    135                 140                 145

att gaa cct gac acg ggt gag ctg gtg gtg ttt aag gtg ccc gcg aaa   595
Ile Glu Pro Asp Thr Gly Glu Leu Val Val Phe Lys Val Pro Ala Lys
150                 155                 160                 165

aat agc gct tcg gca cgc ggt gac att ttt tcc gag gtc ggc gat gtg   643
Asn Ser Ala Ser Ala Arg Gly Asp Ile Phe Ser Glu Val Gly Asp Val
                170                 175                 180

ctt agc ggt gct gct gac ctc gaa gac gtg gtt gat ttt gag gtc att   691
Leu Ser Gly Ala Ala Asp Leu Glu Asp Val Val Asp Phe Glu Val Ile
            185                 190                 195

gcc acc ttc cta gag gtg ctg aat gag acc tct gag gtg gat att gat   739
Ala Thr Phe Leu Glu Val Leu Asn Glu Thr Ser Glu Val Asp Ile Asp
        200                 205                 210

gac gaa gat ggc gac gtg cct tat ggt ctt gag ggt gtc aat gca gcg   787
Asp Glu Asp Gly Asp Val Pro Tyr Gly Leu Glu Gly Val Asn Ala Ala
    215                 220                 225

gga gtt atc acg gat gac ctc att cgc gag aag ctt gat gtg gat tcc   835
Gly Val Ile Thr Asp Asp Leu Ile Arg Glu Lys Leu Asp Val Asp Ser
230                 235                 240                 245

tat ccg agc agt gca gag atc att gac aat att gtg cat gtg ttc acc   883
Tyr Pro Ser Ser Ala Glu Ile Ile Asp Asn Ile Val His Val Phe Thr
                250                 255                 260

aag ttg cag ggc aag cat cat gtg gca cca cag ccg gtg ctt cac agc   931
Lys Leu Gln Gly Lys His His Val Ala Pro Gln Pro Val Leu His Ser
            265                 270                 275
```

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gca gac gta gtg gat gtt gat gca cag gag tcc cat gac aca gtg gtt   979
Ala Asp Val Val Asp Val Asp Ala Gln Glu Ser His Asp Thr Val Val
        280                 285                 290

att gag agc cct gat gat gtc gca cta gca gaa cag gtg gat gta ccg   1027
Ile Glu Ser Pro Asp Asp Val Ala Leu Ala Glu Gln Val Asp Val Pro
    295                 300                 305

gat ttc agt gat gga ttt ggt att gac gat gcc gag gtt act gag cca   1075
Asp Phe Ser Asp Gly Phe Gly Ile Asp Asp Ala Glu Val Thr Glu Pro
310                 315                 320                 325

gag gat gag gag gtt gtc gaa gca aca gct gat gca gat cct ttt ggt   1123
Glu Asp Glu Glu Val Val Glu Ala Thr Ala Asp Ala Asp Pro Phe Gly
                330                 335                 340

gat gta gca gaa gac gat cct ttc ggc agt gat gat gaa cca gat ttt   1171
Asp Val Ala Glu Asp Asp Pro Phe Gly Ser Asp Asp Glu Pro Asp Phe
            345                 350                 355

ggt gca tcc gat gtt gtt gct gca ccg gca cct gta gcc ggc atg tcc   1219
Gly Ala Ser Asp Val Val Ala Ala Pro Ala Pro Val Ala Gly Met Ser
        360                 365                 370

gat gag cag atc cag gcg ctg att cgt ggt gtg tct gag tcc gtg caa   1267
Asp Glu Gln Ile Gln Ala Leu Ile Arg Gly Val Ser Glu Ser Val Gln
    375                 380                 385

gca aag act ggt tca gaa ctt aat gct ttg cga gaa gaa ctt gca caa   1315
Ala Lys Thr Gly Ser Glu Leu Asn Ala Leu Arg Glu Glu Leu Ala Gln
390                 395                 400                 405

gca ctg gct tac aat ccg gtt cag gat tca cag gca gca ttg gca cag   1363
Ala Leu Ala Tyr Asn Pro Val Gln Asp Ser Gln Ala Ala Leu Ala Gln
                410                 415                 420

gtg cac gca gct gat gcc cgc agc ttt gat gcc gat caa gtg ggt gat   1411
Val His Ala Ala Asp Ala Arg Ser Phe Asp Ala Asp Gln Val Gly Asp
            425                 430                 435

gct gtc acc aaa cgt tat gtt aat gac gac ttg ggg ctg tat gtc gat   1459
Ala Val Thr Lys Arg Tyr Val Asn Asp Asp Leu Gly Leu Tyr Val Asp
        440                 445                 450

gag gca aac ttc aat aat gct ttg acc agg gca ccg ttc cag gtg gcg   1507
Glu Ala Asn Phe Asn Asn Ala Leu Thr Arg Ala Pro Phe Gln Val Ala
    455                 460                 465

atg ccg caa ttc cag gag act aca ccg tgg tta ggt gat cag ctt cgt   1555
Met Pro Gln Phe Gln Glu Thr Thr Pro Trp Leu Gly Asp Gln Leu Arg
470                 475                 480                 485

aca ttg gtg gct gtg ttt aat ggt cag ctg ctt gat cag cat cag cgt   1603
Thr Leu Val Ala Val Phe Asn Gly Gln Leu Leu Asp Gln His Gln Arg
                490                 495                 500

gac tac cga aga agt gcg cgc gat gta cat tgc gct taatgatcgc       1649
Asp Tyr Arg Arg Ser Ala Arg Asp Val His Cys Ala
            505                 510

tctaatcttg aga                                                  1662
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<210> 1394
<211> 513
<212> PRT
<213> Corynebacterium glutamicum

<400> 1394

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Met Leu Asp Ser Leu Lys Asn Arg Phe Thr Lys Ala Lys Gly Ser His
  1               5                  10                  15

Gly Val Gly Glu Gly Ala Val Ser Gly Asp Ala Ala Val Lys Pro Leu
             20                  25                  30

Arg Lys Glu Glu Arg Leu Ala Ser Val Ile Gln Glu Thr Glu Pro Gly
         35                  40                  45

Ala Ala Val Glu Val Met Arg Arg Asn Asp Ala Phe Ala Leu Pro Gly
     50                  55                  60

Glu Thr Gly Trp Val Val Met Leu Leu Pro Thr His Asp Ser Gln Phe
 65                  70                  75                  80

Gly Gly Leu Asn Ala Lys Glu Lys Asn Arg Glu Asp Lys Gly Thr Ile
                 85                  90                  95

Ile Asn Leu Val Val Asn Asp Asp Ile His Ser Val Val Thr Pro Glu
            100                 105                 110

Leu Leu Asp Ser Asp Val Leu Gly Val Ile Pro Asp Ala Asp Ser Phe
        115                 120                 125

Asp Arg Met Asp Glu Phe Asp Leu Leu Arg Asn Lys Ala Arg Trp His
    130                 135                 140

Tyr Gly Val Ala Ala Ile Glu Pro Asp Thr Gly Glu Leu Val Val Phe
145                 150                 155                 160

Lys Val Pro Ala Lys Asn Ser Ala Ser Ala Arg Gly Asp Ile Phe Ser
                165                 170                 175

Glu Val Gly Asp Val Leu Ser Gly Ala Ala Asp Leu Glu Asp Val Val
            180                 185                 190

Asp Phe Glu Val Ile Ala Thr Phe Leu Glu Val Leu Asn Glu Thr Ser
        195                 200                 205

Glu Val Asp Ile Asp Asp Glu Asp Gly Asp Val Pro Tyr Gly Leu Glu
    210                 215                 220

Gly Val Asn Ala Ala Gly Val Ile Thr Asp Asp Leu Ile Arg Glu Lys
225                 230                 235                 240

Leu Asp Val Asp Ser Tyr Pro Ser Ser Ala Glu Ile Ile Asp Asn Ile
                245                 250                 255

Val His Val Phe Thr Lys Leu Gln Gly Lys His His Val Ala Pro Gln
            260                 265                 270

Pro Val Leu His Ser Ala Asp Val Val Asp Val Asp Ala Gln Glu Ser
        275                 280                 285
```

His Asp Thr Val Val Ile Glu Ser Pro Asp Asp Val Ala Leu Ala Glu
290 295 300

Gln Val Asp Val Pro Asp Phe Ser Asp Gly Phe Gly Ile Asp Asp Ala
305 310 315 320

Glu Val Thr Glu Pro Glu Asp Glu Glu Val Val Glu Ala Thr Ala Asp
325 330 335

Ala Asp Pro Phe Gly Asp Val Ala Glu Asp Asp Pro Phe Gly Ser Asp
340 345 350

Asp Glu Pro Asp Phe Gly Ala Ser Asp Val Val Ala Ala Pro Ala Pro
355 360 365

Val Ala Gly Met Ser Asp Glu Gln Ile Gln Ala Leu Ile Arg Gly Val
370 375 380

Ser Glu Ser Val Gln Ala Lys Thr Gly Ser Glu Leu Asn Ala Leu Arg
385 390 395 400

Glu Glu Leu Ala Gln Ala Leu Ala Tyr Asn Pro Val Gln Asp Ser Gln
405 410 415

Ala Ala Leu Ala Gln Val His Ala Ala Asp Ala Arg Ser Phe Asp Ala
420 425 430

Asp Gln Val Gly Asp Ala Val Thr Lys Arg Tyr Val Asn Asp Asp Leu
435 440 445

Gly Leu Tyr Val Asp Glu Ala Asn Phe Asn Asn Ala Leu Thr Arg Ala
450 455 460

Pro Phe Gln Val Ala Met Pro Gln Phe Gln Glu Thr Thr Pro Trp Leu
465 470 475 480

Gly Asp Gln Leu Arg Thr Leu Val Ala Val Phe Asn Gly Gln Leu Leu
485 490 495

Asp Gln His Gln Arg Asp Tyr Arg Arg Ser Ala Arg Asp Val His Cys
500 505 510

Ala

<210> 1395
<211> 2616
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(2593)
<223> FRXA02753

<400> 1395
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gaatacgtag attctcgaaa tacagcagaa agcaggggtt atg ctc gat tca ttg 115

```
                                                  Met Leu Asp Ser Leu
                                                    1               5

aaa aat cgc ttc acc aaa gcg aaa ggt tct cat gga gtg ggg gag ggg   163
Lys Asn Arg Phe Thr Lys Ala Lys Gly Ser His Gly Val Gly Glu Gly
                10                  15                  20

gct gtt tct ggc gat gca gca gta aag cca ctg cgc aaa gaa gaa cga   211
Ala Val Ser Gly Asp Ala Ala Val Lys Pro Leu Arg Lys Glu Glu Arg
            25                  30                  35

ctc gcc tca gtc att cag gaa acc gaa cca ggt gct gca gtc gag gtc   259
Leu Ala Ser Val Ile Gln Glu Thr Glu Pro Gly Ala Ala Val Glu Val
        40                  45                  50

atg cgt cgc aat gac gca ttc gct ttg cca ggt gag acc ggt tgg gta   307
Met Arg Arg Asn Asp Ala Phe Ala Leu Pro Gly Glu Thr Gly Trp Val
    55                  60                  65

gtc atg ctg ttg cca act cac gat tca caa ttc ggt ggg ctc aac gct   355
Val Met Leu Leu Pro Thr His Asp Ser Gln Phe Gly Gly Leu Asn Ala
70                  75                  80                  85

aag gaa aag aac cgc gag gat aaa ggc acg atc atc aac ctg gtg gtc   403
Lys Glu Lys Asn Arg Glu Asp Lys Gly Thr Ile Ile Asn Leu Val Val
                90                  95                  100

aac gat gat att cat tcc gtt gtc act cca gaa ctt ctt gac agc gat   451
Asn Asp Asp Ile His Ser Val Val Thr Pro Glu Leu Leu Asp Ser Asp
            105                 110                 115

gtg ctt ggt gtc att cct gat gca gat tct ttc gat cgc atg gat gag   499
Val Leu Gly Val Ile Pro Asp Ala Asp Ser Phe Asp Arg Met Asp Glu
        120                 125                 130

ttt gat tta ctg cgt aac aaa gca cgc tgg cac tac gga gtg gct gca   547
Phe Asp Leu Leu Arg Asn Lys Ala Arg Trp His Tyr Gly Val Ala Ala
    135                 140                 145

att gaa cct gac acg ggt gag ctg gtg gtg ttt aag gtg ccc gcg aaa   595
Ile Glu Pro Asp Thr Gly Glu Leu Val Val Phe Lys Val Pro Ala Lys
150                 155                 160                 165

aat agc gct tcg gca cgc ggt gac att ttt tcc gag gtc ggc gat gtg   643
Asn Ser Ala Ser Ala Arg Gly Asp Ile Phe Ser Glu Val Gly Asp Val
                170                 175                 180

ctt agc ggt gct gct gac ctc gaa gac gtg gtt gat ttt gag gtc att   691
Leu Ser Gly Ala Ala Asp Leu Glu Asp Val Val Asp Phe Glu Val Ile
            185                 190                 195

gcc acc ttc cta gag gtg ctg aat gag acc tct gag gtg gat att gat   739
Ala Thr Phe Leu Glu Val Leu Asn Glu Thr Ser Glu Val Asp Ile Asp
        200                 205                 210

gac gaa gat ggc gac gtg cct tat ggt ctt gag ggt gtc aat gca gcg   787
Asp Glu Asp Gly Asp Val Pro Tyr Gly Leu Glu Gly Val Asn Ala Ala
    215                 220                 225

gga gtt atc acg gat gac ctc att cgc gag aag ctt gat gtg gat tcc   835
Gly Val Ile Thr Asp Asp Leu Ile Arg Glu Lys Leu Asp Val Asp Ser
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230                 235                 240                 245

tat ccg agc agt gca gag atc att gac aat att gtg cat gtg ttc acc   883
Tyr Pro Ser Ser Ala Glu Ile Ile Asp Asn Ile Val His Val Phe Thr
                250                 255                 260

aag ttg cag ggc aag cat cat gtg gca cca cag ccg gtg ctt cac agc   931
Lys Leu Gln Gly Lys His His Val Ala Pro Gln Pro Val Leu His Ser
            265                 270                 275

gca gac gta gtg gat gtt gat gca cag gag tcc cat gac aca gtg gtt   979
Ala Asp Val Val Asp Val Asp Ala Gln Glu Ser His Asp Thr Val Val
        280                 285                 290

att gag agc cct gat gat gtc gca cta gca gaa cag gtg gat gta ccg   1027
Ile Glu Ser Pro Asp Asp Val Ala Leu Ala Glu Gln Val Asp Val Pro
    295                 300                 305

gat ttc agt gat gga ttt ggt att gac gat gcc gag gtt act gag cca   1075
Asp Phe Ser Asp Gly Phe Gly Ile Asp Asp Ala Glu Val Thr Glu Pro
310                 315                 320                 325

gag gat gag gag gtt gtc gaa gca aca gct gat gca gat cct ttt ggt   1123
Glu Asp Glu Glu Val Val Glu Ala Thr Ala Asp Ala Asp Pro Phe Gly
                330                 335                 340

gat gta gca gaa gac gat cct ttc ggc agt gat gat gaa cca gat ttt   1171
Asp Val Ala Glu Asp Asp Pro Phe Gly Ser Asp Asp Glu Pro Asp Phe
            345                 350                 355

ggt gca tcc gat gtt gtt gct gca ccg gca cct gta gcc ggc atg tcc   1219
Gly Ala Ser Asp Val Val Ala Ala Pro Ala Pro Val Ala Gly Met Ser
        360                 365                 370

gat gag cag atc cag gcg ctg att cgt ggt gtg tct gag tcc gtg caa   1267
Asp Glu Gln Ile Gln Ala Leu Ile Arg Gly Val Ser Glu Ser Val Gln
    375                 380                 385

gca aag act ggt tca gaa ctt aat gct ttg cga gaa gaa ctt gca caa   1315
Ala Lys Thr Gly Ser Glu Leu Asn Ala Leu Arg Glu Glu Leu Ala Gln
390                 395                 400                 405

gca ctg gct tac aat ccg gtt cag gat tca cag gca gca ttg gca cag   1363
Ala Leu Ala Tyr Asn Pro Val Gln Asp Ser Gln Ala Ala Leu Ala Gln
                410                 415                 420

gtg cac gca gct gat gcc cgc agc ttt gat gcc gat caa gtg ggt gat   1411
Val His Ala Ala Asp Ala Arg Ser Phe Asp Ala Asp Gln Val Gly Asp
            425                 430                 435

gct gtc acc aaa cgt tat gtt aat gac gac ttg ggg ctg tat gtc gat   1459
Ala Val Thr Lys Arg Tyr Val Asn Asp Asp Leu Gly Leu Tyr Val Asp
        440                 445                 450

gag gca aac ttc aat aat gct ttg acc agg gca ccg ttc cag gtg gcg   1507
Glu Ala Asn Phe Asn Asn Ala Leu Thr Arg Ala Pro Phe Gln Val Ala
    455                 460                 465

atg ccg caa ttc cag gag act aca ccg tgg tta ggt gat cag ctt cgt   1555
Met Pro Gln Phe Gln Glu Thr Thr Pro Trp Leu Gly Asp Gln Leu Arg
470                 475                 480                 485
```

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aca ttg gtg gct gtg ttt aat ggt cag ctg ctt gat cag cat cag cgt   1603
Thr Leu Val Ala Val Phe Asn Gly Gln Leu Leu Asp Gln His Gln Arg
                490                 495                 500

gac tac gaa gaa gtg cgc gcg atg tac att gcg ctt aat gat cgc tct   1651
Asp Tyr Glu Glu Val Arg Ala Met Tyr Ile Ala Leu Asn Asp Arg Ser
            505                 510                 515

aat ctt gag atc gct cgt gat ctt gga ctg gat aat aag gat tcc gaa   1699
Asn Leu Glu Ile Ala Arg Asp Leu Gly Leu Asp Asn Lys Asp Ser Glu
        520                 525                 530

ttc tac gag gtt tac cgt gcc att gag cgt gac cgc gat gtt atg gct   1747
Phe Tyr Glu Val Tyr Arg Ala Ile Glu Arg Asp Arg Asp Val Met Ala
    535                 540                 545

ggt gat caa cag cgt gtg gag tca gag cgt cgt cag caa ttg cag cag   1795
Gly Asp Gln Gln Arg Val Glu Ser Glu Arg Arg Gln Gln Leu Gln Gln
550                 555                 560                 565

gag tat gag gcg aac cgt gaa gaa tat gtc atg gca aag atc gcg gag   1843
Glu Tyr Glu Ala Asn Arg Glu Glu Tyr Val Met Ala Lys Ile Ala Glu
                570                 575                 580

cag cgc gtg gag tat gat cgc cgt cat atg cct cgc cat acc gca tca   1891
Gln Arg Val Glu Tyr Asp Arg Arg His Met Pro Arg His Thr Ala Ser
            585                 590                 595

cta gaa gcg gta ggt cga gag ctg acg agc ctg cgg gat cgc acc att   1939
Leu Glu Ala Val Gly Arg Glu Leu Thr Ser Leu Arg Asp Arg Thr Ile
        600                 605                 610

gag gat tac acc gca cgc atg aac acg ctg cgt cgt gca cgt gct ggt   1987
Glu Asp Tyr Thr Ala Arg Met Asn Thr Leu Arg Arg Ala Arg Ala Gly
    615                 620                 625

gaa cgg gct aac gct gca gaa tct cgc att att gac gaa ttg cgc ccg   2035
Glu Arg Ala Asn Ala Ala Glu Ser Arg Ile Ile Asp Glu Leu Arg Pro
630                 635                 640                 645

att gtg gag cgc cag gca gaa ctg caa cga gca gct ttc gat ggt ttc   2083
Ile Val Glu Arg Gln Ala Glu Leu Gln Arg Ala Ala Phe Asp Gly Phe
                650                 655                 660

att gtt gat ctt gac aag ttt att gct gat cac cgc gaa gat gac ctg   2131
Ile Val Asp Leu Asp Lys Phe Ile Ala Asp His Arg Glu Asp Asp Leu
            665                 670                 675

cgt ttg gca tcg gtg aat gag cag aag ctt gct gca gat aat cgt gtg   2179
Arg Leu Ala Ser Val Asn Glu Gln Lys Leu Ala Ala Asp Asn Arg Val
        680                 685                 690

gca cag ttg acc aag gaa gcc gaa gag cgc atc gag ggt atc cgc gtc   2227
Ala Gln Leu Thr Lys Glu Ala Glu Glu Arg Ile Glu Gly Ile Arg Val
    695                 700                 705

gag acc gat aag atg atc gcc tcc cag cgc aag gca ctt gag cgt cag   2275
Glu Thr Asp Lys Met Ile Ala Ser Gln Arg Lys Ala Leu Glu Arg Gln
710                 715                 720                 725
```

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gaa gcg gaa ttc gca gca gag ctt aag cgt cgc gac act att gtc gct   2323
Glu Ala Glu Phe Ala Ala Glu Leu Lys Arg Arg Asp Thr Ile Val Ala
                730                 735                 740

gca tcg gag gaa cgt gct gag cgg gaa att acc aca gca cgt ctt gat   2371
Ala Ser Glu Glu Arg Ala Glu Arg Glu Ile Thr Thr Ala Arg Leu Asp
            745                 750                 755

gct gag gcg gcg ctc aag cgc atg gaa gag caa att cgt gta aat aat   2419
Ala Glu Ala Ala Leu Lys Arg Met Glu Glu Gln Ile Arg Val Asn Asn
        760                 765                 770

gag gcg cat gag gcg gag att gtt att gag cgc gat cga gcc acc caa   2467
Glu Ala His Glu Ala Glu Ile Val Ile Glu Arg Asp Arg Ala Thr Gln
    775                 780                 785

gca gag gcg aac tcc atg acg ttt gtt gag tca gtc aag cag cag gat   2515
Ala Glu Ala Asn Ser Met Thr Phe Val Glu Ser Val Lys Gln Gln Asp
790                 795                 800                 805

cgc agc aac aac atc att ttg att gcc gtc ctc att gtg ggg ctg att   2563
Arg Ser Asn Asn Ile Ile Leu Ile Ala Val Leu Ile Val Gly Leu Ile
                810                 815                 820

gcc ggc atg gtc gct ggc gca gcc ttc ttc taaaagatcg ttgcgcgggc     2613
Ala Gly Met Val Ala Gly Ala Ala Phe Phe
            825                 830

tgt                                                               2616


<210> 1396
<211> 831
<212> PRT
<213> Corynebacterium glutamicum

<400> 1396
Met Leu Asp Ser Leu Lys Asn Arg Phe Thr Lys Ala Lys Gly Ser His
  1               5                  10                  15

Gly Val Gly Glu Gly Ala Val Ser Gly Asp Ala Ala Val Lys Pro Leu
             20                  25                  30

Arg Lys Glu Glu Arg Leu Ala Ser Val Ile Gln Glu Thr Glu Pro Gly
         35                  40                  45

Ala Ala Val Glu Val Met Arg Arg Asn Asp Ala Phe Ala Leu Pro Gly
     50                  55                  60

Glu Thr Gly Trp Val Val Met Leu Leu Pro Thr His Asp Ser Gln Phe
 65                  70                  75                  80

Gly Gly Leu Asn Ala Lys Glu Lys Asn Arg Glu Asp Lys Gly Thr Ile
                 85                  90                  95

Ile Asn Leu Val Val Asn Asp Asp Ile His Ser Val Val Thr Pro Glu
            100                 105                 110

Leu Leu Asp Ser Asp Val Leu Gly Val Ile Pro Asp Ala Asp Ser Phe
        115                 120                 125
```

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Asp Arg Met Asp Glu Phe Asp Leu Leu Arg Asn Lys Ala Arg Trp His
    130                 135                 140

Tyr Gly Val Ala Ala Ile Glu Pro Asp Thr Gly Glu Leu Val Val Phe
145                 150                 155                 160

Lys Val Pro Ala Lys Asn Ser Ala Ser Ala Arg Gly Asp Ile Phe Ser
                165                 170                 175

Glu Val Gly Asp Val Leu Ser Gly Ala Ala Asp Leu Glu Asp Val Val
            180                 185                 190

Asp Phe Glu Val Ile Ala Thr Phe Leu Glu Val Leu Asn Glu Thr Ser
        195                 200                 205

Glu Val Asp Ile Asp Asp Glu Asp Gly Asp Val Pro Tyr Gly Leu Glu
    210                 215                 220

Gly Val Asn Ala Ala Gly Val Ile Thr Asp Asp Leu Ile Arg Glu Lys
225                 230                 235                 240

Leu Asp Val Asp Ser Tyr Pro Ser Ser Ala Glu Ile Ile Asp Asn Ile
                245                 250                 255

Val His Val Phe Thr Lys Leu Gln Gly Lys His His Val Ala Pro Gln
            260                 265                 270

Pro Val Leu His Ser Ala Asp Val Val Asp Val Asp Ala Gln Glu Ser
        275                 280                 285

His Asp Thr Val Val Ile Glu Ser Pro Asp Asp Val Ala Leu Ala Glu
    290                 295                 300

Gln Val Asp Val Pro Asp Phe Ser Asp Gly Phe Gly Ile Asp Asp Ala
305                 310                 315                 320

Glu Val Thr Glu Pro Glu Asp Glu Glu Val Val Glu Ala Thr Ala Asp
                325                 330                 335

Ala Asp Pro Phe Gly Asp Val Ala Glu Asp Asp Pro Phe Gly Ser Asp
            340                 345                 350

Asp Glu Pro Asp Phe Gly Ala Ser Asp Val Val Ala Ala Pro Ala Pro
        355                 360                 365

Val Ala Gly Met Ser Asp Glu Gln Ile Gln Ala Leu Ile Arg Gly Val
    370                 375                 380

Ser Glu Ser Val Gln Ala Lys Thr Gly Ser Glu Leu Asn Ala Leu Arg
385                 390                 395                 400

Glu Glu Leu Ala Gln Ala Leu Ala Tyr Asn Pro Val Gln Asp Ser Gln
                405                 410                 415

Ala Ala Leu Ala Gln Val His Ala Ala Asp Ala Arg Ser Phe Asp Ala
            420                 425                 430

Asp Gln Val Gly Asp Ala Val Thr Lys Arg Tyr Val Asn Asp Asp Leu
        435                 440                 445

Gly Leu Tyr Val Asp Glu Ala Asn Phe Asn Asn Ala Leu Thr Arg Ala
```

```
    450                 455                 460

Pro Phe Gln Val Ala Met Pro Gln Phe Gln Glu Thr Thr Pro Trp Leu
465                 470                 475                 480

Gly Asp Gln Leu Arg Thr Leu Val Ala Val Phe Asn Gly Gln Leu Leu
                485                 490                 495

Asp Gln His Gln Arg Asp Tyr Glu Glu Val Arg Ala Met Tyr Ile Ala
            500                 505                 510

Leu Asn Asp Arg Ser Asn Leu Glu Ile Ala Arg Asp Leu Gly Leu Asp
        515                 520                 525

Asn Lys Asp Ser Glu Phe Tyr Glu Val Tyr Arg Ala Ile Glu Arg Asp
    530                 535                 540

Arg Asp Val Met Ala Gly Asp Gln Gln Arg Val Glu Ser Glu Arg Arg
545                 550                 555                 560

Gln Gln Leu Gln Gln Glu Tyr Glu Ala Asn Arg Glu Glu Tyr Val Met
                565                 570                 575

Ala Lys Ile Ala Glu Gln Arg Val Glu Tyr Asp Arg Arg His Met Pro
            580                 585                 590

Arg His Thr Ala Ser Leu Glu Ala Val Gly Arg Glu Leu Thr Ser Leu
        595                 600                 605

Arg Asp Arg Thr Ile Glu Asp Tyr Thr Ala Arg Met Asn Thr Leu Arg
    610                 615                 620

Arg Ala Arg Ala Gly Glu Arg Ala Asn Ala Ala Glu Ser Arg Ile Ile
625                 630                 635                 640

Asp Glu Leu Arg Pro Ile Val Glu Arg Gln Ala Glu Leu Gln Arg Ala
                645                 650                 655

Ala Phe Asp Gly Phe Ile Val Asp Leu Asp Lys Phe Ile Ala Asp His
            660                 665                 670

Arg Glu Asp Asp Leu Arg Leu Ala Ser Val Asn Glu Gln Lys Leu Ala
        675                 680                 685

Ala Asp Asn Arg Val Ala Gln Leu Thr Lys Glu Ala Glu Glu Arg Ile
    690                 695                 700

Glu Gly Ile Arg Val Glu Thr Asp Lys Met Ile Ala Ser Gln Arg Lys
705                 710                 715                 720

Ala Leu Glu Arg Gln Glu Ala Glu Phe Ala Ala Glu Leu Lys Arg Arg
                725                 730                 735

Asp Thr Ile Val Ala Ala Ser Glu Glu Arg Ala Glu Arg Glu Ile Thr
            740                 745                 750

Thr Ala Arg Leu Asp Ala Glu Ala Ala Leu Lys Arg Met Glu Glu Gln
        755                 760                 765

Ile Arg Val Asn Asn Glu Ala His Glu Ala Glu Ile Val Ile Glu Arg
    770                 775                 780
```

```
Asp Arg Ala Thr Gln Ala Glu Ala Asn Ser Met Thr Phe Val Glu Ser
785                 790                 795                 800

Val Lys Gln Gln Asp Arg Ser Asn Asn Ile Ile Leu Ile Ala Val Leu
                805                 810                 815

Ile Val Gly Leu Ile Ala Gly Met Val Ala Gly Ala Ala Phe Phe
            820                 825                 830


<210> 1397
<211> 1116
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1093)
<223> RXN03018

<400> 1397
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gtggctgtgt ttaatggtca gctgcttgat cagcatcagc gtg act acc gaa gaa   115
                                        Val Thr Thr Glu Glu
                                          1               5

gtg cgc gcg atg tac att gcg ctt aat gat cgc tct aat ctt gag atc   163
Val Arg Ala Met Tyr Ile Ala Leu Asn Asp Arg Ser Asn Leu Glu Ile
                 10                  15                  20

gct cgt gat ctt gga ctg gat aat aag gat tcc gaa ttc tac gag gtt   211
Ala Arg Asp Leu Gly Leu Asp Asn Lys Asp Ser Glu Phe Tyr Glu Val
             25                  30                  35

tac cgt gcc att gag cgt gac cgc gat gtt atg gct ggt gat caa cag   259
Tyr Arg Ala Ile Glu Arg Asp Arg Asp Val Met Ala Gly Asp Gln Gln
         40                  45                  50

cgt gtg gag tca gag cgt cgt cag caa ttg cag cag gag tat gag gcg   307
Arg Val Glu Ser Glu Arg Arg Gln Gln Leu Gln Gln Glu Tyr Glu Ala
     55                  60                  65

aac cgt gaa gaa tat gtc atg gca aag atc gcg gag cag cgc gtg gag   355
Asn Arg Glu Glu Tyr Val Met Ala Lys Ile Ala Glu Gln Arg Val Glu
 70                  75                  80                  85

tat gat cgc cgt cat atg cct cgc cat acc gca tca cta gaa gcg gta   403
Tyr Asp Arg Arg His Met Pro Arg His Thr Ala Ser Leu Glu Ala Val
                 90                  95                 100

ggt cga gag ctg acg agc ctg cgg gat cgc acc att gag gat tac acc   451
Gly Arg Glu Leu Thr Ser Leu Arg Asp Arg Thr Ile Glu Asp Tyr Thr
            105                 110                 115

gca cgc atg aac acg ctg cgt cgt gca cgt gct ggt gaa cgg gct aac   499
Ala Arg Met Asn Thr Leu Arg Arg Ala Arg Ala Gly Glu Arg Ala Asn
        120                 125                 130

gct gca gaa tct cgc att att gac gaa ttg cgc ccg att gtg gag cgc   547
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Ala Ala Glu Ser Arg Ile Ile Asp Glu Leu Arg Pro Ile Val Glu Arg
    135                 140                 145

cag gca gaa ctg caa cga gca gct ttc gat ggt ttc att gtt gat ctt   595
Gln Ala Glu Leu Gln Arg Ala Ala Phe Asp Gly Phe Ile Val Asp Leu
150                 155                 160                 165

gac aag ttt att gct gat cac cgc gaa gat gac ctg cgt ttg gca tcg   643
Asp Lys Phe Ile Ala Asp His Arg Glu Asp Asp Leu Arg Leu Ala Ser
                170                 175                 180

gtg aat gag cag aag ctt gct gca gat aat cgt gtg gca cag ttg acc   691
Val Asn Glu Gln Lys Leu Ala Ala Asp Asn Arg Val Ala Gln Leu Thr
            185                 190                 195

aag gaa gcc gaa gag cgc atc gag ggt atc cgc gtc gag acc gat aag   739
Lys Glu Ala Glu Glu Arg Ile Glu Gly Ile Arg Val Glu Thr Asp Lys
        200                 205                 210

atg atc gcc tcc cag cgc aag gca ctt gag cgt cag gaa gcg gaa ttc   787
Met Ile Ala Ser Gln Arg Lys Ala Leu Glu Arg Gln Glu Ala Glu Phe
    215                 220                 225

gca gca gag ctt aag cgt cgc gac act att gtc gct gca tcg gag gaa   835
Ala Ala Glu Leu Lys Arg Arg Asp Thr Ile Val Ala Ala Ser Glu Glu
230                 235                 240                 245

cgt gct gag cgg gaa att acc aca gca cgt ctt gat gct gag gcg gcg   883
Arg Ala Glu Arg Glu Ile Thr Thr Ala Arg Leu Asp Ala Glu Ala Ala
                250                 255                 260

ctc aag cgc atg gaa gag caa att cgt gta aat aat gag gcg cat gag   931
Leu Lys Arg Met Glu Glu Gln Ile Arg Val Asn Asn Glu Ala His Glu
            265                 270                 275

gcg gag att gtt att gag cgc gat cga gcc acc caa gca gag gcg aac   979
Ala Glu Ile Val Ile Glu Arg Asp Arg Ala Thr Gln Ala Glu Ala Asn
        280                 285                 290

tcc atg acg ttt gtt gag tca gtc aag cag cag gat cgc agc aac aac   1027
Ser Met Thr Phe Val Glu Ser Val Lys Gln Gln Asp Arg Ser Asn Asn
    295                 300                 305

atc att ttg att gcc gtc ctc att gtg ggg ctg att gcc ggc atg gtc   1075
Ile Ile Leu Ile Ala Val Leu Ile Val Gly Leu Ile Ala Gly Met Val
310                 315                 320                 325

gct ggc gca gcc ttc ttc taaaagatcg ttgcgcgggc tgt                 1116
Ala Gly Ala Ala Phe Phe
                330
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<210> 1398
<211> 331
<212> PRT
<213> Corynebacterium glutamicum

<400> 1398

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Val Thr Thr Glu Glu Val Arg Ala Met Tyr Ile Ala Leu Asn Asp Arg
  1               5                  10                  15
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Ser Asn Leu Glu Ile Ala Arg Asp Leu Gly Leu Asp Asn Lys Asp Ser
20 25 30

Glu Phe Tyr Glu Val Tyr Arg Ala Ile Glu Arg Asp Arg Asp Val Met
35 40 45

Ala Gly Asp Gln Gln Arg Val Glu Ser Glu Arg Arg Gln Gln Leu Gln
50 55 60

Gln Glu Tyr Glu Ala Asn Arg Glu Glu Tyr Val Met Ala Lys Ile Ala
65 70 75 80

Glu Gln Arg Val Glu Tyr Asp Arg Arg His Met Pro Arg His Thr Ala
85 90 95

Ser Leu Glu Ala Val Gly Arg Glu Leu Thr Ser Leu Arg Asp Arg Thr
100 105 110

Ile Glu Asp Tyr Thr Ala Arg Met Asn Thr Leu Arg Arg Ala Arg Ala
115 120 125

Gly Glu Arg Ala Asn Ala Ala Glu Ser Arg Ile Ile Asp Glu Leu Arg
130 135 140

Pro Ile Val Glu Arg Gln Ala Glu Leu Gln Arg Ala Ala Phe Asp Gly
145 150 155 160

Phe Ile Val Asp Leu Asp Lys Phe Ile Ala Asp His Arg Glu Asp Asp
165 170 175

Leu Arg Leu Ala Ser Val Asn Glu Gln Lys Leu Ala Ala Asp Asn Arg
180 185 190

Val Ala Gln Leu Thr Lys Glu Ala Glu Glu Arg Ile Glu Gly Ile Arg
195 200 205

Val Glu Thr Asp Lys Met Ile Ala Ser Gln Arg Lys Ala Leu Glu Arg
210 215 220

Gln Glu Ala Glu Phe Ala Ala Glu Leu Lys Arg Arg Asp Thr Ile Val
225 230 235 240

Ala Ala Ser Glu Glu Arg Ala Glu Arg Glu Ile Thr Thr Ala Arg Leu
245 250 255

Asp Ala Glu Ala Ala Leu Lys Arg Met Glu Glu Gln Ile Arg Val Asn
260 265 270

Asn Glu Ala His Glu Ala Glu Ile Val Ile Glu Arg Asp Arg Ala Thr
275 280 285

Gln Ala Glu Ala Asn Ser Met Thr Phe Val Glu Ser Val Lys Gln Gln
290 295 300

Asp Arg Ser Asn Asn Ile Ile Leu Ile Ala Val Leu Ile Val Gly Leu
305 310 315 320

Ile Ala Gly Met Val Ala Gly Ala Ala Phe Phe
325 330

<210> 1399
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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1516)
<223> RXN03024

<400> 1399
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ttaactcaac gtttactaaa cagaatcgga attaggagcc atg ctt gaa cgc aca 115
Met Leu Glu Arg Thr
1 5

cag gta ttc gtg gat acg tcc tac ctg ctc gca agc ttt tac aac tct 163
Gln Val Phe Val Asp Thr Ser Tyr Leu Leu Ala Ser Phe Tyr Asn Ser
10 15 20

tgg gag aca ggg gca cgt gcc caa tta gaa atc gac ctc ccc gaa gta 211
Trp Glu Thr Gly Ala Arg Ala Gln Leu Glu Ile Asp Leu Pro Glu Val
25 30 35

gtc ggg gta tta gga agg atg att gaa caa caa ctt aaa cag cca gta 259
Val Gly Val Leu Gly Arg Met Ile Glu Gln Gln Leu Lys Gln Pro Val
40 45 50

caa cgc caa atg tgg tac gac gga atc ccc gat tcc ggc ccc cac cgc 307
Gln Arg Gln Met Trp Tyr Asp Gly Ile Pro Asp Ser Gly Pro His Arg
55 60 65

tat caa cga gca cta cgc acc tgc gat ggt gtg caa ctt cgt gct ggc 355
Tyr Gln Arg Ala Leu Arg Thr Cys Asp Gly Val Gln Leu Arg Ala Gly
70 75 80 85

caa tta att gaa tgg ggc gaa cgc cgc aca caa aag gca gta gat acc 403
Gln Leu Ile Glu Trp Gly Glu Arg Arg Thr Gln Lys Ala Val Asp Thr
90 95 100

cgc ctt gtt gca gac ctc gtt ctc gca ggt gtt cgc gga caa tgc tcc 451
Arg Leu Val Ala Asp Leu Val Leu Ala Gly Val Arg Gly Gln Cys Ser
105 110 115

gat atc gtg ctc gtc agt ggc gac gcc gac atg atc ccc ggt gtt caa 499
Asp Ile Val Leu Val Ser Gly Asp Ala Asp Met Ile Pro Gly Val Gln
120 125 130

gaa gct gcc aat gca ggc ctt cgc gtt cac ctc tac ggc ttc ggc tgg 547
Glu Ala Ala Asn Ala Gly Leu Arg Val His Leu Tyr Gly Phe Gly Trp
135 140 145

gat tcc atg tcc tcc caa ctg cgc cac tgc tgt gac acc acc acc att 595
Asp Ser Met Ser Ser Gln Leu Arg His Cys Cys Asp Thr Thr Thr Ile
150 155 160 165

ttg gat cct cga gaa gat ttt gct gaa tgc atg cag ctg cag gtt ctc 643
Leu Asp Pro Arg Glu Asp Phe Ala Glu Cys Met Gln Leu Gln Val Leu
170 175 180

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gaa ggt cca cta ccc cct gtc gtt cgg gta aag ccc atc aac gat gca   691
Glu Gly Pro Leu Pro Pro Val Val Arg Val Lys Pro Ile Asn Asp Ala
            185                 190                 195

gaa ccc atc gag gat ttg gat ttc act cca gtt cca ggc gtc gcc tca   739
Glu Pro Ile Glu Asp Leu Asp Phe Thr Pro Val Pro Gly Val Ala Ser
        200                 205                 210

cca ttt gaa gag gtc agc gcg aaa gat gag aaa ttc tct cca cgc cca   787
Pro Phe Glu Glu Val Ser Ala Lys Asp Glu Lys Phe Ser Pro Arg Pro
    215                 220                 225

agt gaa cct gcc gaa gct ttg tcg gaa cag gtc tgt gaa gcg cag tat   835
Ser Glu Pro Ala Glu Ala Leu Ser Glu Gln Val Cys Glu Ala Gln Tyr
230                 235                 240                 245

gag atc tcc aaa cac gaa ggt caa acc gct gat tca gga gaa atc acc   883
Glu Ile Ser Lys His Glu Gly Gln Thr Ala Asp Ser Gly Glu Ile Thr
                250                 255                 260

gag tct ttc gag gcc gct gaa atc aag gta act gag ttt ttt gga gaa   931
Glu Ser Phe Glu Ala Ala Glu Ile Lys Val Thr Glu Phe Phe Gly Glu
            265                 270                 275

cca gct gct cca gta gcg gaa tca ggc gta gaa gct ccc act ccg gaa   979
Pro Ala Ala Pro Val Ala Glu Ser Gly Val Glu Ala Pro Thr Pro Glu
        280                 285                 290

gct ccc acg gtt cct gaa gca gct aag ccc act ccg gcg aaa cct aag   1027
Ala Pro Thr Val Pro Glu Ala Ala Lys Pro Thr Pro Ala Lys Pro Lys
    295                 300                 305

act cca aag gca gag ccc caa aag caa gaa tcc ccc aag ccg gga act   1075
Thr Pro Lys Ala Glu Pro Gln Lys Gln Glu Ser Pro Lys Pro Gly Thr
310                 315                 320                 325

cca aaa cca aaa gct cca agc cct gcg gat att cca ccg aaa gcc cca   1123
Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile Pro Pro Lys Ala Pro
                330                 335                 340

gct gac act gag gaa cat tcg gaa gtc gaa gct gaa atc gag gac tca   1171
Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala Glu Ile Glu Asp Ser
            345                 350                 355

cgt cca aag atc ccc agc cct tcg atg atg gct ccc cgc cgc aag ctt   1219
Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala Pro Arg Arg Lys Leu
        360                 365                 370

cgt tcc cgc tac gtt ccg ctt ccc aac gaa gtg tgg gca aca gca gga   1267
Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val Trp Ala Thr Ala Gly
    375                 380                 385

ttc caa act cct tac gat gtc ggg caa cag tac gca tcg tgg tgg ttt   1315
Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr Ala Ser Trp Trp Phe
390                 395                 400                 405

gaa aac gca gct acc agc act caa aga gat cag gct cat cta ttg tct   1363
Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln Ala His Leu Leu Ser
                410                 415                 420

ggt ggc gga ctt cca cca gag atc gat cgc ccg ctt ctg cag ttt gct   1411
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Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro Leu Leu Gln Phe Ala
            425                 430                 435

tgt gaa act ctc cac gaa tac acc ctg act gaa gcg cag cgc gta gct   1459
Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu Ala Gln Arg Val Ala
        440                 445                 450

tta cgc gat ggc ttt cac tcc gga atc cgt ggt gta ttg ctc aac cag   1507
Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly Val Leu Leu Asn Gln
    455                 460                 465

cga gat agc tagaatcaca aaaaactggg gct                             1539
Arg Asp Ser
470


<210> 1400
<211> 472
<212> PRT
<213> Corynebacterium glutamicum

<400> 1400
Met Leu Glu Arg Thr Gln Val Phe Val Asp Thr Ser Tyr Leu Leu Ala
  1               5                  10                  15

Ser Phe Tyr Asn Ser Trp Glu Thr Gly Ala Arg Ala Gln Leu Glu Ile
            20                  25                  30

Asp Leu Pro Glu Val Val Gly Val Leu Gly Arg Met Ile Glu Gln Gln
        35                  40                  45

Leu Lys Gln Pro Val Gln Arg Gln Met Trp Tyr Asp Gly Ile Pro Asp
    50                  55                  60

Ser Gly Pro His Arg Tyr Gln Arg Ala Leu Arg Thr Cys Asp Gly Val
65                  70                  75                  80

Gln Leu Arg Ala Gly Gln Leu Ile Glu Trp Gly Glu Arg Arg Thr Gln
                85                  90                  95

Lys Ala Val Asp Thr Arg Leu Val Ala Asp Leu Val Leu Ala Gly Val
            100                 105                 110

Arg Gly Gln Cys Ser Asp Ile Val Leu Val Ser Gly Asp Ala Asp Met
        115                 120                 125

Ile Pro Gly Val Gln Glu Ala Ala Asn Ala Gly Leu Arg Val His Leu
    130                 135                 140

Tyr Gly Phe Gly Trp Asp Ser Met Ser Ser Gln Leu Arg His Cys Cys
145                 150                 155                 160

Asp Thr Thr Thr Ile Leu Asp Pro Arg Glu Asp Phe Ala Glu Cys Met
                165                 170                 175

Gln Leu Gln Val Leu Glu Gly Pro Leu Pro Pro Val Val Arg Val Lys
            180                 185                 190

Pro Ile Asn Asp Ala Glu Pro Ile Glu Asp Leu Asp Phe Thr Pro Val
        195                 200                 205
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Pro Gly Val Ala Ser Pro Phe Glu Glu Val Ser Ala Lys Asp Glu Lys
210 215 220

Phe Ser Pro Arg Pro Ser Glu Pro Ala Glu Ala Leu Ser Glu Gln Val
225 230 235 240

Cys Glu Ala Gln Tyr Glu Ile Ser Lys His Glu Gly Gln Thr Ala Asp
245 250 255

Ser Gly Glu Ile Thr Glu Ser Phe Glu Ala Ala Glu Ile Lys Val Thr
260 265 270

Glu Phe Phe Gly Glu Pro Ala Ala Pro Val Ala Glu Ser Gly Val Glu
275 280 285

Ala Pro Thr Pro Glu Ala Pro Thr Val Pro Glu Ala Ala Lys Pro Thr
290 295 300

Pro Ala Lys Pro Lys Thr Pro Lys Ala Glu Pro Gln Lys Gln Glu Ser
305 310 315 320

Pro Lys Pro Gly Thr Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile
325 330 335

Pro Pro Lys Ala Pro Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala
340 345 350

Glu Ile Glu Asp Ser Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala
355 360 365

Pro Arg Arg Lys Leu Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val
370 375 380

Trp Ala Thr Ala Gly Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr
385 390 395 400

Ala Ser Trp Trp Phe Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln
405 410 415

Ala His Leu Leu Ser Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro
420 425 430

Leu Leu Gln Phe Ala Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu
435 440 445

Ala Gln Arg Val Ala Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly
450 455 460

Val Leu Leu Asn Gln Arg Asp Ser
465 470

<210> 1401
<211> 996
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(973)
<223> RXN03025

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agcgaatcgg attcagtgat ttgcttgcgg gcgcagaaat gatttttcaa ttagacacac 60

ttagacacac gtaactaaaa cctcagggaa gtgactgata atg gct aat ccg ctc 115
Met Ala Asn Pro Leu
1 5

agc aag ggc tgg aag tat ctc atg gca tcg ttc gac aac aag atc gat 163
Ser Lys Gly Trp Lys Tyr Leu Met Ala Ser Phe Asp Asn Lys Ile Asp
10 15 20

gag aat gca gat cca aag atc caa att cag caa gct aca gaa gct gcc 211
Glu Asn Ala Asp Pro Lys Ile Gln Ile Gln Gln Ala Thr Glu Ala Ala
25 30 35

cag aag cag cac cag cag att atg cag cac gct tct cag att atc ggt 259
Gln Lys Gln His Gln Gln Ile Met Gln His Ala Ser Gln Ile Ile Gly
40 45 50

cag cag aag cag ctt gag atg aaa ttg aac cgc ttg gtt act gac cgc 307
Gln Gln Lys Gln Leu Glu Met Lys Leu Asn Arg Leu Val Thr Asp Arg
55 60 65

gat aag ttg cag gaa cag gct cgt cag gca att cag ttg gca gat aag 355
Asp Lys Leu Gln Glu Gln Ala Arg Gln Ala Ile Gln Leu Ala Asp Lys
70 75 80 85

tcc gca aac gaa ggc gac agt gtt aag gct cag gag ttc aac aac act 403
Ser Ala Asn Glu Gly Asp Ser Val Lys Ala Gln Glu Phe Asn Asn Thr
90 95 100

gct gag gtt ttt gct tcc cag ttg gta gct gtg gaa cag cag ttg gag 451
Ala Glu Val Phe Ala Ser Gln Leu Val Ala Val Glu Gln Gln Leu Glu
105 110 115

cag act act gcg ctt cat cag cag gct gag gtt gcg gcg aag gat gct 499
Gln Thr Thr Ala Leu His Gln Gln Ala Glu Val Ala Ala Lys Asp Ala
120 125 130

gtt gcg aag tct aaa gag tct gag atg cgc ctg aaa gag cag atg tct 547
Val Ala Lys Ser Lys Glu Ser Glu Met Arg Leu Lys Glu Gln Met Ser
135 140 145

cag att gat gct cta cgt gcg cag gct gat cag gcg aag atg cag gaa 595
Gln Ile Asp Ala Leu Arg Ala Gln Ala Asp Gln Ala Lys Met Gln Glu
150 155 160 165

agt gtc act aag tct atg gat tct ttg aat cag ttt ggc act cag gat 643
Ser Val Thr Lys Ser Met Asp Ser Leu Asn Gln Phe Gly Thr Gln Asp
170 175 180

tct tct gtt cct acc ctt gat gcg gtg cgt gag aag atc gag cgt cga 691
Ser Ser Val Pro Thr Leu Asp Ala Val Arg Glu Lys Ile Glu Arg Arg
185 190 195

tac gca gat gct ttg ggc gcg cag gaa ctt acc cag aac act gtt agt 739
Tyr Ala Asp Ala Leu Gly Ala Gln Glu Leu Thr Gln Asn Thr Val Ser
200 205 210

gat cgc atg gct gag att gcg cag tcc ggc acc gat atg cgg gcg tca 787

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Asp Arg Met Ala Glu Ile Ala Gln Ser Gly Thr Asp Met Arg Ala Ser
    215                 220                 225

gct cgt ttg gct gaa ctt cgc gcg gag gcg ctg ggc acg tcc gca acg   835
Ala Arg Leu Ala Glu Leu Arg Ala Glu Ala Leu Gly Thr Ser Ala Thr
230                 235                 240                 245

cct aag ggc cag cta gag gca ggt gtc gag gat gcg gaa gaa ctt atc   883
Pro Lys Gly Gln Leu Glu Ala Gly Val Glu Asp Ala Glu Glu Leu Ile
                250                 255                 260

gac gaa acc tcc acc cct tca gct acc cca gaa acc gca agc cca gaa   931
Asp Glu Thr Ser Thr Pro Ser Ala Thr Pro Glu Thr Ala Ser Pro Glu
            265                 270                 275

gct gat gct cca gaa gca tcc gca gac gag tcc gag aag aaa           973
Ala Asp Ala Pro Glu Ala Ser Ala Asp Glu Ser Glu Lys Lys
        280                 285                 290

taacctaaac acaaaaaact ggg                                        996
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<210> 1402
<211> 291
<212> PRT
<213> Corynebacterium glutamicum

<400> 1402

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Asp Asn Lys Ile Asp Glu Asn Ala Asp Pro Lys Ile Gln Ile Gln Gln
             20                  25                  30

Ala Thr Glu Ala Ala Gln Lys Gln His Gln Gln Ile Met Gln His Ala
         35                  40                  45

Ser Gln Ile Ile Gly Gln Gln Lys Gln Leu Glu Met Lys Leu Asn Arg
     50                  55                  60

Leu Val Thr Asp Arg Asp Lys Leu Gln Glu Gln Ala Arg Gln Ala Ile
 65                  70                  75                  80

Gln Leu Ala Asp Lys Ser Ala Asn Glu Gly Asp Ser Val Lys Ala Gln
                 85                  90                  95

Glu Phe Asn Asn Thr Ala Glu Val Phe Ala Ser Gln Leu Val Ala Val
            100                 105                 110

Glu Gln Gln Leu Glu Gln Thr Thr Ala Leu His Gln Gln Ala Glu Val
        115                 120                 125

Ala Ala Lys Asp Ala Val Ala Lys Ser Lys Glu Ser Glu Met Arg Leu
    130                 135                 140

Lys Glu Gln Met Ser Gln Ile Asp Ala Leu Arg Ala Gln Ala Asp Gln
145                 150                 155                 160

Ala Lys Met Gln Glu Ser Val Thr Lys Ser Met Asp Ser Leu Asn Gln
                165                 170                 175
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```
Phe Gly Thr Gln Asp Ser Ser Val Pro Thr Leu Asp Ala Val Arg Glu
            180                 185                 190

Lys Ile Glu Arg Arg Tyr Ala Asp Ala Leu Gly Ala Gln Glu Leu Thr
        195                 200                 205

Gln Asn Thr Val Ser Asp Arg Met Ala Glu Ile Ala Gln Ser Gly Thr
    210                 215                 220

Asp Met Arg Ala Ser Ala Arg Leu Ala Glu Leu Arg Ala Glu Ala Leu
225                 230                 235                 240

Gly Thr Ser Ala Thr Pro Lys Gly Gln Leu Glu Ala Gly Val Glu Asp
                245                 250                 255

Ala Glu Glu Leu Ile Asp Glu Thr Ser Thr Pro Ser Ala Thr Pro Glu
            260                 265                 270

Thr Ala Ser Pro Glu Ala Asp Ala Pro Glu Ala Ser Ala Asp Glu Ser
        275                 280                 285

Glu Lys Lys
    290


<210> 1403
<211> 174
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (17)..(151)
<223> RXN03027

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aataggagaa tttaaaatg gaa aac gtt tac gag ttc ctt gga aac ctt gat  52
                 Met Glu Asn Val Tyr Glu Phe Leu Gly Asn Leu Asp
                   1               5                  10

gtc ctt tcc ggc tcc ggc ctc atc ggc tac gtc ttc gac ttc ctc ggc  100
Val Leu Ser Gly Ser Gly Leu Ile Gly Tyr Val Phe Asp Phe Leu Gly
         15                  20                  25

gct tcc agc aag tgg gct ggc gca gtt gct gac ctc atc ggt ctg ctt  148
Ala Ser Ser Lys Trp Ala Gly Ala Val Ala Asp Leu Ile Gly Leu Leu
     30                  35                  40

ggc taattaactt cgcccacggg caa                                   174
Gly
 45


<210> 1404
<211> 45
<212> PRT
<213> Corynebacterium glutamicum

<400> 1404
Met Glu Asn Val Tyr Glu Phe Leu Gly Asn Leu Asp Val Leu Ser Gly
  1               5                  10                  15
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Ser Gly Leu Ile Gly Tyr Val Phe Asp Phe Leu Gly Ala Ser Ser Lys
            20                  25                  30

Trp Ala Gly Ala Val Ala Asp Leu Ile Gly Leu Leu Gly
        35                  40                  45


<210> 1405
<211> 630
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (95)..(607)
<223> RXN03029

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ggtgtggctt cctattcgct gcatcctgaa tatgccatca aaatcttcac tctgaggccg 60

aaaaatccgg ttatgacatt aagtacctag gacaatg ttt gga gtg ggc tat tat  115
                                      Met Phe Gly Val Gly Tyr Tyr
                                        1               5

aca acc gcc cac cga ttg tcc acc ctg cag cgc ccc aac ttg cgc ggc   163
Thr Thr Ala His Arg Leu Ser Thr Leu Gln Arg Pro Asn Leu Arg Gly
        10                  15                  20

atc ccc tta acc ttc gtg agc gtc gac cga gcc ggc aac atg tcc aaa   211
Ile Pro Leu Thr Phe Val Ser Val Asp Arg Ala Gly Asn Met Ser Lys
    25                  30                  35

cgc caa tcc gcc acg ggc ttc cac ttc acc cat tac ggc ggc acc tgc   259
Arg Gln Ser Ala Thr Gly Phe His Phe Thr His Tyr Gly Gly Thr Cys
40                  45                  50                  55

ccc ctg tgg aac gtg ttt gaa acc ttc acc aac ccc ggc caa gtg ctc   307
Pro Leu Trp Asn Val Phe Glu Thr Phe Thr Asn Pro Gly Gln Val Leu
                60                  65                  70

cgc caa ttc gcg caa atg ccc gac gga cgc aac tac ctg tgg atc tca   355
Arg Gln Phe Ala Gln Met Pro Asp Gly Arg Asn Tyr Leu Trp Ile Ser
            75                  80                  85

cgc acc gtg cga cac cac gaa gcc cgg ttc ggc gaa gta gac aaa atg   403
Arg Thr Val Arg His His Glu Ala Arg Phe Gly Glu Val Asp Lys Met
        90                  95                  100

ttc gcc atc ggc ttg ggc tgc gaa gcg cgc cac gcc gac cgc act gtg   451
Phe Ala Ile Gly Leu Gly Cys Glu Ala Arg His Ala Asp Arg Thr Val
    105                 110                 115

tac tcc cgc ggt ttc aac ctc cag gac ctc tcc acc gcc acc ccc atc   499
Tyr Ser Arg Gly Phe Asn Leu Gln Asp Leu Ser Thr Ala Thr Pro Ile
120                 125                 130                 135

ggg tcc ggc tgc cga gtg tgc acc cgc gag aac tgc gcg cag cgc gca   547
Gly Ser Gly Cys Arg Val Cys Thr Arg Glu Asn Cys Ala Gln Arg Ala
                140                 145                 150
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ttc cca tcc gtc cac ggc cgc atc aac atc gac gcg cac gaa tcc act   595
Phe Pro Ser Val His Gly Arg Ile Asn Ile Asp Ala His Glu Ser Thr
            155                 160                 165

atc gcg ccg tac taagaaaagg agcttgcttt acg                        630
Ile Ala Pro Tyr
        170


<210> 1406
<211> 171
<212> PRT
<213> Corynebacterium glutamicum

<400> 1406
Met Phe Gly Val Gly Tyr Tyr Thr Thr Ala His Arg Leu Ser Thr Leu
  1               5                  10                  15

Gln Arg Pro Asn Leu Arg Gly Ile Pro Leu Thr Phe Val Ser Val Asp
             20                  25                  30

Arg Ala Gly Asn Met Ser Lys Arg Gln Ser Ala Thr Gly Phe His Phe
         35                  40                  45

Thr His Tyr Gly Gly Thr Cys Pro Leu Trp Asn Val Phe Glu Thr Phe
     50                  55                  60

Thr Asn Pro Gly Gln Val Leu Arg Gln Phe Ala Gln Met Pro Asp Gly
 65                  70                  75                  80

Arg Asn Tyr Leu Trp Ile Ser Arg Thr Val Arg His His Glu Ala Arg
                 85                  90                  95

Phe Gly Glu Val Asp Lys Met Phe Ala Ile Gly Leu Gly Cys Glu Ala
            100                 105                 110

Arg His Ala Asp Arg Thr Val Tyr Ser Arg Gly Phe Asn Leu Gln Asp
        115                 120                 125

Leu Ser Thr Ala Thr Pro Ile Gly Ser Gly Cys Arg Val Cys Thr Arg
    130                 135                 140

Glu Asn Cys Ala Gln Arg Ala Phe Pro Ser Val His Gly Arg Ile Asn
145                 150                 155                 160

Ile Asp Ala His Glu Ser Thr Ile Ala Pro Tyr
                165                 170


<210> 1407
<211> 789
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(789)
<223> RXN03031

<400> 1407
aac aac ggc ctt aac gcc atg gcc gcg atg acc aac ctc cca cac ctg   48
```

```
Asn Asn Gly Leu Asn Ala Met Ala Ala Met Thr Asn Leu Pro His Leu
  1               5                  10                  15

cgc gcc atc caa gaa cgc tac tac ttc ctg agc atc cgc tac ctc gcc   96
Arg Ala Ile Gln Glu Arg Tyr Tyr Phe Leu Ser Ile Arg Tyr Leu Ala
            20                  25                  30

tcc atc atg atc gcc gtg gcc aaa gca gac ccc acc ctg tgg gaa gaa   144
Ser Ile Met Ile Ala Val Ala Lys Ala Asp Pro Thr Leu Trp Glu Glu
         35                  40                  45

ctc gac ctg cgc atc acc gac gcc tta aca cca gtc acc gca ggg gaa   192
Leu Asp Leu Arg Ile Thr Asp Ala Leu Thr Pro Val Thr Ala Gly Glu
     50                  55                  60

gtg atg atc caa tcc tcc acc ctg tcc aaa cgc atc gcc gcc tgg atc   240
Val Met Ile Gln Ser Ser Thr Leu Ser Lys Arg Ile Ala Ala Trp Ile
 65                  70                  75                  80

aaa gaa ctc gac ccc gaa ccc aca cca gag ccc ata ccg aaa gag gac   288
Lys Glu Leu Asp Pro Glu Pro Thr Pro Glu Pro Ile Pro Lys Glu Asp
                 85                  90                  95

tat gtt cac gtc cac acc act gat gag gcg acc tat gtc cgc atc aaa   336
Tyr Val His Val His Thr Thr Asp Glu Ala Thr Tyr Val Arg Ile Lys
            100                 105                 110

atc agc ggc ccc aac cgc ctg atc ctc aat gac atc atc acc caa ctc   384
Ile Ser Gly Pro Asn Arg Leu Ile Leu Asn Asp Ile Ile Thr Gln Leu
        115                 120                 125

aaa gac aca gac acc gag gac agc ctg cct gaa gcg ctc atg gcg ttc   432
Lys Asp Thr Asp Thr Glu Asp Ser Leu Pro Glu Ala Leu Met Ala Phe
    130                 135                 140

ctg atg gag aaa atc cag tta aag atc acc aag tac ctt ttc acc cca   480
Leu Met Glu Lys Ile Gln Leu Lys Ile Thr Lys Tyr Leu Phe Thr Pro
145                 150                 155                 160

cat aag cac cct gag cag gtg tgg tca ccg gac tac ggt gac att ggt   528
His Lys His Pro Glu Gln Val Trp Ser Pro Asp Tyr Gly Asp Ile Gly
                165                 170                 175

ccc gaa gcc tat gcc aat gcc acc ctc gtg tgc gcc aag gac tta gat   576
Pro Glu Ala Tyr Ala Asn Ala Thr Leu Val Cys Ala Lys Asp Leu Asp
            180                 185                 190

gag gtc gct gga gcc acg gag aag agc tac acc ccg agt gag aag atg   624
Glu Val Ala Gly Ala Thr Glu Lys Ser Tyr Thr Pro Ser Glu Lys Met
        195                 200                 205

aaa gcc ctg atc aga gct cgg gat ggg cat tgc cgc ttc cca ggg tgt   672
Lys Ala Leu Ile Arg Ala Arg Asp Gly His Cys Arg Phe Pro Gly Cys
    210                 215                 220

tgc gtc ccg gcg agt aaa tgc cag gtc gat cac att atc ccg tgg gcg   720
Cys Val Pro Ala Ser Lys Cys Gln Val Asp His Ile Ile Pro Trp Ala
225                 230                 235                 240

gag ggc ggc ccg aca gcg gcg tgg aac ctg cag ttg ttg tgc cag cgg   768
Glu Gly Gly Pro Thr Ala Ala Trp Asn Leu Gln Leu Leu Cys Gln Arg
```

245 250 255

cat cac aat atg aaa acc gat 789
His His Asn Met Lys Thr Asp
260

<210> 1408
<211> 263
<212> PRT
<213> Corynebacterium glutamicum

<400> 1408
Asn Asn Gly Leu Asn Ala Met Ala Ala Met Thr Asn Leu Pro His Leu
1 5 10 15

Arg Ala Ile Gln Glu Arg Tyr Tyr Phe Leu Ser Ile Arg Tyr Leu Ala
20 25 30

Ser Ile Met Ile Ala Val Ala Lys Ala Asp Pro Thr Leu Trp Glu Glu
35 40 45

Leu Asp Leu Arg Ile Thr Asp Ala Leu Thr Pro Val Thr Ala Gly Glu
50 55 60

Val Met Ile Gln Ser Ser Thr Leu Ser Lys Arg Ile Ala Ala Trp Ile
65 70 75 80

Lys Glu Leu Asp Pro Glu Pro Thr Pro Glu Pro Ile Pro Lys Glu Asp
85 90 95

Tyr Val His Val His Thr Thr Asp Glu Ala Thr Tyr Val Arg Ile Lys
100 105 110

Ile Ser Gly Pro Asn Arg Leu Ile Leu Asn Asp Ile Ile Thr Gln Leu
115 120 125

Lys Asp Thr Asp Thr Glu Asp Ser Leu Pro Glu Ala Leu Met Ala Phe
130 135 140

Leu Met Glu Lys Ile Gln Leu Lys Ile Thr Lys Tyr Leu Phe Thr Pro
145 150 155 160

His Lys His Pro Glu Gln Val Trp Ser Pro Asp Tyr Gly Asp Ile Gly
165 170 175

Pro Glu Ala Tyr Ala Asn Ala Thr Leu Val Cys Ala Lys Asp Leu Asp
180 185 190

Glu Val Ala Gly Ala Thr Glu Lys Ser Tyr Thr Pro Ser Glu Lys Met
195 200 205

Lys Ala Leu Ile Arg Ala Arg Asp Gly His Cys Arg Phe Pro Gly Cys
210 215 220

Cys Val Pro Ala Ser Lys Cys Gln Val Asp His Ile Ile Pro Trp Ala
225 230 235 240

Glu Gly Gly Pro Thr Ala Ala Trp Asn Leu Gln Leu Leu Cys Gln Arg
245 250 255

```
His His Asn Met Lys Thr Asp
            260


<210> 1409
<211> 408
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(385)
<223> RXN03032

<400> 1409
cctggtcata ggatacttag ctcaaccaca cggtcagggc cagcaattcc tcacgtttta 60

ccaactccgt aagcacacca tcatggcctg gtgcgccgct atg acc gac ggg gac   115
                                              Met Thr Asp Gly Asp
                                                1               5

tta gac gct gat atc tca ccc cgc cag atc ggg ttg atg acc acc cga   163
Leu Asp Ala Asp Ile Ser Pro Arg Gln Ile Gly Leu Met Thr Thr Arg
                 10                  15                  20

acc gtg gtc gaa atc gtt cga cta cgc cac atg att gcc caa caa cta   211
Thr Val Val Glu Ile Val Arg Leu Arg His Met Ile Ala Gln Gln Leu
             25                  30                  35

gaa aga gcc acg atc atg gaa aac gag tac ctc aaa gaa atc gca gcg   259
Glu Arg Ala Thr Ile Met Glu Asn Glu Tyr Leu Lys Glu Ile Ala Ala
         40                  45                  50

ctg aag aaa gaa ctc gcg cac tac aag caa aaa gac cat cag aat caa   307
Leu Lys Lys Glu Leu Ala His Tyr Lys Gln Lys Asp His Gln Asn Gln
     55                  60                  65

atg gtg atc gat atc ttg gga aaa gct att ggg acc agg ccc aat cct   355
Met Val Ile Asp Ile Leu Gly Lys Ala Ile Gly Thr Arg Pro Asn Pro
 70                  75                  80                  85

ggc gag ggc tta gac gag gag gac gcc acc taaacgtgga tgagcaacgc     405
Gly Glu Gly Leu Asp Glu Glu Asp Ala Thr
                 90                  95

gcc                                                              408


<210> 1410
<211> 95
<212> PRT
<213> Corynebacterium glutamicum

<400> 1410
Met Thr Asp Gly Asp Leu Asp Ala Asp Ile Ser Pro Arg Gln Ile Gly
  1               5                  10                  15

Leu Met Thr Thr Arg Thr Val Val Glu Ile Val Arg Leu Arg His Met
             20                  25                  30

Ile Ala Gln Gln Leu Glu Arg Ala Thr Ile Met Glu Asn Glu Tyr Leu
```

```
         35                  40                  45

Lys Glu Ile Ala Ala Leu Lys Lys Glu Leu Ala His Tyr Lys Gln Lys
     50                  55                  60

Asp His Gln Asn Gln Met Val Ile Asp Ile Leu Gly Lys Ala Ile Gly
 65                  70                  75                  80

Thr Arg Pro Asn Pro Gly Glu Gly Leu Asp Glu Glu Asp Ala Thr
                 85                  90                  95


<210> 1411
<211> 683
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(660)
<223> RXN03034

<400> 1411
ttc cca cca gat cga atc tcc gcc aac ggg cga cgc tat tac gag cca   48
Phe Pro Pro Asp Arg Ile Ser Ala Asn Gly Arg Arg Tyr Tyr Glu Pro
  1               5                  10                  15

caa aca cga ctc gag ttc atg cgg atc tac acc acc ctg ccg cac ggc   96
Gln Thr Arg Leu Glu Phe Met Arg Ile Tyr Thr Thr Leu Pro His Gly
             20                  25                  30

tac cgc cag ccc ttc ctt aaa gcc aac aac atc ggc cac tgc acc gtt   144
Tyr Arg Gln Pro Phe Leu Lys Ala Asn Asn Ile Gly His Cys Thr Val
         35                  40                  45

cga acc tgg cta gca gca ata agc acc ttc agc cga ctt ccc cat gct   192
Arg Thr Trp Leu Ala Ala Ile Ser Thr Phe Ser Arg Leu Pro His Ala
     50                  55                  60

ttt gat gat gcc cac cgc ttc ggg atc gaa cgc acc acc cca gtc gac   240
Phe Asp Asp Ala His Arg Phe Gly Ile Glu Arg Thr Thr Pro Val Asp
 65                  70                  75                  80

gat gtc acc aca cta acg gct gat gac aaa cgt gac ctg gtc ata gga   288
Asp Val Thr Thr Leu Thr Ala Asp Asp Lys Arg Asp Leu Val Ile Gly
                 85                  90                  95

tac tta gct caa cca cac ggt cag ggc cag caa ttc ctc acg ttt tac   336
Tyr Leu Ala Gln Pro His Gly Gln Gly Gln Gln Phe Leu Thr Phe Tyr
            100                 105                 110

caa ctc cgt aag cac acc atc atg gcc tgg tgc gcc gct atg acc gac   384
Gln Leu Arg Lys His Thr Ile Met Ala Trp Cys Ala Ala Met Thr Asp
        115                 120                 125

ggg gac tta gac gct gat atc tca ccc cgc cag atc ggg ttg atg acc   432
Gly Asp Leu Asp Ala Asp Ile Ser Pro Arg Gln Ile Gly Leu Met Thr
    130                 135                 140

acc cga acc gtg gtc gaa atc gtt cga cta cgc cac atg att gcc caa   480
Thr Arg Thr Val Val Glu Ile Val Arg Leu Arg His Met Ile Ala Gln
```

```
145                 150                 155                 160

caa cta gaa aga gcc acg atc atg gaa aac gag tac ctc aaa gaa atc   528
Gln Leu Glu Arg Ala Thr Ile Met Glu Asn Glu Tyr Leu Lys Glu Ile
                165                 170                 175

gca gcg ctg aag aaa gaa ctc gcg cac tac aag caa aaa gac cat cag   576
Ala Ala Leu Lys Lys Glu Leu Ala His Tyr Lys Gln Lys Asp His Gln
            180                 185                 190

aat caa atg gtg atc gat atc ttg gga aaa gct att ggg acc agg ccc   624
Asn Gln Met Val Ile Asp Ile Leu Gly Lys Ala Ile Gly Thr Arg Pro
        195                 200                 205

aat cct ggc gag ggc tta gac gag gag gac gcc acc taaacgtgga        670
Asn Pro Gly Glu Gly Leu Asp Glu Glu Asp Ala Thr
    210                 215                 220

tgagcaacgc gcc                                                   683


<210> 1412
<211> 220
<212> PRT
<213> Corynebacterium glutamicum

<400> 1412
Phe Pro Pro Asp Arg Ile Ser Ala Asn Gly Arg Arg Tyr Tyr Glu Pro
  1               5                  10                  15

Gln Thr Arg Leu Glu Phe Met Arg Ile Tyr Thr Thr Leu Pro His Gly
             20                  25                  30

Tyr Arg Gln Pro Phe Leu Lys Ala Asn Asn Ile Gly His Cys Thr Val
         35                  40                  45

Arg Thr Trp Leu Ala Ala Ile Ser Thr Phe Ser Arg Leu Pro His Ala
     50                  55                  60

Phe Asp Asp Ala His Arg Phe Gly Ile Glu Arg Thr Thr Pro Val Asp
 65                  70                  75                  80

Asp Val Thr Thr Leu Thr Ala Asp Asp Lys Arg Asp Leu Val Ile Gly
                 85                  90                  95

Tyr Leu Ala Gln Pro His Gly Gln Gly Gln Gln Phe Leu Thr Phe Tyr
            100                 105                 110

Gln Leu Arg Lys His Thr Ile Met Ala Trp Cys Ala Ala Met Thr Asp
        115                 120                 125

Gly Asp Leu Asp Ala Asp Ile Ser Pro Arg Gln Ile Gly Leu Met Thr
    130                 135                 140

Thr Arg Thr Val Val Glu Ile Val Arg Leu Arg His Met Ile Ala Gln
145                 150                 155                 160

Gln Leu Glu Arg Ala Thr Ile Met Glu Asn Glu Tyr Leu Lys Glu Ile
                165                 170                 175

Ala Ala Leu Lys Lys Glu Leu Ala His Tyr Lys Gln Lys Asp His Gln
```

```
            180                 185                 190

Asn Gln Met Val Ile Asp Ile Leu Gly Lys Ala Ile Gly Thr Arg Pro
        195                 200                 205

Asn Pro Gly Glu Gly Leu Asp Glu Glu Asp Ala Thr
    210                 215                 220


<210> 1413
<211> 408
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(385)
<223> FRXA00063

<400> 1413
cctggtcata ggatacttag ctcaaccaca cggtcagggc cagcaattcc tcacgtttta 60

ccaactccgt aagcacacca tcatggcctg gtgcgccgct atg acc gac ggg gac   115
                                              Met Thr Asp Gly Asp
                                                1               5

tta gac gct gat atc tca ccc cgc cag atc ggg ttg atg acc acc cga   163
Leu Asp Ala Asp Ile Ser Pro Arg Gln Ile Gly Leu Met Thr Thr Arg
                10                  15                  20

acc gtg gtc gaa atc gtt cga cta cgc cac atg att gcc caa caa cta   211
Thr Val Val Glu Ile Val Arg Leu Arg His Met Ile Ala Gln Gln Leu
            25                  30                  35

gaa aga gcc acg atc atg gaa aac gag tac ctc aaa gaa atc gca gcg   259
Glu Arg Ala Thr Ile Met Glu Asn Glu Tyr Leu Lys Glu Ile Ala Ala
        40                  45                  50

ctg aag aaa gaa ctc gcg cac tac aag caa aaa gac cat cag aat caa   307
Leu Lys Lys Glu Leu Ala His Tyr Lys Gln Lys Asp His Gln Asn Gln
    55                  60                  65

atg gtg atc gat atc ttg gga aaa gct att ggg acc agg ccc aat cct   355
Met Val Ile Asp Ile Leu Gly Lys Ala Ile Gly Thr Arg Pro Asn Pro
70                  75                  80                  85

ggc gag ggc tta gac gag gag gac gcc acc taaacgtgga tgagcaacgc     405
Gly Glu Gly Leu Asp Glu Glu Asp Ala Thr
                90                  95

gcc                                                              408


<210> 1414
<211> 95
<212> PRT
<213> Corynebacterium glutamicum

<400> 1414
Met Thr Asp Gly Asp Leu Asp Ala Asp Ile Ser Pro Arg Gln Ile Gly
  1               5                  10                  15
```

```
Leu Met Thr Thr Arg Thr Val Val Glu Ile Val Arg Leu Arg His Met
            20                  25                  30

Ile Ala Gln Gln Leu Glu Arg Ala Thr Ile Met Glu Asn Glu Tyr Leu
         35                  40                  45

Lys Glu Ile Ala Ala Leu Lys Lys Glu Leu Ala His Tyr Lys Gln Lys
     50                  55                  60

Asp His Gln Asn Gln Met Val Ile Asp Ile Leu Gly Lys Ala Ile Gly
 65                  70                  75                  80

Thr Arg Pro Asn Pro Gly Glu Gly Leu Asp Glu Glu Asp Ala Thr
                 85                  90                  95


<210> 1415
<211> 309
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(286)
<223> RXN03037

<400> 1415
cgctaaaaga caaatgacag cgaagctgca ttcggataca cacctgaaga acactcttca 60

ccactagcat tccaccaacg cctcggaaag ggctatctcc atg tct gtt gac gat   115
                                            Met Ser Val Asp Asp
                                              1               5

ctt tac gct gtt gct ctc gat act cac acc ggt aag cct atc ccc tgc   163
Leu Tyr Ala Val Ala Leu Asp Thr His Thr Gly Lys Pro Ile Pro Cys
                 10                  15                  20

gta ctc tgt gaa aat gct cca cag att gtt atc tac gat ggt tgc tgc   211
Val Leu Cys Glu Asn Ala Pro Gln Ile Val Ile Tyr Asp Gly Cys Cys
             25                  30                  35

tcg ctt gca tat acc caa gca ctt ggc gat ctc gcc gaa gcg gaa taç   259
Ser Leu Ala Tyr Thr Gln Ala Leu Gly Asp Leu Ala Glu Ala Glu Tyr
         40                  45                  50

tac ggc gcc gat ctt gct gca gct gcc taaacaaact tcatagaacg         306
Tyr Gly Ala Asp Leu Ala Ala Ala Ala
     55                  60

aca                                                               309


<210> 1416
<211> 62
<212> PRT
<213> Corynebacterium glutamicum

<400> 1416
Met Ser Val Asp Asp Leu Tyr Ala Val Ala Leu Asp Thr His Thr Gly
  1               5                  10                  15
```

```
Lys Pro Ile Pro Cys Val Leu Cys Glu Asn Ala Pro Gln Ile Val Ile
            20                  25                  30

Tyr Asp Gly Cys Cys Ser Leu Ala Tyr Thr Gln Ala Leu Gly Asp Leu
         35                  40                  45

Ala Glu Ala Glu Tyr Tyr Gly Ala Asp Leu Ala Ala Ala Ala
     50                  55                  60


<210> 1417
<211> 621
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(598)
<223> RXN03041

<400> 1417
accgaggaac tgaaggaaaa tgtaggtgtc ggggcttaga gaaacaaaaa aggctgctac 60

gcggacagca ttgtcacgtg ctgctgcgga gatcgccttg atg gaa ggc cct gag   115
                                        Met Glu Gly Pro Glu
                                          1               5

gcg ttc acg gtt gcg gcc att gca gct gca gcc ggg gtc tcc ccc agg   163
Ala Phe Thr Val Ala Ala Ile Ala Ala Ala Ala Gly Val Ser Pro Arg
                 10                  15                  20

act ttt cat aac tac ttc cct tct cgg gaa gac gca ttg gtg caa ttt   211
Thr Phe His Asn Tyr Phe Pro Ser Arg Glu Asp Ala Leu Val Gln Phe
             25                  30                  35

gtg gtc att cgc gtt cag gaa ctc acg gat cag cta tac gag ttt cct   259
Val Val Ile Arg Val Gln Glu Leu Thr Asp Gln Leu Tyr Glu Phe Pro
         40                  45                  50

aca agc gtg ccc cca cga gat gcc att gaa caa ttg gtg ata aac caa   307
Thr Ser Val Pro Pro Arg Asp Ala Ile Glu Gln Leu Val Ile Asn Gln
     55                  60                  65

ttg cgg gat ggc gat gac gct atg gat tct ttc agc gca atg ttt cga   355
Leu Arg Asp Gly Asp Asp Ala Met Asp Ser Phe Ser Ala Met Phe Arg
 70                  75                  80                  85

atc ggt gag atc ctt gaa aat ctt gac ccc atc aag tgt gtt atc gat   403
Ile Gly Glu Ile Leu Glu Asn Leu Asp Pro Ile Lys Cys Val Ile Asp
                 90                  95                 100

aag gag cga ctc att gct ccg ttg ctt gag ttc atg gtt gaa cgt gac   451
Lys Glu Arg Leu Ile Ala Pro Leu Leu Glu Phe Met Val Glu Arg Asp
             105                 110                 115

aaa gac ctt gac aag ttc gat ngc ggc aac tct gat cca ttt gca tgc   499
Lys Asp Leu Asp Lys Phe Asp Xaa Gly Asn Ser Asp Pro Phe Ala Cys
         120                 125                 130

agc ggc aat tgc aac ctc gct gca tac gtt tta cca agc ttc cga gcc   547
```

```
Ser Gly Asn Cys Asn Leu Ala Ala Tyr Val Leu Pro Ser Phe Arg Ala
    135                 140                 145

ccg gga cat aga aga tgg agt cgc att gat ccg tcg ggc atg cgc ctg   595
Pro Gly His Arg Arg Trp Ser Arg Ile Asp Pro Ser Gly Met Arg Leu
150                 155                 160                 165

gat taagaaanta aaaatctstg aca                                     621
Asp
```

<210> 1418
<211> 166
<212> PRT
<213> Corynebacterium glutamicum

<400> 1418

```
Met Glu Gly Pro Glu Ala Phe Thr Val Ala Ala Ile Ala Ala Ala Ala
  1               5                  10                  15

Gly Val Ser Pro Arg Thr Phe His Asn Tyr Phe Pro Ser Arg Glu Asp
             20                  25                  30

Ala Leu Val Gln Phe Val Val Ile Arg Val Gln Glu Leu Thr Asp Gln
         35                  40                  45

Leu Tyr Glu Phe Pro Thr Ser Val Pro Pro Arg Asp Ala Ile Glu Gln
     50                  55                  60

Leu Val Ile Asn Gln Leu Arg Asp Gly Asp Asp Ala Met Asp Ser Phe
 65                  70                  75                  80

Ser Ala Met Phe Arg Ile Gly Glu Ile Leu Glu Asn Leu Asp Pro Ile
                 85                  90                  95

Lys Cys Val Ile Asp Lys Glu Arg Leu Ile Ala Pro Leu Leu Glu Phe
            100                 105                 110

Met Val Glu Arg Asp Lys Asp Leu Asp Lys Phe Asp Xaa Gly Asn Ser
        115                 120                 125

Asp Pro Phe Ala Cys Ser Gly Asn Cys Asn Leu Ala Ala Tyr Val Leu
    130                 135                 140

Pro Ser Phe Arg Ala Pro Gly His Arg Arg Trp Ser Arg Ile Asp Pro
145                 150                 155                 160

Ser Gly Met Arg Leu Asp
                165
```

<210> 1419
<211> 627
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(604)
<223> FRXA02892

<400> 1419
accgaggaac tgaaggaaaa tgtaggtgtc ggggcttaga gaaacaaaaa aggctgctac 60

gcggacagca ttgtcacgtg ctgctgcgga tcgccttg atg gaa ggc cct gag 115
Met Glu Gly Pro Glu
1 5

gcg ttc acg gtt gcg gcc att gca gct gca gcc ggg gtc tcc ccc agg 163
Ala Phe Thr Val Ala Ala Ile Ala Ala Ala Ala Gly Val Ser Pro Arg
10 15 20

act ttt cat aac tac ttc cct tct cgg gaa gac gca ttg gtg caa ttt 211
Thr Phe His Asn Tyr Phe Pro Ser Arg Glu Asp Ala Leu Val Gln Phe
25 30 35

gtg gtc att cgc gtt cag gaa ctc acg gat cag cta tac gag ttt cct 259
Val Val Ile Arg Val Gln Glu Leu Thr Asp Gln Leu Tyr Glu Phe Pro
40 45 50

aca agc gtg ccc cca cga gat gcc att gaa caa ttg gtg ata aac caa 307
Thr Ser Val Pro Pro Arg Asp Ala Ile Glu Gln Leu Val Ile Asn Gln
55 60 65

ttg cgg gat ggc gat gac gct atg gat tct ttc agc gca atg ttt cga 355
Leu Arg Asp Gly Asp Asp Ala Met Asp Ser Phe Ser Ala Met Phe Arg
70 75 80 85

atc ggt gag atc ctt gaa aat ctt gac ccc atc aag tgt gtt atc gat 403
Ile Gly Glu Ile Leu Glu Asn Leu Asp Pro Ile Lys Cys Val Ile Asp
90 95 100

aag gag cga ctc att gct ccg ttg ctt gag ttc atg gtt gaa cgt gac 451
Lys Glu Arg Leu Ile Ala Pro Leu Leu Glu Phe Met Val Glu Arg Asp
105 110 115

aaa gac ctt gac aag ttc gat gcg gca act ctg atc cat ttg cat gca 499
Lys Asp Leu Asp Lys Phe Asp Ala Ala Thr Leu Ile His Leu His Ala
120 125 130

gcg gca att gca acc tcg ctg cat acg ttt tac caa gct tcc gag ccc 547
Ala Ala Ile Ala Thr Ser Leu His Thr Phe Tyr Gln Ala Ser Glu Pro
135 140 145

cgg gac ata gaa gat gga gtc gca ttg atc cgt cgg gca tgc gcc tgg 595
Arg Asp Ile Glu Asp Gly Val Ala Leu Ile Arg Arg Ala Cys Ala Trp
150 155 160 165

att aag aaa taaaaattgt ggcgtgtgaa cct 627
Ile Lys Lys

<210> 1420
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 1420
Met Glu Gly Pro Glu Ala Phe Thr Val Ala Ala Ile Ala Ala Ala Ala
1 5 10 15

```
Gly Val Ser Pro Arg Thr Phe His Asn Tyr Phe Pro Ser Arg Glu Asp
            20                  25                  30

Ala Leu Val Gln Phe Val Val Ile Arg Val Gln Glu Leu Thr Asp Gln
        35                  40                  45

Leu Tyr Glu Phe Pro Thr Ser Val Pro Pro Arg Asp Ala Ile Glu Gln
    50                  55                  60

Leu Val Ile Asn Gln Leu Arg Asp Gly Asp Asp Ala Met Asp Ser Phe
65                  70                  75                  80

Ser Ala Met Phe Arg Ile Gly Glu Ile Leu Glu Asn Leu Asp Pro Ile
                85                  90                  95

Lys Cys Val Ile Asp Lys Glu Arg Leu Ile Ala Pro Leu Leu Glu Phe
            100                 105                 110

Met Val Glu Arg Asp Lys Asp Leu Asp Lys Phe Asp Ala Ala Thr Leu
        115                 120                 125

Ile His Leu His Ala Ala Ala Ile Ala Thr Ser Leu His Thr Phe Tyr
    130                 135                 140

Gln Ala Ser Glu Pro Arg Asp Ile Glu Asp Gly Val Ala Leu Ile Arg
145                 150                 155                 160

Arg Ala Cys Ala Trp Ile Lys Lys
                165
```

<210> 1421
<211> 1096
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1096)
<223> RXN03045

<400> 1421
agcttttcta tttcgaaaaa tagccttgta ttcgaaaatt tgatcgggta tggtggttgg 60

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tattagcaca gggaactaaa cgggaaaggg ggaagacacc atg agc atc acc aca   115
                                             Met Ser Ile Thr Thr
                                               1               5

cac gtc caa gca ctc acc aca gca ctc aac gcc atc gac aac cat ttg   163
His Val Gln Ala Leu Thr Thr Ala Leu Asn Ala Ile Asp Asn His Leu
                10                  15                  20

gcc agc atg ctt gac cat ggt gtc acc cca gac caa tac aag gcc atc   211
Ala Ser Met Leu Asp His Gly Val Thr Pro Asp Gln Tyr Lys Ala Ile
            25                  30                  35

gag ccc gac ctc atc gcc cta gaa cac acc atc aac cac cac gcc acc   259
Glu Pro Asp Leu Ile Ala Leu Glu His Thr Ile Asn His His Ala Thr
        40                  45                  50
```

```
atc gcc gcc caa acc acc gcc ctc gcc gaa cgc acc aat gct gcg cag   307
Ile Ala Ala Gln Thr Thr Ala Leu Ala Glu Arg Thr Asn Ala Ala Gln
     55                  60                  65

tcg att ggc tcc acc cac ctc atc gac tac ctc acc acc acc ttc ggc   355
Ser Ile Gly Ser Thr His Leu Ile Asp Tyr Leu Thr Thr Thr Phe Gly
 70                  75                  80                  85

cta tct aaa gca cgc gcc cac cac cgc atc aat ctc gcc cac tcc ctc   403
Leu Ser Lys Ala Arg Ala His His Arg Ile Asn Leu Ala His Ser Leu
                90                  95                 100

tac ccc ata ccg aag cca aac tct gga tct ggc aac ggc ggt aat ggt   451
Tyr Pro Ile Pro Lys Pro Asn Ser Gly Ser Gly Asn Gly Gly Asn Gly
            105                 110                 115

ggc aat ccc gac ggt ggt cct gat ggt ggc gac tcg ggt gat gac gac   499
Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp Ser Gly Asp Asp Asp
        120                 125                 130

tcc ggc gat gat gac ccc gac ccc gaa ccg gac aag cct gaa gac ggc   547
Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp Lys Pro Glu Asp Gly
    135                 140                 145

aaa cct gat agt gat aag ccc cgt agg cca cgg atc agc gcg gaa aaa   595
Lys Pro Asp Ser Asp Lys Pro Arg Arg Pro Arg Ile Ser Ala Glu Lys
150                 155                 160                 165

cac gcc atc atc acc gac gaa ctc gcc cgc ctc aac ccg aat acc aca   643
His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu Asn Pro Asn Thr Thr
                170                 175                 180

ccc agc gcc gag gaa ctg cgc aac caa gcc ctg agt cag gcg atc tgg   691
Pro Ser Ala Glu Glu Leu Arg Asn Gln Ala Leu Ser Gln Ala Ile Trp
            185                 190                 195

cgc acc cca gaa gac ctc cgc acg tgg cta cgc cac cag gtc acc acc   739
Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg His Gln Val Thr Thr
        200                 205                 210

gcg aac aaa aac aac ccc aac ccc atc acc gcc atg aaa agg cgc tac   787
Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala Met Lys Arg Arg Tyr
    215                 220                 225

ctc tca gta ggt aaa ccc gat gcc gac aac atg gtc cgc atc agc ggc   835
Leu Ser Val Gly Lys Pro Asp Ala Asp Asn Met Val Arg Ile Ser Gly
230                 235                 240                 245

ctc gtg ccc gca gcc acc gca gca ctg atc acc gcg aac acc gca ccg   883
Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr Ala Asn Thr Ala Pro
                250                 255                 260

tta acc aaa cgc ggc aac ctc gtg gat cta cca gca gca gaa gat atg   931
Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro Ala Ala Glu Asp Met
            265                 270                 275

cgc acc cgc ggg caa cgc cat gcg gac gcg ttg cat cac atc atg gag   979
Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu His His Ile Met Glu
        280                 285                 290

atc tac aac cac ggt att gtc acc cca gct cgt ggt gga aca gcc agc   1027
```

```
Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg Gly Gly Thr Ala Ser
    295                 300                 305

atc atc atc tcc atg acc acc gat gat ctt gac gag atc aac cac gcc   1075
Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp Glu Ile Asn His Ala
310                 315                 320                 325

aac agc agt ggt gaa agt ctg                                       1096
Asn Ser Ser Gly Glu Ser Leu
                330
```

<210> 1422
<211> 332
<212> PRT
<213> Corynebacterium glutamicum

<400> 1422

```
Met Ser Ile Thr Thr His Val Gln Ala Leu Thr Thr Ala Leu Asn Ala
  1               5                  10                  15

Ile Asp Asn His Leu Ala Ser Met Leu Asp His Gly Val Thr Pro Asp
             20                  25                  30

Gln Tyr Lys Ala Ile Glu Pro Asp Leu Ile Ala Leu Glu His Thr Ile
         35                  40                  45

Asn His His Ala Thr Ile Ala Ala Gln Thr Thr Ala Leu Ala Glu Arg
     50                  55                  60

Thr Asn Ala Ala Gln Ser Ile Gly Ser Thr His Leu Ile Asp Tyr Leu
 65                  70                  75                  80

Thr Thr Thr Phe Gly Leu Ser Lys Ala Arg Ala His His Arg Ile Asn
                 85                  90                  95

Leu Ala His Ser Leu Tyr Pro Ile Pro Lys Pro Asn Ser Gly Ser Gly
            100                 105                 110

Asn Gly Gly Asn Gly Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp
        115                 120                 125

Ser Gly Asp Asp Asp Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp
    130                 135                 140

Lys Pro Glu Asp Gly Lys Pro Asp Ser Asp Lys Pro Arg Arg Pro Arg
145                 150                 155                 160

Ile Ser Ala Glu Lys His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu
                165                 170                 175

Asn Pro Asn Thr Thr Pro Ser Ala Glu Glu Leu Arg Asn Gln Ala Leu
            180                 185                 190

Ser Gln Ala Ile Trp Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg
        195                 200                 205

His Gln Val Thr Thr Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala
    210                 215                 220

Met Lys Arg Arg Tyr Leu Ser Val Gly Lys Pro Asp Ala Asp Asn Met
```

```
225                 230                 235                 240

Val Arg Ile Ser Gly Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr
                245                 250                 255

Ala Asn Thr Ala Pro Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro
            260                 265                 270

Ala Ala Glu Asp Met Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu
        275                 280                 285

His His Ile Met Glu Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg
    290                 295                 300

Gly Gly Thr Ala Ser Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp
305                 310                 315                 320

Glu Ile Asn His Ala Asn Ser Ser Gly Glu Ser Leu
                325                 330
```

<210> 1423
<211> 359
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(336)
<223> RXN03046

<400> 1423

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gcc tca att gct aat tcc acc ctg aat att cca gtg gga ttg ggc ggc   48
Ala Ser Ile Ala Asn Ser Thr Leu Asn Ile Pro Val Gly Leu Gly Gly
  1               5                  10                  15

tcc aat ttg ctg ctc aag gcg caa acc gcg acc cca tct gag cct gcg   96
Ser Asn Leu Leu Leu Lys Ala Gln Thr Ala Thr Pro Ser Glu Pro Ala
             20                  25                  30

aat gct cag gac aaa ctg tac cgt ttc tgc atc gcc aat ggt aag agg   144
Asn Ala Gln Asp Lys Leu Tyr Arg Phe Cys Ile Ala Asn Gly Lys Arg
         35                  40                  45

gca ttt tcc gat gcg cag cga ttc ttg ctc aac gcc gac gag ctc gcg   192
Ala Phe Ser Asp Ala Gln Arg Phe Leu Leu Asn Ala Asp Glu Leu Ala
     50                  55                  60

gag ctt tct gat tat gag cgt ctg gct tat gcc atc acc ttg ctt gat   240
Glu Leu Ser Asp Tyr Glu Arg Leu Ala Tyr Ala Ile Thr Leu Leu Asp
 65                  70                  75                  80

cag cct gga aaa gaa gca gaa gga cgc gaa ctt ttt cct ttc gga gct   288
Gln Pro Gly Lys Glu Ala Glu Gly Arg Glu Leu Phe Pro Phe Gly Ala
                 85                  90                  95

tcg ccg cca ggg cta ccg cgc tgt cga ttt ctt gga atc cca gac tgt   336
Ser Pro Pro Gly Leu Pro Arg Cys Arg Phe Leu Gly Ile Pro Asp Cys
            100                 105                 110

tgaccagctg aataaccccg atg                                        359
```

<210> 1424
<211> 112
<212> PRT
<213> Corynebacterium glutamicum

<400> 1424
Ala Ser Ile Ala Asn Ser Thr Leu Asn Ile Pro Val Gly Leu Gly Gly
1 5 10 15

Ser Asn Leu Leu Leu Lys Ala Gln Thr Ala Thr Pro Ser Glu Pro Ala
20 25 30

Asn Ala Gln Asp Lys Leu Tyr Arg Phe Cys Ile Ala Asn Gly Lys Arg
35 40 45

Ala Phe Ser Asp Ala Gln Arg Phe Leu Leu Asn Ala Asp Glu Leu Ala
50 55 60

Glu Leu Ser Asp Tyr Glu Arg Leu Ala Tyr Ala Ile Thr Leu Leu Asp
65 70 75 80

Gln Pro Gly Lys Glu Ala Glu Gly Arg Glu Leu Phe Pro Phe Gly Ala
85 90 95

Ser Pro Pro Gly Leu Pro Arg Cys Arg Phe Leu Gly Ile Pro Asp Cys
100 105 110

<210> 1425
<211> 1539
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1516)
<223> RXN03047

<400> 1425
ctctacccac ttaaaatgga cgcatattcg caagataagg catgcttgga tgaatagatt 60

ttaactcaac gtttactaaa cagaatcgga attaggagcc atg ctt gaa cgc aca 115
Met Leu Glu Arg Thr
1 5

cag gta ttc gtg gat acg tcc tac ctg ctc gca agc ttt tac aac tct 163
Gln Val Phe Val Asp Thr Ser Tyr Leu Leu Ala Ser Phe Tyr Asn Ser
10 15 20

tgg gag aca ggg gca cgt gcc caa tta gaa atc gac ctc ccc gaa gta 211
Trp Glu Thr Gly Ala Arg Ala Gln Leu Glu Ile Asp Leu Pro Glu Val
25 30 35

gtc ggg gta tta gga agg atg att gaa caa caa ctt aaa cag cca gta 259
Val Gly Val Leu Gly Arg Met Ile Glu Gln Gln Leu Lys Gln Pro Val
40 45 50

```
caa cgc caa atg tgg tac gac gga atc ccc gat tcc ggc ccc cac cgc   307
Gln Arg Gln Met Trp Tyr Asp Gly Ile Pro Asp Ser Gly Pro His Arg
     55                  60                  65

tat caa cga gca cta cgc acc tgc gat ggt gtg caa ctt cgt gct ggc   355
Tyr Gln Arg Ala Leu Arg Thr Cys Asp Gly Val Gln Leu Arg Ala Gly
 70                  75                  80                  85

caa tta att gaa tgg ggc gaa cgc cgc aca caa aag gca gta gat acc   403
Gln Leu Ile Glu Trp Gly Glu Arg Arg Thr Gln Lys Ala Val Asp Thr
                 90                  95                 100

cgc ctt gtt gca gac ctc gtt ctc gca ggt gtt cgc gga caa tgc tcc   451
Arg Leu Val Ala Asp Leu Val Leu Ala Gly Val Arg Gly Gln Cys Ser
            105                 110                 115

gat atc gtg ctc gtc agt ggc gac gcc gac atg atc ccc ggt gtt caa   499
Asp Ile Val Leu Val Ser Gly Asp Ala Asp Met Ile Pro Gly Val Gln
        120                 125                 130

gaa gct gcc aat gca ggc ctt cgc gtt cac ctc tac ggc ttc ggc tgg   547
Glu Ala Ala Asn Ala Gly Leu Arg Val His Leu Tyr Gly Phe Gly Trp
    135                 140                 145

gat tcc atg tcc tcc caa ctg cgc cac tgc tgt gac acc acc acc att   595
Asp Ser Met Ser Ser Gln Leu Arg His Cys Cys Asp Thr Thr Thr Ile
150                 155                 160                 165

ttg gat cct cga gaa gat ttt gct gaa tgc atg cag ctg cag gtt ctc   643
Leu Asp Pro Arg Glu Asp Phe Ala Glu Cys Met Gln Leu Gln Val Leu
                170                 175                 180

gaa ggt cca cta ccc cct gtc gtt cgg gta aag ccc atc aac gat gca   691
Glu Gly Pro Leu Pro Pro Val Val Arg Val Lys Pro Ile Asn Asp Ala
            185                 190                 195

gaa ccc atc gag gat ttg gat ttc act cca gtt cca ggc gtc gcc tca   739
Glu Pro Ile Glu Asp Leu Asp Phe Thr Pro Val Pro Gly Val Ala Ser
        200                 205                 210

cca ttt gaa gag gtc agc gcg aaa gat gag aaa ttc tct cca cgc cca   787
Pro Phe Glu Glu Val Ser Ala Lys Asp Glu Lys Phe Ser Pro Arg Pro
    215                 220                 225

agt gaa cct gcc gaa gct ttg tcg gaa cag gtc tgt gaa gcg cag tat   835
Ser Glu Pro Ala Glu Ala Leu Ser Glu Gln Val Cys Glu Ala Gln Tyr
230                 235                 240                 245

gag atc tcc aaa cac gaa ggt caa acc gct gat tca gga gaa atc acc   883
Glu Ile Ser Lys His Glu Gly Gln Thr Ala Asp Ser Gly Glu Ile Thr
                250                 255                 260

gag tct ttc gag gcc gct gaa atc aag gta act gag ttt ttt gga gaa   931
Glu Ser Phe Glu Ala Ala Glu Ile Lys Val Thr Glu Phe Phe Gly Glu
            265                 270                 275

cca gct gct cca gta gcg gaa tca ggc gta gaa gct ccc act ccg gaa   979
Pro Ala Ala Pro Val Ala Glu Ser Gly Val Glu Ala Pro Thr Pro Glu
        280                 285                 290
```

```
gct ccc acg gtt cct gaa gca gct aag ccc act ccg gcg aaa cct aag   1027
Ala Pro Thr Val Pro Glu Ala Ala Lys Pro Thr Pro Ala Lys Pro Lys
    295                 300                 305

act cca aag gca gag ccc caa aag caa gaa tcc ccc aag ccg gga act   1075
Thr Pro Lys Ala Glu Pro Gln Lys Gln Glu Ser Pro Lys Pro Gly Thr
310                 315                 320                 325

cca aaa cca aaa gct cca agc cct gcg gat att cca ccg aaa gcc cca   1123
Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile Pro Pro Lys Ala Pro
                330                 335                 340

gct gac act gag gaa cat tcg gaa gtc gaa gct gaa atc gag gac tca   1171
Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala Glu Ile Glu Asp Ser
            345                 350                 355

cgt cca aag atc ccc agc cct tcg atg atg gct ccc cgc cgc aag ctt   1219
Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala Pro Arg Arg Lys Leu
        360                 365                 370

cgt tcc cgc tac gtt ccg ctt ccc aac gaa gtg tgg gca aca gca gga   1267
Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val Trp Ala Thr Ala Gly
    375                 380                 385

ttc caa act cct tac gat gtc ggg caa cag tac gca tcg tgg tgg ttt   1315
Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr Ala Ser Trp Trp Phe
390                 395                 400                 405

gaa aac gca gct acc agc act caa aga gat cag gct cat cta ttg tct   1363
Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln Ala His Leu Leu Ser
                410                 415                 420

ggt ggc gga ctt cca cca gag atc gat cgc ccg ctt ctg cag ttt gct   1411
Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro Leu Leu Gln Phe Ala
            425                 430                 435

tgt gaa act ctc cac gaa tac acc ctg act gaa gcg cag cgc gta gct   1459
Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu Ala Gln Arg Val Ala
        440                 445                 450

tta cgc gat ggc ttt cac tcc gga atc cgt ggt gta ttg ctc aac cag   1507
Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly Val Leu Leu Asn Gln
    455                 460                 465

cga gat agc tagaatcaca aaaaactggg gct                            1539
Arg Asp Ser
470
```

<210> 1426
<211> 472
<212> PRT
<213> Corynebacterium glutamicum

<400> 1426

```
Met Leu Glu Arg Thr Gln Val Phe Val Asp Thr Ser Tyr Leu Leu Ala
  1               5                  10                  15

Ser Phe Tyr Asn Ser Trp Glu Thr Gly Ala Arg Ala Gln Leu Glu Ile
             20                  25                  30
```

```
Asp Leu Pro Glu Val Val Gly Val Leu Gly Arg Met Ile Glu Gln Gln
         35                  40                  45

Leu Lys Gln Pro Val Gln Arg Gln Met Trp Tyr Asp Gly Ile Pro Asp
     50                  55                  60

Ser Gly Pro His Arg Tyr Gln Arg Ala Leu Arg Thr Cys Asp Gly Val
 65                  70                  75                  80

Gln Leu Arg Ala Gly Gln Leu Ile Glu Trp Gly Glu Arg Arg Thr Gln
                 85                  90                  95

Lys Ala Val Asp Thr Arg Leu Val Ala Asp Leu Val Leu Ala Gly Val
            100                 105                 110

Arg Gly Gln Cys Ser Asp Ile Val Leu Val Ser Gly Asp Ala Asp Met
        115                 120                 125

Ile Pro Gly Val Gln Glu Ala Ala Asn Ala Gly Leu Arg Val His Leu
    130                 135                 140

Tyr Gly Phe Gly Trp Asp Ser Met Ser Ser Gln Leu Arg His Cys Cys
145                 150                 155                 160

Asp Thr Thr Thr Ile Leu Asp Pro Arg Glu Asp Phe Ala Glu Cys Met
                165                 170                 175

Gln Leu Gln Val Leu Glu Gly Pro Leu Pro Pro Val Val Arg Val Lys
            180                 185                 190

Pro Ile Asn Asp Ala Glu Pro Ile Glu Asp Leu Asp Phe Thr Pro Val
        195                 200                 205

Pro Gly Val Ala Ser Pro Phe Glu Glu Val Ser Ala Lys Asp Glu Lys
    210                 215                 220

Phe Ser Pro Arg Pro Ser Glu Pro Ala Glu Ala Leu Ser Glu Gln Val
225                 230                 235                 240

Cys Glu Ala Gln Tyr Glu Ile Ser Lys His Glu Gly Gln Thr Ala Asp
                245                 250                 255

Ser Gly Glu Ile Thr Glu Ser Phe Glu Ala Ala Glu Ile Lys Val Thr
            260                 265                 270

Glu Phe Phe Gly Glu Pro Ala Ala Pro Val Ala Glu Ser Gly Val Glu
        275                 280                 285

Ala Pro Thr Pro Glu Ala Pro Thr Val Pro Glu Ala Ala Lys Pro Thr
    290                 295                 300

Pro Ala Lys Pro Lys Thr Pro Lys Ala Glu Pro Gln Lys Gln Glu Ser
305                 310                 315                 320

Pro Lys Pro Gly Thr Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile
                325                 330                 335

Pro Pro Lys Ala Pro Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala
            340                 345                 350

Glu Ile Glu Asp Ser Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala
```

```
        355                 360                 365

Pro Arg Arg Lys Leu Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val
    370                 375                 380

Trp Ala Thr Ala Gly Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr
385                 390                 395                 400

Ala Ser Trp Trp Phe Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln
                405                 410                 415

Ala His Leu Leu Ser Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro
            420                 425                 430

Leu Leu Gln Phe Ala Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu
        435                 440                 445

Ala Gln Arg Val Ala Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly
    450                 455                 460

Val Leu Leu Asn Gln Arg Asp Ser
465                 470
```

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<210> 1427
<211> 1539
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1516)
<223> FRXA00036

<400> 1427

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ctctacccac ttaaaatgga cgcatattcg caagataagg catgcttgga tgaatagatt 60

ttaactcaac gtttactaaa cagaatcgga attaggagcc atg ctt gaa cgc aca   115
                                            Met Leu Glu Arg Thr
                                              1               5

cag gta ttc gtg gat acg tcc tac ctg ctc gca agc ttt tac aac tct   163
Gln Val Phe Val Asp Thr Ser Tyr Leu Leu Ala Ser Phe Tyr Asn Ser
                10                  15                  20

tgg gag aca ggg gca cgt gcc caa tta gaa atc gac ctc ccc gaa gta   211
Trp Glu Thr Gly Ala Arg Ala Gln Leu Glu Ile Asp Leu Pro Glu Val
            25                  30                  35

gtc ggg gta tta gga agg atg att gaa caa caa ctt aaa cag cca gta   259
Val Gly Val Leu Gly Arg Met Ile Glu Gln Gln Leu Lys Gln Pro Val
        40                  45                  50

caa cgc caa atg tgg tac gac gga atc ccc gat tcc ggc ccc cac cgc   307
Gln Arg Gln Met Trp Tyr Asp Gly Ile Pro Asp Ser Gly Pro His Arg
    55                  60                  65

tat caa cga gca cta cgc acc tgc gat ggt gtg caa ctt cgt gct ggc   355
Tyr Gln Arg Ala Leu Arg Thr Cys Asp Gly Val Gln Leu Arg Ala Gly
70                  75                  80                  85
```

```
caa tta att gaa tgg ggc gaa cgc cgc aca caa aag gca gta gat acc   403
Gln Leu Ile Glu Trp Gly Glu Arg Arg Thr Gln Lys Ala Val Asp Thr
                 90                  95                 100

cgc ctt gtt gca gac ctc gtt ctc gca ggt gtt cgc gga caa tgc tcc   451
Arg Leu Val Ala Asp Leu Val Leu Ala Gly Val Arg Gly Gln Cys Ser
            105                 110                 115

gat atc gtg ctc gtc agt ggc gac gcc gac atg atc ccc ggt gtt caa   499
Asp Ile Val Leu Val Ser Gly Asp Ala Asp Met Ile Pro Gly Val Gln
        120                 125                 130

gaa gct gcc aat gca ggc ctt cgc gtt cac ctc tac ggc ttc ggc tgg   547
Glu Ala Ala Asn Ala Gly Leu Arg Val His Leu Tyr Gly Phe Gly Trp
    135                 140                 145

gat tcc atg tcc tcc caa ctg cgc cac tgc tgt gac acc acc acc att   595
Asp Ser Met Ser Ser Gln Leu Arg His Cys Cys Asp Thr Thr Thr Ile
150                 155                 160                 165

ttg gat cct cga gaa gat ttt gct gaa tgc atg cag ctg cag gtt ctc   643
Leu Asp Pro Arg Glu Asp Phe Ala Glu Cys Met Gln Leu Gln Val Leu
                170                 175                 180

gaa ggt cca cta ccc cct gtc gtt cgg gta aag ccc atc aac gat gca   691
Glu Gly Pro Leu Pro Pro Val Val Arg Val Lys Pro Ile Asn Asp Ala
            185                 190                 195

gaa ccc atc gag gat ttg gat ttc act cca gtt cca ggc gtc gcc tca   739
Glu Pro Ile Glu Asp Leu Asp Phe Thr Pro Val Pro Gly Val Ala Ser
        200                 205                 210

cca ttt gaa gag gtc agc gcg aaa gat gag aaa ttc tct cca cgc cca   787
Pro Phe Glu Glu Val Ser Ala Lys Asp Glu Lys Phe Ser Pro Arg Pro
    215                 220                 225

agt gaa cct gcc gaa gct ttg tcg gaa cag gtc tgt gaa gcg cag tat   835
Ser Glu Pro Ala Glu Ala Leu Ser Glu Gln Val Cys Glu Ala Gln Tyr
230                 235                 240                 245

gag atc tcc aaa cac gaa ggt caa acc gct gat tca gga gaa atc acc   883
Glu Ile Ser Lys His Glu Gly Gln Thr Ala Asp Ser Gly Glu Ile Thr
                250                 255                 260

gag tct ttc gag gcc gct gaa atc aag gta act gag ttt ttt gga gaa   931
Glu Ser Phe Glu Ala Ala Glu Ile Lys Val Thr Glu Phe Phe Gly Glu
            265                 270                 275

cca gct gct cca gta gcg gaa tca ggc gta gaa gct ccc act ccg gaa   979
Pro Ala Ala Pro Val Ala Glu Ser Gly Val Glu Ala Pro Thr Pro Glu
        280                 285                 290

gct ccc acg gtt cct gaa gca gct aag ccc act ccg gcg aaa cct aag   1027
Ala Pro Thr Val Pro Glu Ala Ala Lys Pro Thr Pro Ala Lys Pro Lys
    295                 300                 305

act cca aag gca gag ccc caa aag caa gaa tcc ccc aag ccg gga act   1075
Thr Pro Lys Ala Glu Pro Gln Lys Gln Glu Ser Pro Lys Pro Gly Thr
310                 315                 320                 325

cca aaa cca aaa gct cca agc cct gcg gat att cca ccg aaa gcc cca   1123
```

```
Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile Pro Pro Lys Ala Pro
                330                 335                 340

gct gac act gag gaa cat tcg gaa gtc gaa gct gaa atc gag gac tca   1171
Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala Glu Ile Glu Asp Ser
            345                 350                 355

cgt cca aag atc ccc agc cct tcg atg atg gct ccc cgc cgc aag ctt   1219
Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala Pro Arg Arg Lys Leu
        360                 365                 370

cgt tcc cgc tac gtt ccg ctt ccc aac gaa gtg tgg gca aca gca gga   1267
Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val Trp Ala Thr Ala Gly
    375                 380                 385

ttc caa act cct tac gat gtc ggg caa cag tac gca tcg tgg tgg ttt   1315
Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr Ala Ser Trp Trp Phe
390                 395                 400                 405

gaa aac gca gct acc agc act caa aga gat cag gct cat cta ttg tct   1363
Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln Ala His Leu Leu Ser
                410                 415                 420

ggt ggc gga ctt cca cca gag atc gat cgc ccg ctt ctg cag ttt gct   1411
Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro Leu Leu Gln Phe Ala
            425                 430                 435

tgt gaa act ctc cac gaa tac acc ctg act gaa gcg cag cgc gta gct   1459
Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu Ala Gln Arg Val Ala
        440                 445                 450

tta cgc gat ggc ttt cac tcc gga atc cgt ggt gta ttg ctc aac cag   1507
Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly Val Leu Leu Asn Gln
    455                 460                 465

cga gat agc tagaatcaca aaaaactggg gct                            1539
Arg Asp Ser
470
```

<210> 1428
<211> 472
<212> PRT
<213> Corynebacterium glutamicum

<400> 1428

```
Met Leu Glu Arg Thr Gln Val Phe Val Asp Thr Ser Tyr Leu Leu Ala
  1               5                  10                  15

Ser Phe Tyr Asn Ser Trp Glu Thr Gly Ala Arg Ala Gln Leu Glu Ile
             20                  25                  30

Asp Leu Pro Glu Val Val Gly Val Leu Gly Arg Met Ile Glu Gln Gln
         35                  40                  45

Leu Lys Gln Pro Val Gln Arg Gln Met Trp Tyr Asp Gly Ile Pro Asp
     50                  55                  60

Ser Gly Pro His Arg Tyr Gln Arg Ala Leu Arg Thr Cys Asp Gly Val
 65                  70                  75                  80
```

```
Gln Leu Arg Ala Gly Gln Leu Ile Glu Trp Gly Glu Arg Arg Thr Gln
                85                  90                  95

Lys Ala Val Asp Thr Arg Leu Val Ala Asp Leu Val Leu Ala Gly Val
            100                 105                 110

Arg Gly Gln Cys Ser Asp Ile Val Leu Val Ser Gly Asp Ala Asp Met
        115                 120                 125

Ile Pro Gly Val Gln Glu Ala Ala Asn Ala Gly Leu Arg Val His Leu
    130                 135                 140

Tyr Gly Phe Gly Trp Asp Ser Met Ser Ser Gln Leu Arg His Cys Cys
145                 150                 155                 160

Asp Thr Thr Thr Ile Leu Asp Pro Arg Glu Asp Phe Ala Glu Cys Met
                165                 170                 175

Gln Leu Gln Val Leu Glu Gly Pro Leu Pro Pro Val Val Arg Val Lys
            180                 185                 190

Pro Ile Asn Asp Ala Glu Pro Ile Glu Asp Leu Asp Phe Thr Pro Val
        195                 200                 205

Pro Gly Val Ala Ser Pro Phe Glu Glu Val Ser Ala Lys Asp Glu Lys
    210                 215                 220

Phe Ser Pro Arg Pro Ser Glu Pro Ala Glu Ala Leu Ser Glu Gln Val
225                 230                 235                 240

Cys Glu Ala Gln Tyr Glu Ile Ser Lys His Glu Gly Gln Thr Ala Asp
                245                 250                 255

Ser Gly Glu Ile Thr Glu Ser Phe Glu Ala Ala Glu Ile Lys Val Thr
            260                 265                 270

Glu Phe Phe Gly Glu Pro Ala Ala Pro Val Ala Glu Ser Gly Val Glu
        275                 280                 285

Ala Pro Thr Pro Glu Ala Pro Thr Val Pro Glu Ala Ala Lys Pro Thr
    290                 295                 300

Pro Ala Lys Pro Lys Thr Pro Lys Ala Glu Pro Gln Lys Gln Glu Ser
305                 310                 315                 320

Pro Lys Pro Gly Thr Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile
                325                 330                 335

Pro Pro Lys Ala Pro Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala
            340                 345                 350

Glu Ile Glu Asp Ser Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala
        355                 360                 365

Pro Arg Arg Lys Leu Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val
    370                 375                 380

Trp Ala Thr Ala Gly Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr
385                 390                 395                 400

Ala Ser Trp Trp Phe Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln
```

```
                405                 410                 415

Ala His Leu Leu Ser Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro
            420                 425                 430

Leu Leu Gln Phe Ala Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu
        435                 440                 445

Ala Gln Arg Val Ala Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly
    450                 455                 460

Val Leu Leu Asn Gln Arg Asp Ser
465                 470


<210> 1429
<211> 996
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(973)
<223> RXN03048

<400> 1429
agcgaatcgg attcagtgat ttgcttgcgg gcgcagaaat gatttttcaa ttagacacac 60

ttagacacac gtaactaaaa cctcagggaa gtgactgata atg gct aat ccg ctc   115
                                            Met Ala Asn Pro Leu
                                              1               5

agc aag ggc tgg aag tat ctc atg gca tcg ttc gac aac aag atc gat   163
Ser Lys Gly Trp Lys Tyr Leu Met Ala Ser Phe Asp Asn Lys Ile Asp
                10                  15                  20

gag aat gca gat cca aag atc caa att cag caa gct aca gaa gct gcc   211
Glu Asn Ala Asp Pro Lys Ile Gln Ile Gln Gln Ala Thr Glu Ala Ala
            25                  30                  35

cag aag cag cac cag cag att atg cag cac gct tct cag att atc ggt   259
Gln Lys Gln His Gln Gln Ile Met Gln His Ala Ser Gln Ile Ile Gly
        40                  45                  50

cag cag aag cag ctt gag atg aaa ttg aac cgc ttg gtt act gac cgc   307
Gln Gln Lys Gln Leu Glu Met Lys Leu Asn Arg Leu Val Thr Asp Arg
    55                  60                  65

gat aag ttg cag gaa cag gct cgt cag gca att cag ttg gca gat aag   355
Asp Lys Leu Gln Glu Gln Ala Arg Gln Ala Ile Gln Leu Ala Asp Lys
70                  75                  80                  85

tcc gca aac gaa ggc gac agt gtt aag gct cag gag ttc aac aac act   403
Ser Ala Asn Glu Gly Asp Ser Val Lys Ala Gln Glu Phe Asn Asn Thr
                90                  95                  100

gct gag gtt ttt gct tcc cag ttg gta gct gtg gaa cag cag ttg gag   451
Ala Glu Val Phe Ala Ser Gln Leu Val Ala Val Glu Gln Gln Leu Glu
            105                 110                 115

cag act act gcg ctt cat cag cag gct gag gtt gcg gcg aag gat gct   499
```

```
Gln Thr Thr Ala Leu His Gln Gln Ala Glu Val Ala Ala Lys Asp Ala
        120                 125                 130

gtt gcg aag tct aaa gag tct gag atg cgc ctg aaa gag cag atg tct   547
Val Ala Lys Ser Lys Glu Ser Glu Met Arg Leu Lys Glu Gln Met Ser
    135                 140                 145

cag att gat gct cta cgt gcg cag gct gat cag gcg aag atg cag gaa   595
Gln Ile Asp Ala Leu Arg Ala Gln Ala Asp Gln Ala Lys Met Gln Glu
150                 155                 160                 165

agt gtc act aag tct atg gat tct ttg aat cag ttt ggc act cag gat   643
Ser Val Thr Lys Ser Met Asp Ser Leu Asn Gln Phe Gly Thr Gln Asp
                170                 175                 180

tct tct gtt cct acc ctt gat gcg gtg cgt gag aag atc gag cgt cga   691
Ser Ser Val Pro Thr Leu Asp Ala Val Arg Glu Lys Ile Glu Arg Arg
            185                 190                 195

tac gca gat gct ttg ggc gcg cag gaa ctt acc cag aac act gtt agt   739
Tyr Ala Asp Ala Leu Gly Ala Gln Glu Leu Thr Gln Asn Thr Val Ser
        200                 205                 210

gat cgc atg gct gag att gcg cag tcc ggc acc gat atg cgg gcg tca   787
Asp Arg Met Ala Glu Ile Ala Gln Ser Gly Thr Asp Met Arg Ala Ser
    215                 220                 225

gct cgt ttg gct gaa ctt cgc gcg gag gcg ctg ggc acg tcc gca acg   835
Ala Arg Leu Ala Glu Leu Arg Ala Glu Ala Leu Gly Thr Ser Ala Thr
230                 235                 240                 245

cct aag ggc cag cta gag gca ggt gtc gag gat gcg gaa gaa ctt atc   883
Pro Lys Gly Gln Leu Glu Ala Gly Val Glu Asp Ala Glu Glu Leu Ile
                250                 255                 260

gac gaa acc tcc acc cct tca gct acc cca gaa acc gca agc cca gaa   931
Asp Glu Thr Ser Thr Pro Ser Ala Thr Pro Glu Thr Ala Ser Pro Glu
            265                 270                 275

gct gat gct cca gaa gca tcc gca gac gag tcc gag aag aaa           973
Ala Asp Ala Pro Glu Ala Ser Ala Asp Glu Ser Glu Lys Lys
        280                 285                 290

taacctaaac acaaaaaact ggg                                        996


<210> 1430
<211> 291
<212> PRT
<213> Corynebacterium glutamicum

<400> 1430
Met Ala Asn Pro Leu Ser Lys Gly Trp Lys Tyr Leu Met Ala Ser Phe
  1               5                  10                  15

Asp Asn Lys Ile Asp Glu Asn Ala Asp Pro Lys Ile Gln Ile Gln Gln
             20                  25                  30

Ala Thr Glu Ala Ala Gln Lys Gln His Gln Gln Ile Met Gln His Ala
         35                  40                  45
```

```
Ser Gln Ile Ile Gly Gln Gln Lys Gln Leu Glu Met Lys Leu Asn Arg
     50                  55                  60

Leu Val Thr Asp Arg Asp Lys Leu Gln Glu Gln Ala Arg Gln Ala Ile
 65                  70                  75                  80

Gln Leu Ala Asp Lys Ser Ala Asn Glu Gly Asp Ser Val Lys Ala Gln
                 85                  90                  95

Glu Phe Asn Asn Thr Ala Glu Val Phe Ala Ser Gln Leu Val Ala Val
            100                 105                 110

Glu Gln Gln Leu Glu Gln Thr Thr Ala Leu His Gln Gln Ala Glu Val
        115                 120                 125

Ala Ala Lys Asp Ala Val Ala Lys Ser Lys Glu Ser Glu Met Arg Leu
    130                 135                 140

Lys Glu Gln Met Ser Gln Ile Asp Ala Leu Arg Ala Gln Ala Asp Gln
145                 150                 155                 160

Ala Lys Met Gln Glu Ser Val Thr Lys Ser Met Asp Ser Leu Asn Gln
                165                 170                 175

Phe Gly Thr Gln Asp Ser Ser Val Pro Thr Leu Asp Ala Val Arg Glu
            180                 185                 190

Lys Ile Glu Arg Arg Tyr Ala Asp Ala Leu Gly Ala Gln Glu Leu Thr
        195                 200                 205

Gln Asn Thr Val Ser Asp Arg Met Ala Glu Ile Ala Gln Ser Gly Thr
    210                 215                 220

Asp Met Arg Ala Ser Ala Arg Leu Ala Glu Leu Arg Ala Glu Ala Leu
225                 230                 235                 240

Gly Thr Ser Ala Thr Pro Lys Gly Gln Leu Glu Ala Gly Val Glu Asp
                245                 250                 255

Ala Glu Glu Leu Ile Asp Glu Thr Ser Thr Pro Ser Ala Thr Pro Glu
            260                 265                 270

Thr Ala Ser Pro Glu Ala Asp Ala Pro Glu Ala Ser Ala Asp Glu Ser
        275                 280                 285

Glu Lys Lys
    290
```

Application as filed - Sequence Listing

<210> 1431
<211> 996
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(973)
<223> FRXA00037

<400> 1431
agcgaatcgg attcagtgat ttgcttgcgg gcgcagaaat gatttttcaa ttagacacac 60

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ttagacacac gtaactaaaa cctcagggaa gtgactgata atg gct aat ccg ctc   115
                                              Met Ala Asn Pro Leu
                                                1               5

agc aag ggc tgg aag tat ctc atg gca tcg ttc gac aac aag atc gat   163
Ser Lys Gly Trp Lys Tyr Leu Met Ala Ser Phe Asp Asn Lys Ile Asp
                10                  15                  20

gag aat gca gat cca aag atc caa att cag caa gct aca gaa gct gcc   211
Glu Asn Ala Asp Pro Lys Ile Gln Ile Gln Gln Ala Thr Glu Ala Ala
            25                  30                  35

cag aag cag cac cag cag att atg cag cac gct tct cag att atc ggt   259
Gln Lys Gln His Gln Gln Ile Met Gln His Ala Ser Gln Ile Ile Gly
        40                  45                  50

cag cag aag cag ctt gag atg aaa ttg aac cgc ttg gtt act gac cgc   307
Gln Gln Lys Gln Leu Glu Met Lys Leu Asn Arg Leu Val Thr Asp Arg
    55                  60                  65

gat aag ttg cag gaa cag gct cgt cag gca att cag ttg gca gat aag   355
Asp Lys Leu Gln Glu Gln Ala Arg Gln Ala Ile Gln Leu Ala Asp Lys
70                  75                  80                  85

tcc gca aac gaa ggc gac agt gtt aag gct cag gag ttc aac aac act   403
Ser Ala Asn Glu Gly Asp Ser Val Lys Ala Gln Glu Phe Asn Asn Thr
                90                  95                 100

gct gag gtt ttt gct tcc cag ttg gta gct gtg gaa cag cag ttg gag   451
Ala Glu Val Phe Ala Ser Gln Leu Val Ala Val Glu Gln Gln Leu Glu
            105                 110                 115

cag act act gcg ctt cat cag cag gct gag gtt gcg gcg aag gat gct   499
Gln Thr Thr Ala Leu His Gln Gln Ala Glu Val Ala Ala Lys Asp Ala
        120                 125                 130

gtt gcg aag tct aaa gag tct gag atg cgc ctg aaa gag cag atg tct   547
Val Ala Lys Ser Lys Glu Ser Glu Met Arg Leu Lys Glu Gln Met Ser
    135                 140                 145

cag att gat gct cta cgt gcg cag gct gat cag gcg aag atg cag gaa   595
Gln Ile Asp Ala Leu Arg Ala Gln Ala Asp Gln Ala Lys Met Gln Glu
150                 155                 160                 165

agt gtc act aag tct atg gat tct ttg aat cag ttt ggc act cag gat   643
Ser Val Thr Lys Ser Met Asp Ser Leu Asn Gln Phe Gly Thr Gln Asp
                170                 175                 180

tct tct gtt cct acc ctt gat gcg gtg cgt gag aag atc gag cgt cga   691
Ser Ser Val Pro Thr Leu Asp Ala Val Arg Glu Lys Ile Glu Arg Arg
            185                 190                 195

tac gca gat gct ttg ggc gcg cag gaa ctt acc cag aac act gtt agt   739
Tyr Ala Asp Ala Leu Gly Ala Gln Glu Leu Thr Gln Asn Thr Val Ser
        200                 205                 210

gat cgc atg gct gag att gcg cag tcc ggc acc gat atg cgg gcg tca   787
Asp Arg Met Ala Glu Ile Ala Gln Ser Gly Thr Asp Met Arg Ala Ser
    215                 220                 225
```

```
gct cgt ttg gct gaa ctt cgc gcg gag gcg ctg ggc acg tcc gca acg   835
Ala Arg Leu Ala Glu Leu Arg Ala Glu Ala Leu Gly Thr Ser Ala Thr
230                 235                 240                 245

cct aag ggc cag cta gag gca ggt gtc gag gat gcg gaa gaa ctt atc   883
Pro Lys Gly Gln Leu Glu Ala Gly Val Glu Asp Ala Glu Glu Leu Ile
                250                 255                 260

gac gaa acc tcc acc cct tca gct acc cca gaa acc gca agc cca gaa   931
Asp Glu Thr Ser Thr Pro Ser Ala Thr Pro Glu Thr Ala Ser Pro Glu
            265                 270                 275

gct gat gct cca gaa gca tcc gca gac gag tcc gag aag aaa           973
Ala Asp Ala Pro Glu Ala Ser Ala Asp Glu Ser Glu Lys Lys
        280                 285                 290

taacctaaac acaaaaaact ggg                                        996


<210> 1432
<211> 291
<212> PRT
<213> Corynebacterium glutamicum

<400> 1432
Met Ala Asn Pro Leu Ser Lys Gly Trp Lys Tyr Leu Met Ala Ser Phe
  1               5                  10                  15

Asp Asn Lys Ile Asp Glu Asn Ala Asp Pro Lys Ile Gln Ile Gln Gln
             20                  25                  30

Ala Thr Glu Ala Ala Gln Lys Gln His Gln Gln Ile Met Gln His Ala
         35                  40                  45

Ser Gln Ile Ile Gly Gln Gln Lys Gln Leu Glu Met Lys Leu Asn Arg
     50                  55                  60

Leu Val Thr Asp Arg Asp Lys Leu Gln Glu Gln Ala Arg Gln Ala Ile
 65                  70                  75                  80

Gln Leu Ala Asp Lys Ser Ala Asn Glu Gly Asp Ser Val Lys Ala Gln
                 85                  90                  95

Glu Phe Asn Asn Thr Ala Glu Val Phe Ala Ser Gln Leu Val Ala Val
            100                 105                 110

Glu Gln Gln Leu Glu Gln Thr Thr Ala Leu His Gln Gln Ala Glu Val
        115                 120                 125

Ala Ala Lys Asp Ala Val Ala Lys Ser Lys Glu Ser Glu Met Arg Leu
    130                 135                 140

Lys Glu Gln Met Ser Gln Ile Asp Ala Leu Arg Ala Gln Ala Asp Gln
145                 150                 155                 160

Ala Lys Met Gln Glu Ser Val Thr Lys Ser Met Asp Ser Leu Asn Gln
                165                 170                 175

Phe Gly Thr Gln Asp Ser Ser Val Pro Thr Leu Asp Ala Val Arg Glu
            180                 185                 190
```

```
Lys Ile Glu Arg Arg Tyr Ala Asp Ala Leu Gly Ala Gln Glu Leu Thr
        195                 200                 205

Gln Asn Thr Val Ser Asp Arg Met Ala Glu Ile Ala Gln Ser Gly Thr
    210                 215                 220

Asp Met Arg Ala Ser Ala Arg Leu Ala Glu Leu Arg Ala Glu Ala Leu
225                 230                 235                 240

Gly Thr Ser Ala Thr Pro Lys Gly Gln Leu Glu Ala Gly Val Glu Asp
                245                 250                 255

Ala Glu Glu Leu Ile Asp Glu Thr Ser Thr Pro Ser Ala Thr Pro Glu
            260                 265                 270

Thr Ala Ser Pro Glu Ala Asp Ala Pro Glu Ala Ser Ala Asp Glu Ser
        275                 280                 285

Glu Lys Lys
    290
```

<210> 1433
<211> 1066
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1066)
<223> RXN03050

<400> 1433

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gttaagccta taggaaaaag tgtttgcata tcacccttgt attcgaacac gtgagcgggt 60

agagtgggtg gtaacaacac ggggaaaggg ggaagacacc atg agc atc acc aca   115
                                          Met Ser Ile Thr Thr
                                            1               5

cac gtc caa gca ctc acc aca gca ctc aac gcc atc gac aac cat ttg   163
His Val Gln Ala Leu Thr Thr Ala Leu Asn Ala Ile Asp Asn His Leu
                10                  15                  20

gcc agc atg ctc gac cat ggt gtc acc cca gac caa tac aag gcc atc   211
Ala Ser Met Leu Asp His Gly Val Thr Pro Asp Gln Tyr Lys Ala Ile
            25                  30                  35

gag ccc gac ctc atc gcc cta gaa cac acc atc aac cac cac gcc acc   259
Glu Pro Asp Leu Ile Ala Leu Glu His Thr Ile Asn His His Ala Thr
        40                  45                  50

atc gcc gcc caa acc aca gcc ctc gcc gaa cgc acc aac gcc gcc cac   307
Ile Ala Ala Gln Thr Thr Ala Leu Ala Glu Arg Thr Asn Ala Ala His
    55                  60                  65

acc att ggc tcc acc cac ctc atc gac tac ctc acc acc acc ttc gga   355
Thr Ile Gly Ser Thr His Leu Ile Asp Tyr Leu Thr Thr Thr Phe Gly
70                  75                  80                  85

cta tcc aaa gca cgc gcc cac cac cgc atc aat ctc gcc cac tcc ctc   403
Leu Ser Lys Ala Arg Ala His His Arg Ile Asn Leu Ala His Ser Leu
```

```
                90                  95                 100

tac ccc ata ccg aag cca aac cct gga tct ggc aac ggc ggt aat ggt   451
Tyr Pro Ile Pro Lys Pro Asn Pro Gly Ser Gly Asn Gly Gly Asn Gly
            105                 110                 115

ggc aat ccc gac ggc ggt cct gat ggt ggc gac tcg ggt gat gac gac   499
Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp Ser Gly Asp Asp Asp
        120                 125                 130

tcc ggc gac gat gac ccc gac ccc gaa ccg gac aag cct gaa gac ggc   547
Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp Lys Pro Glu Asp Gly
    135                 140                 145

aaa cct gat ggt gat aag cct cgt ggg cca cgg atc agc gcg gaa aaa   595
Lys Pro Asp Gly Asp Lys Pro Arg Gly Pro Arg Ile Ser Ala Glu Lys
150                 155                 160                 165

cac gcc atc atc acc gac gaa ctc gcc cgc ctc aac ccg aat acc aca   643
His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu Asn Pro Asn Thr Thr
                170                 175                 180

ccc agc gcc gag gag cta cgc acc caa gcc ctg agt caa gcg atc tgg   691
Pro Ser Ala Glu Glu Leu Arg Thr Gln Ala Leu Ser Gln Ala Ile Trp
            185                 190                 195

cgc acc cca gaa gac ctc cgc acg tgg cta cgc cac cac gtc acc acc   739
Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg His His Val Thr Thr
        200                 205                 210

gcc aat aaa aac aac ccc aac ccc atc acc gcc atg aaa agg cgc tac   787
Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala Met Lys Arg Arg Tyr
    215                 220                 225

ctc gct gta ggt aaa ccc gat gcc gac aac atg gtc cgc atc agc ggc   835
Leu Ala Val Gly Lys Pro Asp Ala Asp Asn Met Val Arg Ile Ser Gly
230                 235                 240                 245

ctc gtg ccc gca gcc acc gca gca ctg atc acc gcg aac acc gca ccg   883
Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr Ala Asn Thr Ala Pro
                250                 255                 260

tta acc aaa cgc ggc aac ctc gtg gat cta ccc gca gca gaa gat atg   931
Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro Ala Ala Glu Asp Met
            265                 270                 275

cgc acc cgc ggg caa cgc cat gcg gac gcg ttg cat cac atc atg gag   979
Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu His His Ile Met Glu
        280                 285                 290

atc tac aac cac ggt att gtc acc cca gct cgt ggt gga aca gcc agc   1027
Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg Gly Gly Thr Ala Ser
    295                 300                 305

atc atc atc tcc atg acc acc gat gat ctt gat gag atc               1066
Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp Glu Ile
310                 315                 320
```

<210> 1434
<211> 322

<212> PRT
<213> Corynebacterium glutamicum

<400> 1434

```
Met Ser Ile Thr Thr His Val Gln Ala Leu Thr Thr Ala Leu Asn Ala
  1               5                  10                  15

Ile Asp Asn His Leu Ala Ser Met Leu Asp His Gly Val Thr Pro Asp
             20                  25                  30

Gln Tyr Lys Ala Ile Glu Pro Asp Leu Ile Ala Leu Glu His Thr Ile
         35                  40                  45

Asn His His Ala Thr Ile Ala Ala Gln Thr Thr Ala Leu Ala Glu Arg
     50                  55                  60

Thr Asn Ala Ala His Thr Ile Gly Ser Thr His Leu Ile Asp Tyr Leu
 65                  70                  75                  80

Thr Thr Thr Phe Gly Leu Ser Lys Ala Arg Ala His His Arg Ile Asn
                 85                  90                  95

Leu Ala His Ser Leu Tyr Pro Ile Pro Lys Pro Asn Pro Gly Ser Gly
            100                 105                 110

Asn Gly Gly Asn Gly Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp
        115                 120                 125

Ser Gly Asp Asp Asp Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp
    130                 135                 140

Lys Pro Glu Asp Gly Lys Pro Asp Gly Asp Lys Pro Arg Gly Pro Arg
145                 150                 155                 160

Ile Ser Ala Glu Lys His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu
                165                 170                 175

Asn Pro Asn Thr Thr Pro Ser Ala Glu Glu Leu Arg Thr Gln Ala Leu
            180                 185                 190

Ser Gln Ala Ile Trp Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg
        195                 200                 205

His His Val Thr Thr Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala
    210                 215                 220

Met Lys Arg Arg Tyr Leu Ala Val Gly Lys Pro Asp Ala Asp Asn Met
225                 230                 235                 240

Val Arg Ile Ser Gly Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr
                245                 250                 255

Ala Asn Thr Ala Pro Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro
            260                 265                 270

Ala Ala Glu Asp Met Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu
        275                 280                 285

His His Ile Met Glu Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg
    290                 295                 300
```

```
Gly Gly Thr Ala Ser Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp
305                 310                 315                 320

Glu Ile



<210> 1435
<211> 1558
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (12)..(1535)
<223> RXN03053

<400> 1435
gaggtaaagg attc cac ttc acc tcg act gag ttt gcc ggt tct tat tct   50
            Phe His Phe Thr Ser Thr Glu Phe Ala Gly Ser Tyr Ser
              1               5                  10

ttg gtc acc aat ggt ctt aac gat gtt gct ggc gaa tac gtc ggt gtc   98
Leu Val Thr Asn Gly Leu Asn Asp Val Ala Gly Glu Tyr Val Gly Val
     15                  20                  25

atg cgt ggc gat gtc aac aac tcc gct gtg ctt ttt gat gtg gat cgc   146
Met Arg Gly Asp Val Asn Asn Ser Ala Val Leu Phe Asp Val Asp Arg
 30                  35                  40                  45

tgg tcg gga cat gtc gta tgc gca gat agc tcg att aat aca tca cca   194
Trp Ser Gly His Val Val Cys Ala Asp Ser Ser Ile Asn Thr Ser Pro
                 50                  55                  60

cta ctt aag cgt ccc cgt gtc gtt gac atg tgg ggg tcg aag att tct   242
Leu Leu Lys Arg Pro Arg Val Val Asp Met Trp Gly Ser Lys Ile Ser
            65                  70                  75

cag gca gcg cta ctg aat aac cgt cgc gta gtg cac ctg gtg ctc aat   290
Gln Ala Ala Leu Leu Asn Asn Arg Arg Val Val His Leu Val Leu Asn
        80                  85                  90

ggt gcc aag ctc gat gaa atg gga cca aag cta gaa tcc atg acc gct   338
Gly Ala Lys Leu Asp Glu Met Gly Pro Lys Leu Glu Ser Met Thr Ala
     95                  100                 105

cat gtg gat atg act agc gga gat ctc aac atg ttc gag ctg ttt ggt   386
His Val Asp Met Thr Ser Gly Asp Leu Asn Met Phe Glu Leu Phe Gly
110                 115                 120                 125

aag caa gaa gat gag ctg tcg ctg tat tcc aca cac atg gac aaa atc   434
Lys Gln Glu Asp Glu Leu Ser Leu Tyr Ser Thr His Met Asp Lys Ile
                130                 135                 140

gtg ttt atg acc gag cag gca ttg ggc gat aag acc tct gag ctg gcg   482
Val Phe Met Thr Glu Gln Ala Leu Gly Asp Lys Thr Ser Glu Leu Ala
            145                 150                 155

cta ttg cgc gga aag ctc aaa gaa att att aca gcc ttt tat gtg gat   530
Leu Leu Arg Gly Lys Leu Lys Glu Ile Ile Thr Ala Phe Tyr Val Asp
        160                 165                 170
```

```
atg aaa atg tgg gct ctt aat gcc ggt gaa aac cgt gac aag ctg cgt   578
Met Lys Met Trp Ala Leu Asn Ala Gly Glu Asn Arg Asp Lys Leu Arg
    175                 180                 185

ctt gtt ggt gtg cct cat gag cag atc ccg ttg ctc tct gtc ttc gtg   626
Leu Val Gly Val Pro His Glu Gln Ile Pro Leu Leu Ser Val Phe Val
190                 195                 200                 205

tcc tat ttg gat caa gaa tat gag cgc cag aaa tat gag gga acc aaa   674
Ser Tyr Leu Asp Gln Glu Tyr Glu Arg Gln Lys Tyr Glu Gly Thr Lys
                210                 215                 220

gac cct gaa atg ttt cgt gcc att tct gtg ctg cga ctg acc tat aag   722
Asp Pro Glu Met Phe Arg Ala Ile Ser Val Leu Arg Leu Thr Tyr Lys
            225                 230                 235

gat ttg ctc gat act cat ggc gat ctg ttt aat cag cac acg gca gat   770
Asp Leu Leu Asp Thr His Gly Asp Leu Phe Asn Gln His Thr Ala Asp
        240                 245                 250

ggc att gat tct gtg aac tct gca cgc cgc gtg atc tat gat ttt tct   818
Gly Ile Asp Ser Val Asn Ser Ala Arg Arg Val Ile Tyr Asp Phe Ser
    255                 260                 265

gga gtg ctg cga cgt ggc gca ggt gtc gcg atg gca cag ctg gtt aac   866
Gly Val Leu Arg Arg Gly Ala Gly Val Ala Met Ala Gln Leu Val Asn
270                 275                 280                 285

gtg att ggt ttt gct gtg gag acg ctt ggt caa ggc gat gtg gtc atc   914
Val Ile Gly Phe Ala Val Glu Thr Leu Gly Gln Gly Asp Val Val Ile
                290                 295                 300

att cac ggt gct gat ggc att gtc gat gtt gat gtt cag gat tat ttg   962
Ile His Gly Ala Asp Gly Ile Val Asp Val Asp Val Gln Asp Tyr Leu
            305                 310                 315

gct aat cag ttc gca tat atg gct gag cgt ggt ggg cga gtg gcg tat  1010
Ala Asn Gln Phe Ala Tyr Met Ala Glu Arg Gly Gly Arg Val Ala Tyr
        320                 325                 330

ctc tac agc tcg atg gac gcg atg ctt ggc act gtt ggc ttc aat caa  1058
Leu Tyr Ser Ser Met Asp Ala Met Leu Gly Thr Val Gly Phe Asn Gln
    335                 340                 345

ttc caa cgt gct gcg tac acc att ttg ggc ccg atg aac gtt gac tcg  1106
Phe Gln Arg Ala Ala Tyr Thr Ile Leu Gly Pro Met Asn Val Asp Ser
350                 355                 360                 365

gtg gat act tat caa tct ctg att aat agt cag atc ccg atg gac ttg  1154
Val Asp Thr Tyr Gln Ser Leu Ile Asn Ser Gln Ile Pro Met Asp Leu
                370                 375                 380

gca cgg ttg gtg aca acg cag aat tct ggt gcg agc tat ttg cgc cga  1202
Ala Arg Leu Val Thr Thr Gln Asn Ser Gly Ala Ser Tyr Leu Arg Arg
            385                 390                 395

gga tct acc aat gtg gtg ttt gaa acc aac ctt gcg ttg ggc gtt aat  1250
Gly Ser Thr Asn Val Val Phe Glu Thr Asn Leu Ala Leu Gly Val Asn
        400                 405                 410
```

```
cct tat atg gag cag cgt cgc aag att gaa gca cag cga ggt cag cga   1298
Pro Tyr Met Glu Gln Arg Arg Lys Ile Glu Ala Gln Arg Gly Gln Arg
    415                 420                 425

cga tcc aag cga gac aag cac tac ggt ggt ggc acg acg atg gtg ggc   1346
Arg Ser Lys Arg Asp Lys His Tyr Gly Gly Gly Thr Thr Met Val Gly
430                 435                 440                 445

aca gcg gat ctt gat gtt gtc gca att cag gcg aag gcc gag cac cgc   1394
Thr Ala Asp Leu Asp Val Val Ala Ile Gln Ala Lys Ala Glu His Arg
                450                 455                 460

gaa gag cgc ttt gat gag aaa tct gcg cgc aag atg aag gag ctt gat   1442
Glu Glu Arg Phe Asp Glu Lys Ser Ala Arg Lys Met Lys Glu Leu Asp
            465                 470                 475

gat gta gaa gcg aaa gaa cta gct ttg aaa act ggg ccg aag aat ctt   1490
Asp Val Glu Ala Lys Glu Leu Ala Leu Lys Thr Gly Pro Lys Asn Leu
        480                 485                 490

gat gat gcg ctt gca cag gtg gag aag aag cgc ctg gcg aag cgg       1535
Asp Asp Ala Leu Ala Gln Val Glu Lys Lys Arg Leu Ala Lys Arg
    495                 500                 505

tagttgttgg ctgtggtgaa taa                                        1558
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<210> 1436
<211> 508
<212> PRT
<213> Corynebacterium glutamicum

<400> 1436

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Phe His Phe Thr Ser Thr Glu Phe Ala Gly Ser Tyr Ser Leu Val Thr
  1               5                  10                  15

Asn Gly Leu Asn Asp Val Ala Gly Glu Tyr Val Gly Val Met Arg Gly
             20                  25                  30

Asp Val Asn Asn Ser Ala Val Leu Phe Asp Val Asp Arg Trp Ser Gly
         35                  40                  45

His Val Val Cys Ala Asp Ser Ser Ile Asn Thr Ser Pro Leu Leu Lys
     50                  55                  60

Arg Pro Arg Val Val Asp Met Trp Gly Ser Lys Ile Ser Gln Ala Ala
 65                  70                  75                  80

Leu Leu Asn Asn Arg Arg Val Val His Leu Val Leu Asn Gly Ala Lys
                 85                  90                  95

Leu Asp Glu Met Gly Pro Lys Leu Glu Ser Met Thr Ala His Val Asp
            100                 105                 110

Met Thr Ser Gly Asp Leu Asn Met Phe Glu Leu Phe Gly Lys Gln Glu
        115                 120                 125

Asp Glu Leu Ser Leu Tyr Ser Thr His Met Asp Lys Ile Val Phe Met
    130                 135                 140

Thr Glu Gln Ala Leu Gly Asp Lys Thr Ser Glu Leu Ala Leu Leu Arg
```

```
145                 150                 155                 160

Gly Lys Leu Lys Glu Ile Ile Thr Ala Phe Tyr Val Asp Met Lys Met
                165                 170                 175

Trp Ala Leu Asn Ala Gly Glu Asn Arg Asp Lys Leu Arg Leu Val Gly
            180                 185                 190

Val Pro His Glu Gln Ile Pro Leu Leu Ser Val Phe Val Ser Tyr Leu
        195                 200                 205

Asp Gln Glu Tyr Glu Arg Gln Lys Tyr Glu Gly Thr Lys Asp Pro Glu
    210                 215                 220

Met Phe Arg Ala Ile Ser Val Leu Arg Leu Thr Tyr Lys Asp Leu Leu
225                 230                 235                 240

Asp Thr His Gly Asp Leu Phe Asn Gln His Thr Ala Asp Gly Ile Asp
                245                 250                 255

Ser Val Asn Ser Ala Arg Arg Val Ile Tyr Asp Phe Ser Gly Val Leu
            260                 265                 270

Arg Arg Gly Ala Gly Val Ala Met Ala Gln Leu Val Asn Val Ile Gly
        275                 280                 285

Phe Ala Val Glu Thr Leu Gly Gln Gly Asp Val Val Ile Ile His Gly
    290                 295                 300

Ala Asp Gly Ile Val Asp Val Asp Val Gln Asp Tyr Leu Ala Asn Gln
305                 310                 315                 320

Phe Ala Tyr Met Ala Glu Arg Gly Gly Arg Val Ala Tyr Leu Tyr Ser
                325                 330                 335

Ser Met Asp Ala Met Leu Gly Thr Val Gly Phe Asn Gln Phe Gln Arg
            340                 345                 350

Ala Ala Tyr Thr Ile Leu Gly Pro Met Asn Val Asp Ser Val Asp Thr
        355                 360                 365

Tyr Gln Ser Leu Ile Asn Ser Gln Ile Pro Met Asp Leu Ala Arg Leu
    370                 375                 380

Val Thr Thr Gln Asn Ser Gly Ala Ser Tyr Leu Arg Arg Gly Ser Thr
385                 390                 395                 400

Asn Val Val Phe Glu Thr Asn Leu Ala Leu Gly Val Asn Pro Tyr Met
                405                 410                 415

Glu Gln Arg Arg Lys Ile Glu Ala Gln Arg Gly Gln Arg Arg Ser Lys
            420                 425                 430

Arg Asp Lys His Tyr Gly Gly Gly Thr Thr Met Val Gly Thr Ala Asp
        435                 440                 445

Leu Asp Val Val Ala Ile Gln Ala Lys Ala Glu His Arg Glu Glu Arg
    450                 455                 460

Phe Asp Glu Lys Ser Ala Arg Lys Met Lys Glu Leu Asp Asp Val Glu
465                 470                 475                 480
```

```
Ala Lys Glu Leu Ala Leu Lys Thr Gly Pro Lys Asn Leu Asp Asp Ala
                485                 490                 495

Leu Ala Gln Val Glu Lys Lys Arg Leu Ala Lys Arg
            500                 505
```

<210> 1437
<211> 1559
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1536)
<223> FRXA02885

<400> 1437

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cga ggt aaa gga ttc cac ttc acc tcg act gag ttt gcc ggt tct tat   48
Arg Gly Lys Gly Phe His Phe Thr Ser Thr Glu Phe Ala Gly Ser Tyr
  1               5                  10                  15

tct ttg gtc acc aat ggt ctt aac gat gtt gct ggc gaa tac gtc ggt   96
Ser Leu Val Thr Asn Gly Leu Asn Asp Val Ala Gly Glu Tyr Val Gly
             20                  25                  30

gtc atg cgt ggc gat gtc aac aac tcc gct gtg ctt ttt gat gtg gat   144
Val Met Arg Gly Asp Val Asn Asn Ser Ala Val Leu Phe Asp Val Asp
         35                  40                  45

cgc tgg tcg gga cat gtc gta tgc gca gat agc tcg att aat aca tca   192
Arg Trp Ser Gly His Val Val Cys Ala Asp Ser Ser Ile Asn Thr Ser
     50                  55                  60

cca cta ctt aag cgt ccc cgt gtc gtt gac atg tgg ggg tcg aag att   240
Pro Leu Leu Lys Arg Pro Arg Val Val Asp Met Trp Gly Ser Lys Ile
 65                  70                  75                  80

tct cag gca gcg cta ctg aat aac cgt cgc gta gtg cac ctg gtg ctc   288
Ser Gln Ala Ala Leu Leu Asn Asn Arg Arg Val Val His Leu Val Leu
                 85                  90                  95

aat ggt gcc aag ctc gat gaa atg gga cca aag cta gaa tcc atg acc   336
Asn Gly Ala Lys Leu Asp Glu Met Gly Pro Lys Leu Glu Ser Met Thr
            100                 105                 110

gct cat gtg gat atg act agc gga gat ctc aac atg ttc gag ctg ttt   384
Ala His Val Asp Met Thr Ser Gly Asp Leu Asn Met Phe Glu Leu Phe
        115                 120                 125

ggt aag caa gaa gat gag ctg tcg ctg tat tcc aca cac atg gac aaa   432
Gly Lys Gln Glu Asp Glu Leu Ser Leu Tyr Ser Thr His Met Asp Lys
    130                 135                 140

atc gtg ttt atg acc gag cag gca ttg ggc gat aag acc tct gag ctg   480
Ile Val Phe Met Thr Glu Gln Ala Leu Gly Asp Lys Thr Ser Glu Leu
145                 150                 155                 160

gcg cta ttg cgc gga aag ctc aaa gaa att att aca gcc ttt tat gtg   528
Ala Leu Leu Arg Gly Lys Leu Lys Glu Ile Ile Thr Ala Phe Tyr Val
```

```
                  165                 170                 175

gat atg aaa atg tgg gct ctt aat gcc ggt gaa aac cgt gac aag ctg   576
Asp Met Lys Met Trp Ala Leu Asn Ala Gly Glu Asn Arg Asp Lys Leu
            180                 185                 190

cgt ctt gtt ggt gtg cct cat gag cag atc ccg ttg ctc tct gtc ttc   624
Arg Leu Val Gly Val Pro His Glu Gln Ile Pro Leu Leu Ser Val Phe
        195                 200                 205

gtg tcc tat ttg gat caa gaa tat gag cgc cag aaa tat gag gga acc   672
Val Ser Tyr Leu Asp Gln Glu Tyr Glu Arg Gln Lys Tyr Glu Gly Thr
    210                 215                 220

aaa gac cct gaa atg ttt cgt gcc att tct gtg ctg cga ctg acc tat   720
Lys Asp Pro Glu Met Phe Arg Ala Ile Ser Val Leu Arg Leu Thr Tyr
225                 230                 235                 240

aag gat ttg ctc gat act cat ggc gat ctg ttt aat cag cac acg gca   768
Lys Asp Leu Leu Asp Thr His Gly Asp Leu Phe Asn Gln His Thr Ala
                245                 250                 255

gat ggc att gat tct gtg aac tct gca cgc cgc gtg atc tat gat ttt   816
Asp Gly Ile Asp Ser Val Asn Ser Ala Arg Arg Val Ile Tyr Asp Phe
            260                 265                 270

tct gga gtg ctg cga cgt ggc gca ggt gtc gcg atg gca cag ctg gtt   864
Ser Gly Val Leu Arg Arg Gly Ala Gly Val Ala Met Ala Gln Leu Val
        275                 280                 285

aac gtg att ggt ttt gct gtg gag acg ctt ggt caa ggc gat gtg gtc   912
Asn Val Ile Gly Phe Ala Val Glu Thr Leu Gly Gln Gly Asp Val Val
    290                 295                 300

atc att cac ggt gct gat ggc att gtc gat gtt gat gtt cag gat tat   960
Ile Ile His Gly Ala Asp Gly Ile Val Asp Val Asp Val Gln Asp Tyr
305                 310                 315                 320

ttg gct aat cag ttc gca tat atg gct gag cgt ggt ggg cga gtg gcg   1008
Leu Ala Asn Gln Phe Ala Tyr Met Ala Glu Arg Gly Gly Arg Val Ala
                325                 330                 335

tat ctc tac agc tcg atg gac gcg atg ctt ggc act gtt ggc ttc aat   1056
Tyr Leu Tyr Ser Ser Met Asp Ala Met Leu Gly Thr Val Gly Phe Asn
            340                 345                 350

caa ttc caa cgt gct gcg tac acc att ttg ggc ccg atg aac gtt gac   1104
Gln Phe Gln Arg Ala Ala Tyr Thr Ile Leu Gly Pro Met Asn Val Asp
        355                 360                 365

tcg gtg gat act tat caa tct ctg att aat agt cag atc ccg atg gac   1152
Ser Val Asp Thr Tyr Gln Ser Leu Ile Asn Ser Gln Ile Pro Met Asp
    370                 375                 380

ttg gca cgg ttg gtg aca acg cag aat tct ggt gcg agc tat ttg cgc   1200
Leu Ala Arg Leu Val Thr Thr Gln Asn Ser Gly Ala Ser Tyr Leu Arg
385                 390                 395                 400

cga gga tct acc aat gtg gtg ttt gaa acc aac ctt gcg ttg ggc gtt   1248
Arg Gly Ser Thr Asn Val Val Phe Glu Thr Asn Leu Ala Leu Gly Val
                405                 410                 415
```

```
aat cct tat atg gag cag cgt cgc aag att gaa gca cag cga ggt cag   1296
Asn Pro Tyr Met Glu Gln Arg Arg Lys Ile Glu Ala Gln Arg Gly Gln
            420                 425                 430

cga cga tcc aag cga gac aag cac tac ggt ggt ggc acg acg atg gtg   1344
Arg Arg Ser Lys Arg Asp Lys His Tyr Gly Gly Gly Thr Thr Met Val
        435                 440                 445

ggc aca gcg gat ctt gat gtt gtc gca att cag gcg aag gcc gag cac   1392
Gly Thr Ala Asp Leu Asp Val Val Ala Ile Gln Ala Lys Ala Glu His
    450                 455                 460

cgc gaa gag cgc ttt gat gag aaa tct gcg cgc aag atg aag gag ctt   1440
Arg Glu Glu Arg Phe Asp Glu Lys Ser Ala Arg Lys Met Lys Glu Leu
465                 470                 475                 480

gat gat gta gaa gcg aaa gaa cta gct ttg aaa act ggg ccg aag aat   1488
Asp Asp Val Glu Ala Lys Glu Leu Ala Leu Lys Thr Gly Pro Lys Asn
                485                 490                 495

ctt gat gat gcg ctt gca cag gtg gag aag aag cgc ctg gcg aag cgg   1536
Leu Asp Asp Ala Leu Ala Gln Val Glu Lys Lys Arg Leu Ala Lys Arg
            500                 505                 510

tagttgttgg ctgtggtgaa taa                                       1559


<210> 1438
<211> 512
<212> PRT
<213> Corynebacterium glutamicum

<400> 1438
Arg Gly Lys Gly Phe His Phe Thr Ser Thr Glu Phe Ala Gly Ser Tyr
  1               5                  10                  15

Ser Leu Val Thr Asn Gly Leu Asn Asp Val Ala Gly Glu Tyr Val Gly
             20                  25                  30

Val Met Arg Gly Asp Val Asn Asn Ser Ala Val Leu Phe Asp Val Asp
         35                  40                  45

Arg Trp Ser Gly His Val Val Cys Ala Asp Ser Ser Ile Asn Thr Ser
     50                  55                  60

Pro Leu Leu Lys Arg Pro Arg Val Val Asp Met Trp Gly Ser Lys Ile
 65                  70                  75                  80

Ser Gln Ala Ala Leu Leu Asn Asn Arg Arg Val Val His Leu Val Leu
                 85                  90                  95

Asn Gly Ala Lys Leu Asp Glu Met Gly Pro Lys Leu Glu Ser Met Thr
            100                 105                 110

Ala His Val Asp Met Thr Ser Gly Asp Leu Asn Met Phe Glu Leu Phe
        115                 120                 125

Gly Lys Gln Glu Asp Glu Leu Ser Leu Tyr Ser Thr His Met Asp Lys
    130                 135                 140
```

```
Ile Val Phe Met Thr Glu Gln Ala Leu Gly Asp Lys Thr Ser Glu Leu
145                 150                 155                 160

Ala Leu Leu Arg Gly Lys Leu Lys Glu Ile Ile Thr Ala Phe Tyr Val
                165                 170                 175

Asp Met Lys Met Trp Ala Leu Asn Ala Gly Glu Asn Arg Asp Lys Leu
            180                 185                 190

Arg Leu Val Gly Val Pro His Glu Gln Ile Pro Leu Leu Ser Val Phe
        195                 200                 205

Val Ser Tyr Leu Asp Gln Glu Tyr Glu Arg Gln Lys Tyr Glu Gly Thr
    210                 215                 220

Lys Asp Pro Glu Met Phe Arg Ala Ile Ser Val Leu Arg Leu Thr Tyr
225                 230                 235                 240

Lys Asp Leu Leu Asp Thr His Gly Asp Leu Phe Asn Gln His Thr Ala
                245                 250                 255

Asp Gly Ile Asp Ser Val Asn Ser Ala Arg Arg Val Ile Tyr Asp Phe
            260                 265                 270

Ser Gly Val Leu Arg Arg Gly Ala Gly Val Ala Met Ala Gln Leu Val
        275                 280                 285

Asn Val Ile Gly Phe Ala Val Glu Thr Leu Gly Gln Gly Asp Val Val
    290                 295                 300

Ile Ile His Gly Ala Asp Gly Ile Val Asp Val Asp Val Gln Asp Tyr
305                 310                 315                 320

Leu Ala Asn Gln Phe Ala Tyr Met Ala Glu Arg Gly Gly Arg Val Ala
                325                 330                 335

Tyr Leu Tyr Ser Ser Met Asp Ala Met Leu Gly Thr Val Gly Phe Asn
            340                 345                 350

Gln Phe Gln Arg Ala Ala Tyr Thr Ile Leu Gly Pro Met Asn Val Asp
        355                 360                 365

Ser Val Asp Thr Tyr Gln Ser Leu Ile Asn Ser Gln Ile Pro Met Asp
    370                 375                 380

Leu Ala Arg Leu Val Thr Thr Gln Asn Ser Gly Ala Ser Tyr Leu Arg
385                 390                 395                 400

Arg Gly Ser Thr Asn Val Val Phe Glu Thr Asn Leu Ala Leu Gly Val
                405                 410                 415

Asn Pro Tyr Met Glu Gln Arg Arg Lys Ile Glu Ala Gln Arg Gly Gln
            420                 425                 430

Arg Arg Ser Lys Arg Asp Lys His Tyr Gly Gly Gly Thr Thr Met Val
        435                 440                 445

Gly Thr Ala Asp Leu Asp Val Val Ala Ile Gln Ala Lys Ala Glu His
    450                 455                 460

Arg Glu Glu Arg Phe Asp Glu Lys Ser Ala Arg Lys Met Lys Glu Leu
```

```
465                 470                 475                 480

Asp Asp Val Glu Ala Lys Glu Leu Ala Leu Lys Thr Gly Pro Lys Asn
                485                 490                 495

Leu Asp Asp Ala Leu Ala Gln Val Glu Lys Lys Arg Leu Ala Lys Arg
            500                 505                 510
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<210> 1439
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(529)
<223> RXN03055

<400> 1439

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aaggtcagcc gtatttcggt cagtcagcaa ctaattacgc ttatcttccg tgtacgatag 60

accgtagtta acataaggaa tggaatagga gaattgcggc atg tat tcc gac aag   115
                                              Met Tyr Ser Asp Lys
                                                1               5

ctg att ctc ttg ttc ctt tct gag cag gat tca agc tat gaa tgc tgc   163
Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser Ser Tyr Glu Cys Cys
                10                  15                  20

gta ggt tta tta gat ggc tca gat gga cgt gat tat att gaa aag ctt   211
Val Gly Leu Leu Asp Gly Ser Asp Gly Arg Asp Tyr Ile Glu Lys Leu
            25                  30                  35

ctg aag ggt agg aag ctg aag aac cat ttt ctt gaa tgg gaa gat att   259
Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu Glu Trp Glu Asp Ile
        40                  45                  50

aac aag gct gat gtt gct cgt gaa gaa ata tat aaa ggg caa ttg gtg   307
Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr Lys Gly Gln Leu Val
    55                  60                  65

cat ctg gtg ttt gtg acg gct ctt tcc acg cct ggt gaa att tct ttt   355
His Leu Val Phe Val Thr Ala Leu Ser Thr Pro Gly Glu Ile Ser Phe
70                  75                  80                  85

gtt ttt cca ggt caa tct ctt atg agt gca aca ctc gaa gaa gac ttt   403
Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr Leu Glu Glu Asp Phe
                90                  95                  100

gct gcg ctt gtg ctc gaa gag gag cgc aca tca ttt aga cct gaa ctg   451
Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser Phe Arg Pro Glu Leu
            105                 110                 115

tct cac ctg tgg tca ctc ccc gta ggg tgg gta gct ccg ggg ctt gag   499
Ser His Leu Trp Ser Leu Pro Val Gly Trp Val Ala Pro Gly Leu Glu
        120                 125                 130
```

```
ggt ttc gtg gag cgt aat tcc gag gca gct tgaaccaccg ctttctgagc     549
Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
    135                 140

cgg                                                              552


<210> 1440
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 1440
Met Tyr Ser Asp Lys Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser
  1               5                  10                  15

Ser Tyr Glu Cys Cys Val Gly Leu Leu Asp Gly Ser Asp Gly Arg Asp
             20                  25                  30

Tyr Ile Glu Lys Leu Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu
         35                  40                  45

Glu Trp Glu Asp Ile Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr
     50                  55                  60

Lys Gly Gln Leu Val His Leu Val Phe Val Thr Ala Leu Ser Thr Pro
 65                  70                  75                  80

Gly Glu Ile Ser Phe Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr
                 85                  90                  95

Leu Glu Glu Asp Phe Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser
            100                 105                 110

Phe Arg Pro Glu Leu Ser His Leu Trp Ser Leu Pro Val Gly Trp Val
        115                 120                 125

Ala Pro Gly Leu Glu Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
    130                 135                 140


<210> 1441
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(529)
<223> FRXA00261

<400> 1441
aaggtcagcc gtatttcggt cagtcagcaa ctaattacgc ttatcttccg tgtacgatag 60

accgtagtta acataaggaa tggaatagga gaattgcggc atg tat tcc gac aag   115
                                            Met Tyr Ser Asp Lys
                                              1               5

ctg att ctc ttg ttc ctt tct gag cag gat tca agc tat gaa tgc tgc   163
Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser Ser Tyr Glu Cys Cys
                 10                  15                  20
```

```
gta ggt tta tta gat ggc tca gat gga cgt gat tat att gaa aag ctt   211
Val Gly Leu Leu Asp Gly Ser Asp Gly Arg Asp Tyr Ile Glu Lys Leu
            25                  30                  35

ctg aag ggt agg aag ctg aag aac cat ttt ctt gaa tgg gaa gat att   259
Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu Glu Trp Glu Asp Ile
        40                  45                  50

aac aag gct gat gtt gct cgt gaa gaa ata tat aaa ggg caa ttg gtg   307
Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr Lys Gly Gln Leu Val
    55                  60                  65

cat ctg gtg ttt gtg acg gct ctt tcc acg cct ggt gaa att tct ttt   355
His Leu Val Phe Val Thr Ala Leu Ser Thr Pro Gly Glu Ile Ser Phe
70                  75                  80                  85

gtt ttt cca ggt caa tct ctc atg agt gca aca ctc gaa gaa gac ttt   403
Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr Leu Glu Glu Asp Phe
            90                  95                  100

gct gca ctt gtg ctc gaa gag gag cgc aca tca ttt aga cct gat ctg   451
Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser Phe Arg Pro Asp Leu
        105                 110                 115

tct cac ttg tgg tca ctc ccc gta ggg tgg gta gct ccg ggg ctt gag   499
Ser His Leu Trp Ser Leu Pro Val Gly Trp Val Ala Pro Gly Leu Glu
    120                 125                 130

ggt ttc gtg gag cgt aat tca gag gca gct tgaaccaccg ctctttgagc     549
Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
135                 140

cgg                                                               552
```

Sequence Listing.ST25.txt

<210> 1442
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 1442

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Met Tyr Ser Asp Lys Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser
  1               5                  10                  15

Ser Tyr Glu Cys Cys Val Gly Leu Leu Asp Gly Ser Asp Gly Arg Asp
            20                  25                  30

Tyr Ile Glu Lys Leu Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu
        35                  40                  45

Glu Trp Glu Asp Ile Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr
    50                  55                  60

Lys Gly Gln Leu Val His Leu Val Phe Val Thr Ala Leu Ser Thr Pro
65                  70                  75                  80

Gly Glu Ile Ser Phe Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr
                85                  90                  95

Leu Glu Glu Asp Phe Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser
```

```
            100                 105                 110

Phe Arg Pro Asp Leu Ser His Leu Trp Ser Leu Pro Val Gly Trp Val
        115                 120                 125

Ala Pro Gly Leu Glu Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
    130                 135                 140


<210> 1443
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(529)
<223> FRXA02888

<400> 1443
aaggtcagcc gtatttcggt cagtcagcaa ctaattacgc ttatcttccg tgtacgatag 60

accgtagtta acataaggaa tggaatagga gaattgcggc atg tat tcc gac aag   115
                                            Met Tyr Ser Asp Lys
                                              1               5

ctg att ctc ttg ttc ctt tct gag cag gat tca agc tat gaa tgc tgc   163
Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser Ser Tyr Glu Cys Cys
                10                  15                  20

gta ggt tta tta gat ggc tca gat gga cgt gat tat att gaa aag ctt   211
Val Gly Leu Leu Asp Gly Ser Asp Gly Arg Asp Tyr Ile Glu Lys Leu
            25                  30                  35

ctg aag ggt agg aag ctg aag aac cat ttt ctt gaa tgg gaa gat att   259
Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu Glu Trp Glu Asp Ile
        40                  45                  50

aac aag gct gat gtt gct cgt gaa gaa ata tat aaa ggg caa ttg gtg   307
Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr Lys Gly Gln Leu Val
    55                  60                  65

cat ctg gtg ttt gtg acg gct ctt tcc acg cct ggt gaa att tct ttt   355
His Leu Val Phe Val Thr Ala Leu Ser Thr Pro Gly Glu Ile Ser Phe
70                  75                  80                  85

gtt ttt cca ggt caa tct ctt atg agt gca aca ctc gaa gaa gac ttt   403
Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr Leu Glu Glu Asp Phe
                90                  95                  100

gct gcg ctt gtg ctc gaa gag gag cgc aca tca ttt aga cct gaa ctg   451
Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser Phe Arg Pro Glu Leu
            105                 110                 115

tct cac ctg tgg tca ctc ccc gta ggg tgg gta gct ccg ggg ctt gag   499
Ser His Leu Trp Ser Leu Pro Val Gly Trp Val Ala Pro Gly Leu Glu
        120                 125                 130

ggt ttc gtg gag cgt aat tcc gag gca gct tgaaccaccg ctttctgagc     549
Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
    135                 140
```

cgg 552

<210> 1444
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 1444
Met Tyr Ser Asp Lys Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser
1 5 10 15

Ser Tyr Glu Cys Cys Val Gly Leu Leu Asp Gly Ser Asp Gly Arg Asp
20 25 30

Tyr Ile Glu Lys Leu Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu
35 40 45

Glu Trp Glu Asp Ile Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr
50 55 60

Lys Gly Gln Leu Val His Leu Val Phe Val Thr Ala Leu Ser Thr Pro
65 70 75 80

Gly Glu Ile Ser Phe Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr
85 90 95

Leu Glu Glu Asp Phe Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser
100 105 110

Phe Arg Pro Glu Leu Ser His Leu Trp Ser Leu Pro Val Gly Trp Val
115 120 125

Ala Pro Gly Leu Glu Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
130 135 140

<210> 1445
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(580)
<223> RXN03059

<400> 1445
gtgtcatttt cttggcggac ggtcgtatcg tgaaccagtt gtttgatccc accatcgagg 60

aaatcttggc cacgatgaac ggaattgagg atattgccta atg aat tcc ggt tcc 115
Met Asn Ser Gly Ser
1 5

aca atg cgc aga atc agt ctg cgc aat att ggc gcg cac aag gtc agg 163
Thr Met Arg Arg Ile Ser Leu Arg Asn Ile Gly Ala His Lys Val Arg
10 15 20

ctg ttt ttg aca gtt ctg gca gtg gtg ctc ggc acg tct ttt gtt tcc 211
Leu Phe Leu Thr Val Leu Ala Val Val Leu Gly Thr Ser Phe Val Ser

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            25                  30                  35

ggc gcg atg atg ttt acc aac gcg ctg tcc tcc act ttt gat gag gct   259
Gly Ala Met Met Phe Thr Asn Ala Leu Ser Ser Thr Phe Asp Glu Ala
         40                  45                  50

att gcc agc agc ttt gac ggc gtg gat gtg gtg gtt tca cca aac ggt   307
Ile Ala Ser Ser Phe Asp Gly Val Asp Val Val Val Ser Pro Asn Gly
     55                  60                  65

gca tca gag gtg cag ggt gtt cct gtt gag acg gtt gaa tct ttg cgt   355
Ala Ser Glu Val Gln Gly Val Pro Val Glu Thr Val Glu Ser Leu Arg
 70                  75                  80                  85

gag gat tcc cgc atc aac cat ctc aac atc aac ggt tcc cag act gtc   403
Glu Asp Ser Arg Ile Asn His Leu Asn Ile Asn Gly Ser Gln Thr Val
                 90                  95                 100

gtt ctg gcg gat gct gat tcc aag gca att caa acg act ggg gga tcg   451
Val Leu Ala Asp Ala Asp Ser Lys Ala Ile Gln Thr Thr Gly Gly Ser
            105                 110                 115

tcg tta agc att tat tac agc gcg gac gac gcg gtt gcc cag gca cct   499
Ser Leu Ser Ile Tyr Tyr Ser Ala Asp Asp Ala Val Ala Gln Ala Pro
        120                 125                 130

gaa ttg gct gag gga gag gca ccg act ggc acc gaa gag gtg ctt gcc   547
Glu Leu Ala Glu Gly Glu Ala Pro Thr Gly Thr Glu Glu Val Leu Ala
    135                 140                 145

tcg aag gcg ggc gct gag gcg aat ggc ctg gag taggggacca gatcttggtc 600
Ser Lys Ala Gly Ala Glu Ala Asn Gly Leu Glu
150                 155                 160

gtg                                                               603


<210> 1446
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 1446
Met Asn Ser Gly Ser Thr Met Arg Arg Ile Ser Leu Arg Asn Ile Gly
  1               5                  10                  15

Ala His Lys Val Arg Leu Phe Leu Thr Val Leu Ala Val Val Leu Gly
             20                  25                  30

Thr Ser Phe Val Ser Gly Ala Met Met Phe Thr Asn Ala Leu Ser Ser
         35                  40                  45

Thr Phe Asp Glu Ala Ile Ala Ser Ser Phe Asp Gly Val Asp Val Val
     50                  55                  60

Val Ser Pro Asn Gly Ala Ser Glu Val Gln Gly Val Pro Val Glu Thr
 65                  70                  75                  80

Val Glu Ser Leu Arg Glu Asp Ser Arg Ile Asn His Leu Asn Ile Asn
                 85                  90                  95
```

```
Gly Ser Gln Thr Val Val Leu Ala Asp Ala Asp Ser Lys Ala Ile Gln
            100                 105                 110

Thr Thr Gly Gly Ser Ser Leu Ser Ile Tyr Tyr Ser Ala Asp Asp Ala
        115                 120                 125

Val Ala Gln Ala Pro Glu Leu Ala Glu Gly Glu Ala Pro Thr Gly Thr
    130                 135                 140

Glu Glu Val Leu Ala Ser Lys Ala Gly Ala Glu Ala Asn Gly Leu Glu
145                 150                 155                 160
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<210> 1447
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(580)
<223> FRXA02899

<400> 1447

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aaatcttggc cacgatgaac ggaattgagg atattgccta atg aat tcc ggt tcc   115
                                            Met Asn Ser Gly Ser
                                              1               5

aca atg cgc aga atc agt ctg cgc aat att ggc gcg cac aag gtc agg   163
Thr Met Arg Arg Ile Ser Leu Arg Asn Ile Gly Ala His Lys Val Arg
                10                  15                  20

ctg ttt ttg aca gtt ctg gca gtg gtg ctc ggc acg tct ttt gtt tcc   211
Leu Phe Leu Thr Val Leu Ala Val Val Leu Gly Thr Ser Phe Val Ser
            25                  30                  35

ggc gcg atg atg ttt acc aac gcg ctg tcc tcc act ttt gat gag gct   259
Gly Ala Met Met Phe Thr Asn Ala Leu Ser Ser Thr Phe Asp Glu Ala
        40                  45                  50

att gcc agc agc ttt gac ggc gtg gat gtg gtg gtt tca cca aac ggt   307
Ile Ala Ser Ser Phe Asp Gly Val Asp Val Val Val Ser Pro Asn Gly
    55                  60                  65

gca tca gag gtg cag ggt gtt cct gtt gag acg gtt gaa tct ttg cgt   355
Ala Ser Glu Val Gln Gly Val Pro Val Glu Thr Val Glu Ser Leu Arg
70                  75                  80                  85

gag gat tcc cgc atc aac cat ctc aac atc aac ggt tcc cag act gtc   403
Glu Asp Ser Arg Ile Asn His Leu Asn Ile Asn Gly Ser Gln Thr Val
                90                  95                  100

gtt ctg gcg gat gct gat tcc aag gca att caa acg act ggg gga tcg   451
Val Leu Ala Asp Ala Asp Ser Lys Ala Ile Gln Thr Thr Gly Gly Ser
            105                 110                 115
```

```
tcg tta agc att tat tac agc gcg gac gac gcg gtt gcc cag gca cct   499
Ser Leu Ser Ile Tyr Tyr Ser Ala Asp Asp Ala Val Ala Gln Ala Pro
        120                 125                 130

gaa ttg gct gag gga gag gca ccg act ggc acc gaa gag gtg ctt gcc   547
Glu Leu Ala Glu Gly Glu Ala Pro Thr Gly Thr Glu Glu Val Leu Ala
    135                 140                 145

tcg aag gcg ggc gct gag gcg aat ggc ctg gag taggggacca gatcttggtc 600
Ser Lys Ala Gly Ala Glu Ala Asn Gly Leu Glu
150                 155                 160

gtg                                                               603
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<210> 1448
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 1448

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Met Asn Ser Gly Ser Thr Met Arg Arg Ile Ser Leu Arg Asn Ile Gly
  1               5                  10                  15

Ala His Lys Val Arg Leu Phe Leu Thr Val Leu Ala Val Val Leu Gly
             20                  25                  30

Thr Ser Phe Val Ser Gly Ala Met Met Phe Thr Asn Ala Leu Ser Ser
         35                  40                  45

Thr Phe Asp Glu Ala Ile Ala Ser Ser Phe Asp Gly Val Asp Val Val
     50                  55                  60

Val Ser Pro Asn Gly Ala Ser Glu Val Gln Gly Val Pro Val Glu Thr
 65                  70                  75                  80

Val Glu Ser Leu Arg Glu Asp Ser Arg Ile Asn His Leu Asn Ile Asn
                 85                  90                  95

Gly Ser Gln Thr Val Val Leu Ala Asp Ala Asp Ser Lys Ala Ile Gln
            100                 105                 110

Thr Thr Gly Gly Ser Ser Leu Ser Ile Tyr Tyr Ser Ala Asp Asp Ala
        115                 120                 125

Val Ala Gln Ala Pro Glu Leu Ala Glu Gly Glu Ala Pro Thr Gly Thr
    130                 135                 140

Glu Glu Val Leu Ala Ser Lys Ala Gly Ala Glu Ala Asn Gly Leu Glu
145                 150                 155                 160
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<210> 1449
<211> 622
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(622)
<223> RXN03062

<400> 1449
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atatttggcc catatggata attgacagga gtttaacgcc atg gaa acc cca acc 115
Met Glu Thr Pro Thr
1 5

caa gac atg gat gtc cgc tgg tta tac acc caa agc cag ctc aaa ctc 163
Gln Asp Met Asp Val Arg Trp Leu Tyr Thr Gln Ser Gln Leu Lys Leu
10 15 20

cgc gaa att ctc ccc aca aac aaa acc ttc gat gtc atc caa atc agc 211
Arg Glu Ile Leu Pro Thr Asn Lys Thr Phe Asp Val Ile Gln Ile Ser
25 30 35

gaa ctc gtt gac ccc acc gac ttc atc agg ccc aac agc gtg gtc tta 259
Glu Leu Val Asp Pro Thr Asp Phe Ile Arg Pro Asn Ser Val Val Leu
40 45 50

tcc gtt ggc atc gcc ttc gca gaa acg ccc gac ggg ctt cgc gat tgg 307
Ser Val Gly Ile Ala Phe Ala Glu Thr Pro Asp Gly Leu Arg Asp Trp
55 60 65

gca cac cga ctc gcc gac gca ggg gtc atc gcg atc ggg ttc ggc tcc 355
Ala His Arg Leu Ala Asp Ala Gly Val Ile Ala Ile Gly Phe Gly Ser
70 75 80 85

ggc ctc acc ttc cca cag gtt ccg cag gcg ctt atc gac gcc tcc ctc 403
Gly Leu Thr Phe Pro Gln Val Pro Gln Ala Leu Ile Asp Ala Ser Leu
90 95 100

cac ctt ggc ctc ggc ctc ttt gaa gtc ccc cgt gaa att cca ttt atc 451
His Leu Gly Leu Gly Leu Phe Glu Val Pro Arg Glu Ile Pro Phe Ile
105 110 115

tcg atc acc tcc agc gtg cgt gat gag caa acc cgc cgt gcc ggc cgc 499
Ser Ile Thr Ser Ser Val Arg Asp Glu Gln Thr Arg Arg Ala Gly Arg
120 125 130

ctg caa caa gaa ctc ctc ctg gaa cag gaa cgg ctt aac tcc atc gcc 547
Leu Gln Gln Glu Leu Leu Leu Glu Gln Glu Arg Leu Asn Ser Ile Ala
135 140 145

atc tcc ggt ggc atc gaa gcc ctg tgc cgt gct gcc gcc gac tat ttg 595
Ile Ser Gly Gly Ile Glu Ala Leu Cys Arg Ala Ala Ala Asp Tyr Leu
150 155 160 165

ggt ggt gca gta acc atc gtg gac agc 622
Gly Gly Ala Val Thr Ile Val Asp Ser
170

<210> 1450
<211> 174
<212> PRT
<213> Corynebacterium glutamicum

<400> 1450
Met Glu Thr Pro Thr Gln Asp Met Asp Val Arg Trp Leu Tyr Thr Gln
1 5 10 15

Ser Gln Leu Lys Leu Arg Glu Ile Leu Pro Thr Asn Lys Thr Phe Asp
20 25 30

Val Ile Gln Ile Ser Glu Leu Val Asp Pro Thr Asp Phe Ile Arg Pro
35 40 45

Asn Ser Val Val Leu Ser Val Gly Ile Ala Phe Ala Glu Thr Pro Asp
50 55 60

Gly Leu Arg Asp Trp Ala His Arg Leu Ala Asp Ala Gly Val Ile Ala
65 70 75 80

Ile Gly Phe Gly Ser Gly Leu Thr Phe Pro Gln Val Pro Gln Ala Leu
85 90 95

Ile Asp Ala Ser Leu His Leu Gly Leu Gly Leu Phe Glu Val Pro Arg
100 105 110

Glu Ile Pro Phe Ile Ser Ile Thr Ser Ser Val Arg Asp Glu Gln Thr
115 120 125

Arg Arg Ala Gly Arg Leu Gln Gln Glu Leu Leu Leu Glu Gln Glu Arg
130 135 140

Leu Asn Ser Ile Ala Ile Ser Gly Gly Ile Glu Ala Leu Cys Arg Ala
145 150 155 160

Ala Ala Asp Tyr Leu Gly Gly Ala Val Thr Ile Val Asp Ser
165 170

<210> 1451
<211> 786
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(763)
<223> RXN03066

<400> 1451
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cgaaatcacc gcggcgtaat agcaccagct taaaaacctt atg aca tca gac aaa 115
Met Thr Ser Asp Lys
1 5

gac act gaa caa ttg gaa gcg gca ggc act gaa att tta atg cct cgc 163
Asp Thr Glu Gln Leu Glu Ala Ala Gly Thr Glu Ile Leu Met Pro Arg
10 15 20

cgc cgt ccg gca cag cag cgc agt cgt gaa cga ttc aat cga atc ctc 211
Arg Arg Pro Ala Gln Gln Arg Ser Arg Glu Arg Phe Asn Arg Ile Leu
25 30 35

acc gct gcg cgt tca gtg ctt gtc gat cta ggt ttt gaa tcg ttc acg 259

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Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly Phe Glu Ser Phe Thr
         40                  45                  50

ttt gat gaa gtc gct aag cgt gca gag gta ccg atc ggc acg ctg tac   307
Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro Ile Gly Thr Leu Tyr
     55                  60                  65

caa ttc ttt gcc aat aag tat gta ttg atc tgc gaa ttg gat cgt gtg   355
Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys Glu Leu Asp Arg Val
 70                  75                  80                  85

gat acc gca gaa gct gtc gcg gag ttg aag aaa ttc tcc gat cag gtt   403
Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys Phe Ser Asp Gln Val
                 90                  95                 100

cct gcg ttg cag tgg ccg gat atc ctt gat gaa ttc att gag cac ttg   451
Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu Phe Ile Glu His Leu
            105                 110                 115

gct agg ctc tgg cgc gat gat ccg tct cgg cgg gcc gtg tgg cat gcc   499
Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg Ala Val Trp His Ala
        120                 125                 130

atc cag tcc acg ccg gca act cgt gcg aca gct gcg gcg acg gaa aaa   547
Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala Ala Ala Thr Glu Lys
    135                 140                 145

gag atg ctg gaa atc atc gcg gaa gtt atg cgc ccg ctt gcc cgc ggt   595
Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg Pro Leu Ala Arg Gly
150                 155                 160                 165

gcc ggc tac gag gag cgc atg tca ctg gcg gga ttg ctg gtg cac acg   643
Ala Gly Tyr Glu Glu Arg Met Ser Leu Ala Gly Leu Leu Val His Thr
                170                 175                 180

gta agt tcc ctg ctt aac tat gcc gtg cgt gat gtc aat agt tcc gaa   691
Val Ser Ser Leu Leu Asn Tyr Ala Val Arg Asp Val Asn Ser Ser Glu
            185                 190                 195

gag gat ttc gac agc atc gtg gaa gaa ata aaa cga atg ctg att tct   739
Glu Asp Phe Asp Ser Ile Val Glu Glu Ile Lys Arg Met Leu Ile Ser
        200                 205                 210

tac ctc ttc tcc gtg gct act gga tagtcaacac gcacgttcca ccg         786
Tyr Leu Phe Ser Val Ala Thr Gly
    215                 220
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<210> 1452
<211> 221
<212> PRT
<213> Corynebacterium glutamicum

<400> 1452

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Met Thr Ser Asp Lys Asp Thr Glu Gln Leu Glu Ala Ala Gly Thr Glu
  1               5                  10                  15

Ile Leu Met Pro Arg Arg Arg Pro Ala Gln Gln Arg Ser Arg Glu Arg
             20                  25                  30

Phe Asn Arg Ile Leu Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly
```

```
         35                  40                  45

Phe Glu Ser Phe Thr Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro
     50                  55                  60

Ile Gly Thr Leu Tyr Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys
 65                  70                  75                  80

Glu Leu Asp Arg Val Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys
                 85                  90                  95

Phe Ser Asp Gln Val Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu
            100                 105                 110

Phe Ile Glu His Leu Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg
        115                 120                 125

Ala Val Trp His Ala Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala
    130                 135                 140

Ala Ala Thr Glu Lys Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg
145                 150                 155                 160

Pro Leu Ala Arg Gly Ala Gly Tyr Glu Glu Arg Met Ser Leu Ala Gly
                165                 170                 175

Leu Leu Val His Thr Val Ser Ser Leu Leu Asn Tyr Ala Val Arg Asp
            180                 185                 190

Val Asn Ser Ser Glu Glu Asp Phe Asp Ser Ile Val Glu Glu Ile Lys
        195                 200                 205

Arg Met Leu Ile Ser Tyr Leu Phe Ser Val Ala Thr Gly
    210                 215                 220


<210> 1453
<211> 786
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(763)
<223> FRXA02876

<400> 1453
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cgaaatcacc gcggcgtaat agcaccagct taaaaacctt atg aca tca gac aaa   115
                                              Met Thr Ser Asp Lys
                                                1               5

gac act gaa caa ttg gaa gcg gca ggc act gaa att tta atg cct cgc   163
Asp Thr Glu Gln Leu Glu Ala Ala Gly Thr Glu Ile Leu Met Pro Arg
                10                  15                  20

cgc cgt ccg gca cag cag cgc agt cgt gaa cga ttc aat cga atc ctc   211
Arg Arg Pro Ala Gln Gln Arg Ser Arg Glu Arg Phe Asn Arg Ile Leu
            25                  30                  35
```

```
acc gct gcg cgt tca gtg ctt gtc gat cta ggt ttt gaa tcg ttc acg   259
Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly Phe Glu Ser Phe Thr
         40                  45                  50

ttt gat gaa gtc gct aag cgt gca gag gta ccg atc ggc acg ctg tac   307
Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro Ile Gly Thr Leu Tyr
     55                  60                  65

caa ttc ttt gcc aat aag tat gta ttg atc tgc gaa ttg gat cgt gtg   355
Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys Glu Leu Asp Arg Val
 70                  75                  80                  85

gat acc gca gaa gct gtc gcg gag ttg aag aaa ttc tcc gat cag gtt   403
Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys Phe Ser Asp Gln Val
                 90                  95                 100

cct gcg ttg cag tgg ccg gat atc ctt gat gaa ttc att gag cac ttg   451
Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu Phe Ile Glu His Leu
            105                 110                 115

gct agg ctc tgg cgc gat gat ccg tct cgg cgg gcc gtg tgg cat gcc   499
Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg Ala Val Trp His Ala
        120                 125                 130

atc cag tcc acg ccg gca act cgt gcg aca gct gcg gcg acg gaa aaa   547
Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala Ala Ala Thr Glu Lys
    135                 140                 145

gag atg ctg gaa atc atc gcg gaa gtt atg cgc ccg ctt gcc cgc ggt   595
Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg Pro Leu Ala Arg Gly
150                 155                 160                 165

gcc ggc tac gag gag cgc atg tca ctg gcg gga ttg ctg gtg cac acg   643
Ala Gly Tyr Glu Glu Arg Met Ser Leu Ala Gly Leu Leu Val His Thr
                170                 175                 180

gta agt tcc ctg ctt aac tat gcc gtg cgt gat gtc aat agt tcc gaa   691
Val Ser Ser Leu Leu Asn Tyr Ala Val Arg Asp Val Asn Ser Ser Glu
            185                 190                 195

gag gat ttc gac agc atc gtg gaa gaa atc aaa cga atg ctg att tct   739
Glu Asp Phe Asp Ser Ile Val Glu Glu Ile Lys Arg Met Leu Ile Ser
        200                 205                 210

tac ctc ttc tcc gtg gct act gga tagtcaacac gcacgtcgcc acc         786
Tyr Leu Phe Ser Val Ala Thr Gly
    215                 220
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<210> 1454
<211> 221
<212> PRT
<213> Corynebacterium glutamicum

<400> 1454

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Met Thr Ser Asp Lys Asp Thr Glu Gln Leu Glu Ala Ala Gly Thr Glu
  1               5                  10                  15

Ile Leu Met Pro Arg Arg Arg Pro Ala Gln Gln Arg Ser Arg Glu Arg
             20                  25                  30
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Phe Asn Arg Ile Leu Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly
         35                  40                  45

Phe Glu Ser Phe Thr Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro
     50                  55                  60

Ile Gly Thr Leu Tyr Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys
 65                  70                  75                  80

Glu Leu Asp Arg Val Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys
                 85                  90                  95

Phe Ser Asp Gln Val Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu
            100                 105                 110

Phe Ile Glu His Leu Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg
        115                 120                 125

Ala Val Trp His Ala Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala
    130                 135                 140

Ala Ala Thr Glu Lys Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg
145                 150                 155                 160

Pro Leu Ala Arg Gly Ala Gly Tyr Glu Glu Arg Met Ser Leu Ala Gly
                165                 170                 175

Leu Leu Val His Thr Val Ser Ser Leu Leu Asn Tyr Ala Val Arg Asp
            180                 185                 190

Val Asn Ser Ser Glu Glu Asp Phe Asp Ser Ile Val Glu Glu Ile Lys
        195                 200                 205

Arg Met Leu Ile Ser Tyr Leu Phe Ser Val Ala Thr Gly
    210                 215                 220
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<210> 1455
<211> 294
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(271)
<223> RXN03067

<400> 1455
ttgctgttgt tggcatttcc ccggatccgg tggacaagct ggtaagttcc gtgaggacca 60

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tgagctgaac ttccctcttc tttccgatga ggacaagtct gtg atg act gcg tgg   115
                                              Val Met Thr Ala Trp
                                                1               5

ggt gcg ttt ggt gag aag aag aat tac ggc aag att gtt cag ggt gta   163
Gly Ala Phe Gly Glu Lys Lys Asn Tyr Gly Lys Ile Val Gln Gly Val
                  10                  15                  20

att cgt tcc aca ttc ctc atc aat gct gac gga act gtt ggc atg gcg   211
Ile Arg Ser Thr Phe Leu Ile Asn Ala Asp Gly Thr Val Gly Met Ala
             25                  30                  35
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aag tac aat gtt cgt gca act ggt cac gtg gag cgc atc gtc cgc gaa   259
Lys Tyr Asn Val Arg Ala Thr Gly His Val Glu Arg Ile Val Arg Glu
         40                  45                  50

atc acc gcg gcg taatagcacc agcttaaaaa cct                        294
Ile Thr Ala Ala
     55


<210> 1456
<211> 57
<212> PRT
<213> Corynebacterium glutamicum

<400> 1456
Val Met Thr Ala Trp Gly Ala Phe Gly Glu Lys Lys Asn Tyr Gly Lys
  1               5                  10                  15

Ile Val Gln Gly Val Ile Arg Ser Thr Phe Leu Ile Asn Ala Asp Gly
             20                  25                  30

Thr Val Gly Met Ala Lys Tyr Asn Val Arg Ala Thr Gly His Val Glu
         35                  40                  45

Arg Ile Val Arg Glu Ile Thr Ala Ala
     50                  55


<210> 1457
<211> 143
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(120)
<223> RXN03068

<400> 1457
acc aag gaa gca tgc gat ttc cgt gat tct ttg agc aac ctc aac gat   48
Thr Lys Glu Ala Cys Asp Phe Arg Asp Ser Leu Ser Asn Leu Asn Asp
  1               5                  10                  15

ctc gac att gct gtt gtt ggc att tcc ccg gat ccg gtg gac aag ctg   96
Leu Asp Ile Ala Val Val Gly Ile Ser Pro Asp Pro Val Asp Lys Leu
             20                  25                  30

gta agt tcc gtg agg acc atg agc tgaacttccc tcttctttcc gat        143
Val Ser Ser Val Arg Thr Met Ser
         35                  40


<210> 1458
<211> 40
<212> PRT
<213> Corynebacterium glutamicum

<400> 1458
Thr Lys Glu Ala Cys Asp Phe Arg Asp Ser Leu Ser Asn Leu Asn Asp
  1               5                  10                  15
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Leu Asp Ile Ala Val Val Gly Ile Ser Pro Asp Pro Val Asp Lys Leu
            20                  25                  30

Val Ser Ser Val Arg Thr Met Ser
         35                  40


<210> 1459
<211> 753
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(730)
<223> RXN03073

<400> 1459
cgaaacatct aggcaacccg acttttatgt ccctgcttga gttgaaaact gctgtcgatc 60

aaaggtgccc caattgtttc atgccgtgag ttttgcatta atg gac tcc gta aat   115
                                        Met Asp Ser Val Asn
                                          1               5

gtc ctg ctc att ggc ata atc gtc gcg att gct gct ttg ctg cct cgc   163
Val Leu Leu Ile Gly Ile Ile Val Ala Ile Ala Ala Leu Leu Pro Arg
                10                  15                  20

aag ggt aaa tat ggg cca atc gcc acg cta ctg gtt gcc ggc gat tgg   211
Lys Gly Lys Tyr Gly Pro Ile Ala Thr Leu Leu Val Ala Gly Asp Trp
            25                  30                  35

ctt ggc gtt ttc ctc ctc agt att ttg gtg atg ctc gtt ttt gat gga   259
Leu Gly Val Phe Leu Leu Ser Ile Leu Val Met Leu Val Phe Asp Gly
         40                  45                  50

cta gag gat tta gtt cag ggc ttt ttg gat tca atc tgg ttc gga gtc   307
Leu Glu Asp Leu Val Gln Gly Phe Leu Asp Ser Ile Trp Phe Gly Val
     55                  60                  65

atc ctt ctt gta act ggc atc gtt tcc ttc gtt gcg aca ctg gtt tct   355
Ile Leu Leu Val Thr Gly Ile Val Ser Phe Val Ala Thr Leu Val Ser
 70                  75                  80                  85

aaa acc gac agc act aga aag ctt gat gga ttc cta gcg cca gta aaa   403
Lys Thr Asp Ser Thr Arg Lys Leu Asp Gly Phe Leu Ala Pro Val Lys
                90                  95                  100

act cct agt tgg aaa act gtt gga gcc gga ttg atc ctt gga atc gtt   451
Thr Pro Ser Trp Lys Thr Val Gly Ala Gly Leu Ile Leu Gly Ile Val
            105                 110                 115

cag tca gcg aca tct gta cct ttt tat gca ggg ctt gga tat ttg agc   499
Gln Ser Ala Thr Ser Val Pro Phe Tyr Ala Gly Leu Gly Tyr Leu Ser
        120                 125                 130

gtt ggc aat ttc agt cca gaa att agg tat ggc gga ctt gtg gtc tat   547
Val Gly Asn Phe Ser Pro Glu Ile Arg Tyr Gly Gly Leu Val Val Tyr
    135                 140                 145
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gcg acc ttg gct ctg agt ctg ccg att atc gtg gca att ctc gtt gga   595
Ala Thr Leu Ala Leu Ser Leu Pro Ile Ile Val Ala Ile Leu Val Gly
150                 155                 160                 165

atg gtt cgc aaa tac cct gaa agt cct gtt ggt agg ttg ttt gaa ctg   643
Met Val Arg Lys Tyr Pro Glu Ser Pro Val Gly Arg Leu Phe Glu Leu
                170                 175                 180

att ggt caa aat aaa gag aga gtc acc aaa tgg tcg ggc tat ctc gtg   691
Ile Gly Gln Asn Lys Glu Arg Val Thr Lys Trp Ser Gly Tyr Leu Val
            185                 190                 195

tca ctg gtt ctg tgc ata atg ggc att act tcg atc ctg taactagcgc   740
Ser Leu Val Leu Cys Ile Met Gly Ile Thr Ser Ile Leu
        200                 205                 210

atgtactcat gag                                                  753
```

<210> 1460
<211> 210
<212> PRT
<213> Corynebacterium glutamicum

<400> 1460

```
Met Asp Ser Val Asn Val Leu Leu Ile Gly Ile Ile Val Ala Ile Ala
  1               5                  10                  15

Ala Leu Leu Pro Arg Lys Gly Lys Tyr Gly Pro Ile Ala Thr Leu Leu
             20                  25                  30

Val Ala Gly Asp Trp Leu Gly Val Phe Leu Leu Ser Ile Leu Val Met
         35                  40                  45

Leu Val Phe Asp Gly Leu Glu Asp Leu Val Gln Gly Phe Leu Asp Ser
     50                  55                  60

Ile Trp Phe Gly Val Ile Leu Leu Val Thr Gly Ile Val Ser Phe Val
 65                  70                  75                  80

Ala Thr Leu Val Ser Lys Thr Asp Ser Thr Arg Lys Leu Asp Gly Phe
                 85                  90                  95

Leu Ala Pro Val Lys Thr Pro Ser Trp Lys Thr Val Gly Ala Gly Leu
            100                 105                 110

Ile Leu Gly Ile Val Gln Ser Ala Thr Ser Val Pro Phe Tyr Ala Gly
        115                 120                 125

Leu Gly Tyr Leu Ser Val Gly Asn Phe Ser Pro Glu Ile Arg Tyr Gly
    130                 135                 140

Gly Leu Val Val Tyr Ala Thr Leu Ala Leu Ser Leu Pro Ile Ile Val
145                 150                 155                 160

Ala Ile Leu Val Gly Met Val Arg Lys Tyr Pro Glu Ser Pro Val Gly
                165                 170                 175

Arg Leu Phe Glu Leu Ile Gly Gln Asn Lys Glu Arg Val Thr Lys Trp
            180                 185                 190
```

```
Ser Gly Tyr Leu Val Ser Leu Val Leu Cys Ile Met Gly Ile Thr Ser
        195                 200                 205

Ile Leu
    210


<210> 1461
<211> 574
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(574)
<223> FRXA02905

<400> 1461
cgaaacatct aggcaacccg acttttatgt ccctgcttga gttgaaaact gctgtcgatc 60

aaaggtgccc caattgtttc atgccgtgag ttttgcatta atg gac tcc gta aat   115
                                            Met Asp Ser Val Asn
                                              1               5

gtc ctg ctc att ggc ata atc gtc gcg att gct gct ttg ctg cct cgc   163
Val Leu Leu Ile Gly Ile Ile Val Ala Ile Ala Ala Leu Leu Pro Arg
                10                  15                  20

aag ggt aaa tat ggg cca atc gcc acg cta ctg gtt gcc ggc gat tgg   211
Lys Gly Lys Tyr Gly Pro Ile Ala Thr Leu Leu Val Ala Gly Asp Trp
            25                  30                  35

ctt ggc gtt ttc ctc ctc agt att ttg gtg atg ctc gtt ttt gat gga   259
Leu Gly Val Phe Leu Leu Ser Ile Leu Val Met Leu Val Phe Asp Gly
        40                  45                  50

cta gag gat tta gtt cag ggc ttt ttg gat tca atc tgg ttc gga gtc   307
Leu Glu Asp Leu Val Gln Gly Phe Leu Asp Ser Ile Trp Phe Gly Val
    55                  60                  65

atc ctt ctt gta act ggc atc gtt tcc ttc gtt gcg aca ctg gtt tct   355
Ile Leu Leu Val Thr Gly Ile Val Ser Phe Val Ala Thr Leu Val Ser
70                  75                  80                  85

aaa acc gac agc act aga aag ctt gat gga ttc cta gcg cca gta aaa   403
Lys Thr Asp Ser Thr Arg Lys Leu Asp Gly Phe Leu Ala Pro Val Lys
                90                  95                  100

act cct agt tgg aaa act gtt gga gcc gga ttg atc ctt gga atc gtt   451
Thr Pro Ser Trp Lys Thr Val Gly Ala Gly Leu Ile Leu Gly Ile Val
            105                 110                 115

cag tca gcg aca tct gta cct ttt tat gca ggg ctt gga tat ttg agc   499
Gln Ser Ala Thr Ser Val Pro Phe Tyr Ala Gly Leu Gly Tyr Leu Ser
        120                 125                 130

gtt ggc aat ttc agt cca gaa att agg tat ggc gga ctt gtg gtc tat   547
Val Gly Asn Phe Ser Pro Glu Ile Arg Tyr Gly Gly Leu Val Val Tyr
    135                 140                 145

gcg acc ttg gct ctg agt ctg ccg att                              574
```

```
Ala Thr Leu Ala Leu Ser Leu Pro Ile
150                 155


<210> 1462
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 1462
Met Asp Ser Val Asn Val Leu Leu Ile Gly Ile Ile Val Ala Ile Ala
  1               5                  10                  15

Ala Leu Leu Pro Arg Lys Gly Lys Tyr Gly Pro Ile Ala Thr Leu Leu
             20                  25                  30

Val Ala Gly Asp Trp Leu Gly Val Phe Leu Leu Ser Ile Leu Val Met
         35                  40                  45

Leu Val Phe Asp Gly Leu Glu Asp Leu Val Gln Gly Phe Leu Asp Ser
     50                  55                  60

Ile Trp Phe Gly Val Ile Leu Leu Val Thr Gly Ile Val Ser Phe Val
 65                  70                  75                  80

Ala Thr Leu Val Ser Lys Thr Asp Ser Thr Arg Lys Leu Asp Gly Phe
                 85                  90                  95

Leu Ala Pro Val Lys Thr Pro Ser Trp Lys Thr Val Gly Ala Gly Leu
            100                 105                 110

Ile Leu Gly Ile Val Gln Ser Ala Thr Ser Val Pro Phe Tyr Ala Gly
        115                 120                 125

Leu Gly Tyr Leu Ser Val Gly Asn Phe Ser Pro Glu Ile Arg Tyr Gly
    130                 135                 140

Gly Leu Val Val Tyr Ala Thr Leu Ala Leu Ser Leu Pro Ile
145                 150                 155


<210> 1463
<211> 474
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(451)
<223> RXN03085

<400> 1463
taagcaggat tacgacaagc gccaagatat caagcgtcgc accgaagaac gcgaagtcac 60

ccgtgagctc ggccgtcgca ttaagggaat caacgcgtaa atg agt att cac atc   115
                                              Met Ser Ile His Ile
                                                1               5

gca aaa gtc cac gac gtc ctc aaa ggt gaa aaa acc tac gga acc acc   163
Ala Lys Val His Asp Val Leu Lys Gly Glu Lys Thr Tyr Gly Thr Thr
            10                  15                  20
```

```
att ttg gtg gat cgg ctc tgg cca cgc ggt gtg aaa aaa gac gac ctt   211
Ile Leu Val Asp Arg Leu Trp Pro Arg Gly Val Lys Lys Asp Asp Leu
             25                  30                  35

gag cca gac ctc tgg ctc aaa agc gtc gcc ccc aca acc gaa ctc cga   259
Glu Pro Asp Leu Trp Leu Lys Ser Val Ala Pro Thr Thr Glu Leu Arg
         40                  45                  50

aaa tgg ttc ggc cac gac cca gct aaa ttc tcc gaa ttc agc acc cgt   307
Lys Trp Phe Gly His Asp Pro Ala Lys Phe Ser Glu Phe Ser Thr Arg
     55                  60                  65

tac acc gaa gag ctc aac gcc agc aac gac aaa gac cta gag acg ctt   355
Tyr Thr Glu Glu Leu Asn Ala Ser Asn Asp Lys Asp Leu Glu Thr Leu
 70                  75                  80                  85

gtc gac gcc acc tcc cgc cac ccc gta acc ctc ctc tac ggt gct gcc   403
Val Asp Ala Thr Ser Arg His Pro Val Thr Leu Leu Tyr Gly Ala Ala
                 90                  95                 100

gac cgc gac cac aac cac gcc att gtt cta gcc aag tgg cta aag aaa   451
Asp Arg Asp His Asn His Ala Ile Val Leu Ala Lys Trp Leu Lys Lys
            105                 110                 115

taactccttg caaatagttg caa                                       474


<210> 1464
<211> 117
<212> PRT
<213> Corynebacterium glutamicum

<400> 1464
Met Ser Ile His Ile Ala Lys Val His Asp Val Leu Lys Gly Glu Lys
  1               5                  10                  15

Thr Tyr Gly Thr Thr Ile Leu Val Asp Arg Leu Trp Pro Arg Gly Val
             20                  25                  30

Lys Lys Asp Asp Leu Glu Pro Asp Leu Trp Leu Lys Ser Val Ala Pro
         35                  40                  45

Thr Thr Glu Leu Arg Lys Trp Phe Gly His Asp Pro Ala Lys Phe Ser
     50                  55                  60

Glu Phe Ser Thr Arg Tyr Thr Glu Glu Leu Asn Ala Ser Asn Asp Lys
 65                  70                  75                  80

Asp Leu Glu Thr Leu Val Asp Ala Thr Ser Arg His Pro Val Thr Leu
                 85                  90                  95

Leu Tyr Gly Ala Ala Asp Arg Asp His Asn His Ala Ile Val Leu Ala
            100                 105                 110

Lys Trp Leu Lys Lys
        115


<210> 1465
<211> 1181
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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1158)
<223> RXN03089

<400> 1465

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cac tcc ctc tac ccc ata ccg aag cca aac tct gga tct ggc aac ggc   48
His Ser Leu Tyr Pro Ile Pro Lys Pro Asn Ser Gly Ser Gly Asn Gly
  1               5                  10                  15

ggt aat ggt ggc aat ccc gat ggc ggt cct gat ggt ggc gac tcg ggt   96
Gly Asn Gly Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp Ser Gly
             20                  25                  30

gat gac gac tcc ggc gat gat gac ccc gac ccc gaa ccg gac aag cct   144
Asp Asp Asp Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp Lys Pro
         35                  40                  45

gaa gac ggc aaa cct gat agt gat aag ccc cgt agg cca cgg atc agc   192
Glu Asp Gly Lys Pro Asp Ser Asp Lys Pro Arg Arg Pro Arg Ile Ser
     50                  55                  60

gcg gaa aaa cac gcc atc atc acc gac gaa ctc gcc cgc ctc aac ccg   240
Ala Glu Lys His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu Asn Pro
 65                  70                  75                  80

aat acc aca ccc agc gcc gag gaa cta cgc acc caa gcc ctg agt caa   288
Asn Thr Thr Pro Ser Ala Glu Glu Leu Arg Thr Gln Ala Leu Ser Gln
                 85                  90                  95

gcg atc tgg cgc acc cca gaa gac ctc cgc acg tgg cta cgc cac cag   336
Ala Ile Trp Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg His Gln
            100                 105                 110

gtc acc acc gcg aac aaa aac aac ccc aac ccc atc acc gcc atg aaa   384
Val Thr Thr Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala Met Lys
        115                 120                 125

agg cgc tac ctc tca gta ggt aaa ccc gat gcc gac aac atg gtc cgc   432
Arg Arg Tyr Leu Ser Val Gly Lys Pro Asp Ala Asp Asn Met Val Arg
    130                 135                 140

atc agc ggc ctc gtg ccc gca gcc acc gca gca ctg atc acc gcg aac   480
Ile Ser Gly Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr Ala Asn
145                 150                 155                 160

acc gca ccg tta acc aaa cgt ggc aac ctc gtg gat cta cca gca gca   528
Thr Ala Pro Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro Ala Ala
                165                 170                 175

gaa gat atg cgc acc cgc ggg caa cgc cat gcg gat gcg ttg cat cac   576
Glu Asp Met Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu His His
            180                 185                 190

atc atg gag atc tac aac cac ggt att gtc acc cca gct cgt ggt gga   624
Ile Met Glu Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg Gly Gly
        195                 200                 205
```

```
aca gcc agc atc atc atc tcc atg acc acc gat gat ctt gac gag atc   672
Thr Ala Ser Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp Glu Ile
    210                 215                 220

aac cac ggt gat cat ggc gat ggc agt cta ctt aac aac ctg tac ccc   720
Asn His Gly Asp His Gly Asp Gly Ser Leu Leu Asn Asn Leu Tyr Pro
225                 230                 235                 240

acg aac acg ggt tac tca ttg aac ttg gcg gag atc atg aac ctc atc   768
Thr Asn Thr Gly Tyr Ser Leu Asn Leu Ala Glu Ile Met Asn Leu Ile
                245                 250                 255

gct gcg aaa tac gac ttc gct gtg ctc ctc gat ggt gag acg ggg cag   816
Ala Ala Lys Tyr Asp Phe Ala Val Leu Leu Asp Gly Glu Thr Gly Gln
            260                 265                 270

ccg ttg aac gtc aat agg atg cag cgc tca gcg aac ctg act caa cgc   864
Pro Leu Asn Val Asn Arg Met Gln Arg Ser Ala Asn Leu Thr Gln Arg
        275                 280                 285

atc gcg ttg ttt gct tct gag ttg gtg tgc tcg gca ccc aat tgt gac   912
Ile Ala Leu Phe Ala Ser Glu Leu Val Cys Ser Ala Pro Asn Cys Asp
    290                 295                 300

agg ccg cag tta gag tgc gag gtt cat cat tta gat ccc tgg atg aga   960
Arg Pro Gln Leu Glu Cys Glu Val His His Leu Asp Pro Trp Met Arg
305                 310                 315                 320

ggt ggg ctg acc aac ctg gtc aat ctc acg cat cag tgc ttt aat cac  1008
Gly Gly Leu Thr Asn Leu Val Asn Leu Thr His Gln Cys Phe Asn His
                325                 330                 335

cac cca cgc aac gat gat tcc agg agt ggg gtc aat ggt aaa ggg ttt  1056
His Pro Arg Asn Asp Asp Ser Arg Ser Gly Val Asn Gly Lys Gly Phe
            340                 345                 350

atg gac cgc gat ccc gtc act ggc aga gta ggt cac tac tca gca agt  1104
Met Asp Arg Asp Pro Val Thr Gly Arg Val Gly His Tyr Ser Ala Ser
        355                 360                 365

ggt gag ggg ccg gtg ttt aac cgg tcg gct gct gct gat cgt tcc ggt  1152
Gly Glu Gly Pro Val Phe Asn Arg Ser Ala Ala Ala Asp Arg Ser Gly
    370                 375                 380

ggt gca tagtccagac gtaagcatta tgg                               1181
Gly Ala
385
```

<210> 1466
<211> 386
<212> PRT
<213> Corynebacterium glutamicum

<400> 1466

```
His Ser Leu Tyr Pro Ile Pro Lys Pro Asn Ser Gly Ser Gly Asn Gly
  1               5                  10                  15

Gly Asn Gly Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp Ser Gly
            20                  25                  30
```

```
Asp Asp Asp Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp Lys Pro
         35                  40                  45

Glu Asp Gly Lys Pro Asp Ser Asp Lys Pro Arg Arg Pro Arg Ile Ser
     50                  55                  60

Ala Glu Lys His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu Asn Pro
 65                  70                  75                  80

Asn Thr Thr Pro Ser Ala Glu Glu Leu Arg Thr Gln Ala Leu Ser Gln
                 85                  90                  95

Ala Ile Trp Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg His Gln
            100                 105                 110

Val Thr Thr Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala Met Lys
        115                 120                 125

Arg Arg Tyr Leu Ser Val Gly Lys Pro Asp Ala Asp Asn Met Val Arg
    130                 135                 140

Ile Ser Gly Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr Ala Asn
145                 150                 155                 160

Thr Ala Pro Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro Ala Ala
                165                 170                 175

Glu Asp Met Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu His His
            180                 185                 190

Ile Met Glu Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg Gly Gly
        195                 200                 205

Thr Ala Ser Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp Glu Ile
    210                 215                 220

Asn His Gly Asp His Gly Asp Gly Ser Leu Leu Asn Asn Leu Tyr Pro
225                 230                 235                 240

Thr Asn Thr Gly Tyr Ser Leu Asn Leu Ala Glu Ile Met Asn Leu Ile
                245                 250                 255

Ala Ala Lys Tyr Asp Phe Ala Val Leu Leu Asp Gly Glu Thr Gly Gln
            260                 265                 270

Pro Leu Asn Val Asn Arg Met Gln Arg Ser Ala Asn Leu Thr Gln Arg
        275                 280                 285

Ile Ala Leu Phe Ala Ser Glu Leu Val Cys Ser Ala Pro Asn Cys Asp
    290                 295                 300

Arg Pro Gln Leu Glu Cys Glu Val His His Leu Asp Pro Trp Met Arg
305                 310                 315                 320

Gly Gly Leu Thr Asn Leu Val Asn Leu Thr His Gln Cys Phe Asn His
                325                 330                 335

His Pro Arg Asn Asp Asp Ser Arg Ser Gly Val Asn Gly Lys Gly Phe
            340                 345                 350

Met Asp Arg Asp Pro Val Thr Gly Arg Val Gly His Tyr Ser Ala Ser
```

```
        355                 360                 365

Gly Glu Gly Pro Val Phe Asn Arg Ser Ala Ala Ala Asp Arg Ser Gly
    370                 375                 380

Gly Ala
385
```

<210> 1467
<211> 1575
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1552)
<223> FRXA00071

<400> 1467

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gcttttctat ttcgaaaaat agccttgtat tcgaaaattt gatcgggtat ggtggttggt 60

akwrksrswg gkaacwamac ggggaaaggg ggaagacacc atg agc atc acc aca   115
                                              Met Ser Ile Thr Thr
                                                1               5

cac gtc caa gca ctc acc aca gca ctc aac gcc atc gac aac cat ttg   163
His Val Gln Ala Leu Thr Thr Ala Leu Asn Ala Ile Asp Asn His Leu
                10                  15                  20

gcc agc atg cty gac cat ggt gtc acc cca gac caa tac aag gcc atc   211
Ala Ser Met Xaa Asp His Gly Val Thr Pro Asp Gln Tyr Lys Ala Ile
            25                  30                  35

gag ccc gac ctc atc gcc cta gaa cac acc atc aac cac cac gcc acc   259
Glu Pro Asp Leu Ile Ala Leu Glu His Thr Ile Asn His His Ala Thr
        40                  45                  50

atc gcc gcc caa acc acm gcc ctc gcc gaa cgc acc aay gcy gcs cas   307
Ile Ala Ala Gln Thr Xaa Ala Leu Ala Glu Arg Thr Xaa Xaa Xaa Xaa
    55                  60                  65

wcs att ggc tcc acc cac ctc atc gac tac ctc acc acc acc ttc ggc   355
Xaa Ile Gly Ser Thr His Leu Ile Asp Tyr Leu Thr Thr Thr Phe Gly
70                  75                  80                  85

cta tct aaa gca cgc gcc cac cac cgc atc aat ctc gcc cac tcc ctc   403
Leu Ser Lys Ala Arg Ala His His Arg Ile Asn Leu Ala His Ser Leu
                90                  95                  100

tac ccc ata ccg aag cca aac tct gga tct ggc aac ggc ggt aat ggt   451
Tyr Pro Ile Pro Lys Pro Asn Ser Gly Ser Gly Asn Gly Gly Asn Gly
            105                 110                 115

ggc aat ccc gac ggc ggt cct gat ggt ggc gac tcg ggt gat gac gac   499
Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp Ser Gly Asp Asp Asp
        120                 125                 130

tcc ggc gat gat gac ccc gac ccc gaa ccg gac aag cct gaa gac ggc   547
Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp Lys Pro Glu Asp Gly
    135                 140                 145
```

```
aaa cct gat agt gat aag ccc cgt agg cca cgg atc agc gcg gaa aaa   595
Lys Pro Asp Ser Asp Lys Pro Arg Arg Pro Arg Ile Ser Ala Glu Lys
150                 155                 160                 165

cac gcc atc atc acc gac gaa ctc gcc cgc ctc aac ccg aat acc aca   643
His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu Asn Pro Asn Thr Thr
                170                 175                 180

ccc agc gcc gag gaa ctr cgc amc caa gcc ctg agt car gcg atc tgg   691
Pro Ser Ala Glu Glu Xaa Arg Xaa Gln Ala Leu Ser Xaa Ala Ile Trp
            185                 190                 195

cgc acc cca gaa gac ctc cgc acg tgg cta cgc cac cag gtc acc acc   739
Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg His Gln Val Thr Thr
        200                 205                 210

gcg aac aaa aac aac ccc aac ccc atc acc gcc atg aaa agg cgc tac   787
Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala Met Lys Arg Arg Tyr
    215                 220                 225

ctc tca gta ggt aaa ccc gat gcc gac aac atg gtc cgc atc agc ggc   835
Leu Ser Val Gly Lys Pro Asp Ala Asp Asn Met Val Arg Ile Ser Gly
230                 235                 240                 245

ctc gtg ccc gca gcc acc gca gca ctg atc acc gcg aac acc gca ccg   883
Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr Ala Asn Thr Ala Pro
                250                 255                 260

tta acc aaa cgt ggc aac ctc gtg gat cta cca gca gca gaa gat atg   931
Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro Ala Ala Glu Asp Met
            265                 270                 275

cgc acc cgc ggg caa cgc cat gcg gat gcg ttg cat cac atc atg gag   979
Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu His His Ile Met Glu
        280                 285                 290

atc tac aac cac ggt att gtc acc cca gct cgt ggt gga aca gcc agc   1027
Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg Gly Gly Thr Ala Ser
    295                 300                 305

atc atc atc tcc atg acc acc gat gat ctt gac gag atc aac cac ggt   1075
Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp Glu Ile Asn His Gly
310                 315                 320                 325

gat cat ggc gat ggc agt cta ctt aac aac ctg tac ccc acg aac acg   1123
Asp His Gly Asp Gly Ser Leu Leu Asn Asn Leu Tyr Pro Thr Asn Thr
                330                 335                 340

ggt tac tca ttg aac ttg gcg gag atc atg aac ctc atc gct gcg aaa   1171
Gly Tyr Ser Leu Asn Leu Ala Glu Ile Met Asn Leu Ile Ala Ala Lys
            345                 350                 355

tac gac ttc gct gtg ctc ctc gat ggt gag acg ggg cag ccg ttg aac   1219
Tyr Asp Phe Ala Val Leu Leu Asp Gly Glu Thr Gly Gln Pro Leu Asn
        360                 365                 370

gtc aat agg atg cag cgc tca gcg aac ctg act caa cgc atc gcg ttg   1267
Val Asn Arg Met Gln Arg Ser Ala Asn Leu Thr Gln Arg Ile Ala Leu
    375                 380                 385
```

```
ttt gct tct gag ttg gtg tgc tcg gca ccc aat tgt gac agg ccg cag   1315
Phe Ala Ser Glu Leu Val Cys Ser Ala Pro Asn Cys Asp Arg Pro Gln
390                 395                 400                 405

tta gag tgc gag gtt cat cat tta gat ccc tgg atg aga ggt ggg ctg   1363
Leu Glu Cys Glu Val His His Leu Asp Pro Trp Met Arg Gly Gly Leu
                410                 415                 420

acc aac ctg gtc aat ctc acg cat cag tgc ttt aat cac cac cca cgc   1411
Thr Asn Leu Val Asn Leu Thr His Gln Cys Phe Asn His His Pro Arg
            425                 430                 435

aac gat gat tcc agg agt ggg gtc aat ggt aaa ggg ttt atg gac cgc   1459
Asn Asp Asp Ser Arg Ser Gly Val Asn Gly Lys Gly Phe Met Asp Arg
        440                 445                 450

gat ccc gtc act ggc aga gta ggt cac tac tca gca agt ggt gag ggg   1507
Asp Pro Val Thr Gly Arg Val Gly His Tyr Ser Ala Ser Gly Glu Gly
    455                 460                 465

ccg gtg ttt aac cgg tcg gct gct gct gat cgt tcc ggt ggt gca       1552
Pro Val Phe Asn Arg Ser Ala Ala Ala Asp Arg Ser Gly Gly Ala
470                 475                 480

tagtccagac gtaagcatta tgg                                        1575


<210> 1468
<211> 484
<212> PRT
<213> Corynebacterium glutamicum

<400> 1468
Met Ser Ile Thr Thr His Val Gln Ala Leu Thr Thr Ala Leu Asn Ala
  1               5                  10                  15

Ile Asp Asn His Leu Ala Ser Met Xaa Asp His Gly Val Thr Pro Asp
             20                  25                  30

Gln Tyr Lys Ala Ile Glu Pro Asp Leu Ile Ala Leu Glu His Thr Ile
         35                  40                  45

Asn His His Ala Thr Ile Ala Ala Gln Thr Xaa Ala Leu Ala Glu Arg
     50                  55                  60

Thr Xaa Xaa Xaa Xaa Xaa Ile Gly Ser Thr His Leu Ile Asp Tyr Leu
 65                  70                  75                  80

Thr Thr Thr Phe Gly Leu Ser Lys Ala Arg Ala His His Arg Ile Asn
                 85                  90                  95

Leu Ala His Ser Leu Tyr Pro Ile Pro Lys Pro Asn Ser Gly Ser Gly
            100                 105                 110

Asn Gly Gly Asn Gly Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp
        115                 120                 125

Ser Gly Asp Asp Asp Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp
    130                 135                 140

Lys Pro Glu Asp Gly Lys Pro Asp Ser Asp Lys Pro Arg Arg Pro Arg
```

```
145                 150                 155                 160

Ile Ser Ala Glu Lys His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu
                165                 170                 175

Asn Pro Asn Thr Thr Pro Ser Ala Glu Glu Xaa Arg Xaa Gln Ala Leu
            180                 185                 190

Ser Xaa Ala Ile Trp Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg
        195                 200                 205

His Gln Val Thr Thr Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala
    210                 215                 220

Met Lys Arg Arg Tyr Leu Ser Val Gly Lys Pro Asp Ala Asp Asn Met
225                 230                 235                 240

Val Arg Ile Ser Gly Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr
                245                 250                 255

Ala Asn Thr Ala Pro Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro
            260                 265                 270

Ala Ala Glu Asp Met Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu
        275                 280                 285

His His Ile Met Glu Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg
    290                 295                 300

Gly Gly Thr Ala Ser Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp
305                 310                 315                 320

Glu Ile Asn His Gly Asp His Gly Asp Gly Ser Leu Leu Asn Asn Leu
                325                 330                 335

Tyr Pro Thr Asn Thr Gly Tyr Ser Leu Asn Leu Ala Glu Ile Met Asn
            340                 345                 350

Leu Ile Ala Ala Lys Tyr Asp Phe Ala Val Leu Leu Asp Gly Glu Thr
        355                 360                 365

Gly Gln Pro Leu Asn Val Asn Arg Met Gln Arg Ser Ala Asn Leu Thr
    370                 375                 380

Gln Arg Ile Ala Leu Phe Ala Ser Glu Leu Val Cys Ser Ala Pro Asn
385                 390                 395                 400

Cys Asp Arg Pro Gln Leu Glu Cys Glu Val His His Leu Asp Pro Trp
                405                 410                 415

Met Arg Gly Gly Leu Thr Asn Leu Val Asn Leu Thr His Gln Cys Phe
            420                 425                 430

Asn His His Pro Arg Asn Asp Asp Ser Arg Ser Gly Val Asn Gly Lys
        435                 440                 445

Gly Phe Met Asp Arg Asp Pro Val Thr Gly Arg Val Gly His Tyr Ser
    450                 455                 460

Ala Ser Gly Glu Gly Pro Val Phe Asn Arg Ser Ala Ala Ala Asp Arg
465                 470                 475                 480
```

Ser Gly Gly Ala

<210> 1469
<211> 747
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(724)
<223> RXN03098

<400> 1469
gaccgttttg tcgatcgcac cgctgctggc tcgcaccatc aacgagatct tcgaaaacgg 60

ttccgtcacc accctcttcg agggcgaggc ctaaacaccc atg ccc acc acg gac 115
Met Pro Thr Thr Asp
1 5

gtc ttc aac cgc gtc cgg ttg gca ttg gaa cct cta gct gat ccc gca 163
Val Phe Asn Arg Val Arg Leu Ala Leu Glu Pro Leu Ala Asp Pro Ala
10 15 20

cgt gcc acc gga atg gca agc tac atg cgg gat cag ttt tct ttt ctc 211
Arg Ala Thr Gly Met Ala Ser Tyr Met Arg Asp Gln Phe Ser Phe Leu
25 30 35

ggc atc cca tcc acc ccc aga aaa gaa gcc tgc aaa ccc gtg ctg tcc 259
Gly Ile Pro Ser Thr Pro Arg Lys Glu Ala Cys Lys Pro Val Leu Ser
40 45 50

gcg cta aaa gag ttg gac act gac ttt gtc tca gac tgc ttt ggc gca 307
Ala Leu Lys Glu Leu Asp Thr Asp Phe Val Ser Asp Cys Phe Gly Ala
55 60 65

gct gaa cgg gaa tac cag tat gtc gcc tgc gat cac atc aat cgc gtc 355
Ala Glu Arg Glu Tyr Gln Tyr Val Ala Cys Asp His Ile Asn Arg Val
70 75 80 85

ggc atc acc gat tta ggt ttt gcc aaa gca tta gtg cag acc aaa tcc 403
Gly Ile Thr Asp Leu Gly Phe Ala Lys Ala Leu Val Gln Thr Lys Ser
90 95 100

tgg tgg gac acc gtc gat tcc cta gca aaa ccg atc ggc gcc aaa cac 451
Trp Trp Asp Thr Val Asp Ser Leu Ala Lys Pro Ile Gly Ala Lys His
105 110 115

gat gat gat ctg atg aaa acg tgg gcg ctt gat gag gac ttc tgg gtg 499
Asp Asp Asp Leu Met Lys Thr Trp Ala Leu Asp Glu Asp Phe Trp Val
120 125 130

cgc cgc atc gcg atc atc cac caa ctg ggc cgc aag aaa aac acc gac 547
Arg Arg Ile Ala Ile Ile His Gln Leu Gly Arg Lys Lys Asn Thr Asp
135 140 145

gct gcc ctg ctg gcc tgg atc atc gag cag aac ctc ggc tcc agc gag 595
Ala Ala Leu Leu Ala Trp Ile Ile Glu Gln Asn Leu Gly Ser Ser Glu
150 155 160 165

```
ttc ttc atc aac aaa gcg atc ggc tgg gca ctg cgg gat ttc gcc cgc   643
Phe Phe Ile Asn Lys Ala Ile Gly Trp Ala Leu Arg Asp Phe Ala Arg
                170                 175                 180

cac gac ccc agc tgg gtc cgg gct ttt gtc gac gcc acg gac ctt tcc   691
His Asp Pro Ser Trp Val Arg Ala Phe Val Asp Ala Thr Asp Leu Ser
            185                 190                 195

cca ctg agc cgg cga gaa gcc ctg aag aat att tagccctcag gcatcatctg 744
Pro Leu Ser Arg Arg Glu Ala Leu Lys Asn Ile
        200                 205

agc                                                               747
```

<210> 1470
<211> 208
<212> PRT
<213> Corynebacterium glutamicum

<400> 1470

```
Met Pro Thr Thr Asp Val Phe Asn Arg Val Arg Leu Ala Leu Glu Pro
  1               5                  10                  15

Leu Ala Asp Pro Ala Arg Ala Thr Gly Met Ala Ser Tyr Met Arg Asp
             20                  25                  30

Gln Phe Ser Phe Leu Gly Ile Pro Ser Thr Pro Arg Lys Glu Ala Cys
         35                  40                  45

Lys Pro Val Leu Ser Ala Leu Lys Glu Leu Asp Thr Asp Phe Val Ser
     50                  55                  60

Asp Cys Phe Gly Ala Ala Glu Arg Glu Tyr Gln Tyr Val Ala Cys Asp
 65                  70                  75                  80

His Ile Asn Arg Val Gly Ile Thr Asp Leu Gly Phe Ala Lys Ala Leu
                 85                  90                  95

Val Gln Thr Lys Ser Trp Trp Asp Thr Val Asp Ser Leu Ala Lys Pro
            100                 105                 110

Ile Gly Ala Lys His Asp Asp Asp Leu Met Lys Thr Trp Ala Leu Asp
        115                 120                 125

Glu Asp Phe Trp Val Arg Arg Ile Ala Ile Ile His Gln Leu Gly Arg
    130                 135                 140

Lys Lys Asn Thr Asp Ala Ala Leu Leu Ala Trp Ile Ile Glu Gln Asn
145                 150                 155                 160

Leu Gly Ser Ser Glu Phe Phe Ile Asn Lys Ala Ile Gly Trp Ala Leu
                165                 170                 175

Arg Asp Phe Ala Arg His Asp Pro Ser Trp Val Arg Ala Phe Val Asp
            180                 185                 190

Ala Thr Asp Leu Ser Pro Leu Ser Arg Arg Glu Ala Leu Lys Asn Ile
        195                 200                 205
```

<210> 1471
<211> 798
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(775)
<223> RXN03099

<400> 1471
ccacgccgta gcgatcattg atcaccttga gcactggggt aatggcattg gtggtgcatg 60

atgctgcgga aacgatctga tcatctgcgg tgatgtcggt gtg gtt gat gcc gta 115
Val Val Asp Ala Val
1 5

cac gat gtt ctt cag atc gcc ctt gcc cgg cgc ggt gag tac aac ctt 163
His Asp Val Leu Gln Ile Ala Leu Ala Arg Arg Gly Glu Tyr Asn Leu
10 15 20

ggc aac gcc ctt gga ctt gag gtg ctg gga cag gcc ttc gcg gtc acg 211
Gly Asn Ala Leu Gly Leu Glu Val Leu Gly Gln Ala Phe Ala Val Thr
25 30 35

cca gcg gcc ggt gtt gtc tac cac gac ggc gtc att gat gcc gta ttc 259
Pro Ala Ala Gly Val Val Tyr His Asp Gly Val Ile Asp Ala Val Phe
40 45 50

ggt gta atc aat ggt ggc tgg gtc att gga gta gat gac ctt gat tgg 307
Gly Val Ile Asn Gly Gly Trp Val Ile Gly Val Asp Asp Leu Asp Trp
55 60 65

ggt gcc gtt ggc cca gat gat gtt gtt gtc ata atc ggt ggt gat ggt 355
Gly Ala Val Gly Pro Asp Asp Val Val Val Ile Ile Gly Gly Asp Gly
70 75 80 85

gcc atc gaa tcc acc gtg gac aga atc acg acg cag caa gga tgc gcg 403
Ala Ile Glu Ser Thr Val Asp Arg Ile Thr Thr Gln Gln Gly Cys Ala
90 95 100

ctt gac cag gtc ttc ttc acc att ttt gcg gac cac gat ggc gcg cag 451
Leu Asp Gln Val Phe Phe Thr Ile Phe Ala Asp His Asp Gly Ala Gln
105 110 115

acg agc acc gtc ata cag tgc ctc gcg gga aac cag gat gcg ggc cag 499
Thr Ser Thr Val Ile Gln Cys Leu Ala Gly Asn Gln Asp Ala Gly Gln
120 125 130

cag gcg acc gat gcg gcc gaa acc gta cag cac gat atc agt tgg gtt 547
Gln Ala Thr Asp Ala Ala Glu Thr Val Gln His Asp Ile Ser Trp Val
135 140 145

gat gtc ggt ttc cgc acc aat gac cgg cgc gag agc gtc ctc cag gaa 595
Asp Val Gly Phe Arg Thr Asn Asp Arg Arg Glu Ser Val Leu Gln Glu
150 155 160 165

```
ggc acg cag gtc ggt gct ttc gga ttc ttc gaa gct gta ggc cag ctg   643
Gly Thr Gln Val Gly Ala Phe Gly Phe Phe Glu Ala Val Gly Gln Leu
                170                 175                 180

tcc cag gtc gat cga tgc ggt acc aag gtt cat atc tac cag ttc gcg   691
Ser Gln Val Asp Arg Cys Gly Thr Lys Val His Ile Tyr Gln Phe Ala
            185                 190                 195

caa aat atc caa gga gct ttc cag tgg aag ttc ctt gga tat gat gtg   739
Gln Asn Ile Gln Gly Ala Phe Gln Trp Lys Phe Leu Gly Tyr Asp Val
        200                 205                 210

gcg ggc gta gcg gtg aga ctt gat gat atc gat gtc tgagacattc        785
Ala Gly Val Ala Val Arg Leu Asp Asp Ile Asp Val
    215                 220                 225

acaaggagac gac                                                   798
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<210> 1472
<211> 225
<212> PRT
<213> Corynebacterium glutamicum

<400> 1472

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Val Val Asp Ala Val His Asp Val Leu Gln Ile Ala Leu Ala Arg Arg
  1               5                  10                  15

Gly Glu Tyr Asn Leu Gly Asn Ala Leu Gly Leu Glu Val Leu Gly Gln
             20                  25                  30

Ala Phe Ala Val Thr Pro Ala Ala Gly Val Val Tyr His Asp Gly Val
         35                  40                  45

Ile Asp Ala Val Phe Gly Val Ile Asn Gly Gly Trp Val Ile Gly Val
     50                  55                  60

Asp Asp Leu Asp Trp Gly Ala Val Gly Pro Asp Asp Val Val Val Ile
 65                  70                  75                  80

Ile Gly Gly Asp Gly Ala Ile Glu Ser Thr Val Asp Arg Ile Thr Thr
                 85                  90                  95

Gln Gln Gly Cys Ala Leu Asp Gln Val Phe Phe Thr Ile Phe Ala Asp
            100                 105                 110

His Asp Gly Ala Gln Thr Ser Thr Val Ile Gln Cys Leu Ala Gly Asn
        115                 120                 125

Gln Asp Ala Gly Gln Gln Ala Thr Asp Ala Ala Glu Thr Val Gln His
    130                 135                 140

Asp Ile Ser Trp Val Asp Val Gly Phe Arg Thr Asn Asp Arg Arg Glu
145                 150                 155                 160

Ser Val Leu Gln Glu Gly Thr Gln Val Gly Ala Phe Gly Phe Phe Glu
                165                 170                 175

Ala Val Gly Gln Leu Ser Gln Val Asp Arg Cys Gly Thr Lys Val His
            180                 185                 190
```

```
Ile Tyr Gln Phe Ala Gln Asn Ile Gln Gly Ala Phe Gln Trp Lys Phe
        195                 200                 205

Leu Gly Tyr Asp Val Ala Gly Val Ala Val Arg Leu Asp Asp Ile Asp
    210                 215                 220

Val
225


<210> 1473
<211> 300
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(277)
<223> RXN03104

<400> 1473
actgctggga gtagccgaag aggatggtgg cgtcagtggt cagggcgtca acgttgccct 60

gggacagtgc ctcaacacag gaagagtagg tgtcgtattc ttg gag ctg aac gcc   115
                                        Leu Glu Leu Asn Ala
                                          1               5

tgg gag gac atc ctt gac ctt ctg agc tgg agt gga tcc gga aac gga   163
Trp Glu Asp Ile Leu Asp Leu Leu Ser Trp Ser Gly Ser Gly Asn Gly
                10                  15                  20

gca cag gat caa acc gtt atc caa gtc ctc gag ggt ttc aat gcg atc   211
Ala Gln Asp Gln Thr Val Ile Gln Val Leu Glu Gly Phe Asn Ala Ile
            25                  30                  35

gtc atc ttg gcg aac aag cag agc ctg gtg ggt aag cag gta tgg gcc   259
Val Ile Leu Ala Asn Lys Gln Ser Leu Val Gly Lys Gln Val Trp Ala
        40                  45                  50

acc gaa gtt gac gga ctc tgaacggcca gcgttgatgg agt                 300
Thr Glu Val Asp Gly Leu
     55


<210> 1474
<211> 59
<212> PRT
<213> Corynebacterium glutamicum

<400> 1474
Leu Glu Leu Asn Ala Trp Glu Asp Ile Leu Asp Leu Leu Ser Trp Ser
  1               5                  10                  15

Gly Ser Gly Asn Gly Ala Gln Asp Gln Thr Val Ile Gln Val Leu Glu
            20                  25                  30

Gly Phe Asn Ala Ile Val Ile Leu Ala Asn Lys Gln Ser Leu Val Gly
        35                  40                  45

Lys Gln Val Trp Ala Thr Glu Val Asp Gly Leu
     50                  55
```

<210> 1475
<211> 292
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(292)
<223> RXN03106

<400> 1475
aaatgccctc ctgaactgga agaatcaagc ttgcttagag tcctgattca cctgccagaa 60

aggcacctca caggtgcaat tattacacaa ccccacagcg atg tcc gca tcc ttt 115
Met Ser Ala Ser Phe
1 5

gat gac ccc aac ctc atc tcg ctt gct gga ctg gtt cca acc atg cac 163
Asp Asp Pro Asn Leu Ile Ser Leu Ala Gly Leu Val Pro Thr Met His
10 15 20

tta gcc gat gct gcc agc ctg tcc acc ttg gcc cag gac cgg ttg agc 211
Leu Ala Asp Ala Ala Ser Leu Ser Thr Leu Ala Gln Asp Arg Leu Ser
25 30 35

atc acc ggt gat aaa ggt gcc aat gct ggt gcg aag atc gcc tcc cta 259
Ile Thr Gly Asp Lys Gly Ala Asn Ala Gly Ala Lys Ile Ala Ser Leu
40 45 50

gtc gcg ggc atg gtc gcc ggt gct gat tcc atc 292
Val Ala Gly Met Val Ala Gly Ala Asp Ser Ile
55 60

<210> 1476
<211> 64
<212> PRT
<213> Corynebacterium glutamicum

<400> 1476
Met Ser Ala Ser Phe Asp Asp Pro Asn Leu Ile Ser Leu Ala Gly Leu
1 5 10 15

Val Pro Thr Met His Leu Ala Asp Ala Ala Ser Leu Ser Thr Leu Ala
20 25 30

Gln Asp Arg Leu Ser Ile Thr Gly Asp Lys Gly Ala Asn Ala Gly Ala
35 40 45

Lys Ile Ala Ser Leu Val Ala Gly Met Val Ala Gly Ala Asp Ser Ile
50 55 60

<210> 1477
<211> 324
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(301)
<223> RXN03107

<400> 1477
ggatttatat caatttcagg gcgtggcgag cttttagtga ttcacgctcc tacggtgggt 60

atcacaaata cctcaactag aagtaggaga tgagcaccac atg agc gat ttt tcc 115
Met Ser Asp Phe Ser
1 5

aac aag gca gag gac ctc aca ggt aag gct aaa gaa gga ttc ggc gag 163
Asn Lys Ala Glu Asp Leu Thr Gly Lys Ala Lys Glu Gly Phe Gly Glu
10 15 20

gca act gat aac gag tcc ctc gct gat gag ggc cgt gcg gat cag gct 211
Ala Thr Asp Asn Glu Ser Leu Ala Asp Glu Gly Arg Ala Asp Gln Ala
25 30 35

aag gca gac atc aag gat gct gtc gaa aac gcc ggt gaa aag gta aag 259
Lys Ala Asp Ile Lys Asp Ala Val Glu Asn Ala Gly Glu Lys Val Lys
40 45 50

gac gca gct aac aag gtt ctg ggt gcg ttc aag aag gac gac 301
Asp Ala Ala Asn Lys Val Leu Gly Ala Phe Lys Lys Asp Asp
55 60 65

taatcccgta cttgttcagg att 324

<210> 1478
<211> 67
<212> PRT
<213> Corynebacterium glutamicum

<400> 1478
Met Ser Asp Phe Ser Asn Lys Ala Glu Asp Leu Thr Gly Lys Ala Lys
1 5 10 15

Glu Gly Phe Gly Glu Ala Thr Asp Asn Glu Ser Leu Ala Asp Glu Gly
20 25 30

Arg Ala Asp Gln Ala Lys Ala Asp Ile Lys Asp Ala Val Glu Asn Ala
35 40 45

Gly Glu Lys Val Lys Asp Ala Ala Asn Lys Val Leu Gly Ala Phe Lys
50 55 60

Lys Asp Asp
65

<210> 1479
<211> 1722
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(1699)
<223> RXN03113

<400> 1479
gttggatctt gcattgaaaa aatgaaaacc tcgtcgggaa tgcaacttgg gatcacgtct 60

cgggcaagaa acgtccttaa aaaaagggga gtgattgtga gtg ctt gat ttc tta 115
Val Leu Asp Phe Leu
1 5

gct gcg aac ccg ctg att gcg ctg gtg gtt att ttg gcc gtt ggt tta 163
Ala Ala Asn Pro Leu Ile Ala Leu Val Val Ile Leu Ala Val Gly Leu
10 15 20

gca att ggt cag att agg gtc ttt ggc ctt tct tta ggt gcc gcc gcg 211
Ala Ile Gly Gln Ile Arg Val Phe Gly Leu Ser Leu Gly Ala Ala Ala
25 30 35

gtg ctg ttt gtg gcc ctg gtg gtt tca act gca aat acc gac atc gtc 259
Val Leu Phe Val Ala Leu Val Val Ser Thr Ala Asn Thr Asp Ile Val
40 45 50

atc ccc atg att gtt tat cag ctg ggc ttg gcg atg ttc gtt tat gtc 307
Ile Pro Met Ile Val Tyr Gln Leu Gly Leu Ala Met Phe Val Tyr Val
55 60 65

atc ggt ttg tcc gcc gga cca gca ttt ttc agt gag ttc gct aaa aag 355
Ile Gly Leu Ser Ala Gly Pro Ala Phe Phe Ser Glu Phe Ala Lys Lys
70 75 80 85

ggc tgg aag ctc acc atc ttt atg ctc ctg ctg ctg gca aca ctg att 403
Gly Trp Lys Leu Thr Ile Phe Met Leu Leu Leu Leu Ala Thr Leu Ile
90 95 100

ggt ttg gcg tgg gtg ctt att aag tca ctg ggg ctt gat gca gcg atc 451
Gly Leu Ala Trp Val Leu Ile Lys Ser Leu Gly Leu Asp Ala Ala Ile
105 110 115

ggt acc ggt atg ttc acc ggc gcg ctg acc tcg act ccc ggt atg gca 499
Gly Thr Gly Met Phe Thr Gly Ala Leu Thr Ser Thr Pro Gly Met Ala
120 125 130

gcg gtc gtg gaa ttg att gaa gga atc gat cca agc ctt gcc agt gaa 547
Ala Val Val Glu Leu Ile Glu Gly Ile Asp Pro Ser Leu Ala Ser Glu
135 140 145

cct gtt att ggt tat tcc ttg gca tat ccg gga gcc gtg ctg gga tcc 595
Pro Val Ile Gly Tyr Ser Leu Ala Tyr Pro Gly Ala Val Leu Gly Ser
150 155 160 165

att gtg gtg gcc gcg gtt gga gcg aaa ctg ctc aaa gta aat cac cgg 643
Ile Val Val Ala Ala Val Gly Ala Lys Leu Leu Lys Val Asn His Arg
170 175 180

gaa gat gct cga aaa gaa ggc atg atc acc gca ccg ctg gtg tgg aag 691
Glu Asp Ala Arg Lys Glu Gly Met Ile Thr Ala Pro Leu Val Trp Lys
185 190 195

ggt gtg cag ctc aaa cct gga atc aca ggc agg gtg gga gat ctt cca 739
Gly Val Gln Leu Lys Pro Gly Ile Thr Gly Arg Val Gly Asp Leu Pro

```
        200                 205                 210

cgc ctt gca ggt gaa agt atc atc gca acc cgc att gtg gat gat cca   787
Arg Leu Ala Gly Glu Ser Ile Ile Ala Thr Arg Ile Val Asp Asp Pro
    215                 220                 225

cat aca cac cgc ctc gcg gat cca gat ctg ccg att act gaa ggc atg   835
His Thr His Arg Leu Ala Asp Pro Asp Leu Pro Ile Thr Glu Gly Met
230                 235                 240                 245

gaa ctg ttg atc aac ggc act gaa gaa gcc gtg gat cgg gca att aag   883
Glu Leu Leu Ile Asn Gly Thr Glu Glu Ala Val Asp Arg Ala Ile Lys
                250                 255                 260

gcg ttg ggt gaa gaa cgc gaa acc aaa att gag gac aca gag ctg atc   931
Ala Leu Gly Glu Glu Arg Glu Thr Lys Ile Glu Asp Thr Glu Leu Ile
            265                 270                 275

tac acc cgc ctg acg gta tct agc cct gag gtt gca ggt aga acc gtt   979
Tyr Thr Arg Leu Thr Val Ser Ser Pro Glu Val Ala Gly Arg Thr Val
        280                 285                 290

gct gag ctt gat act gta gct cac gga ttc atg att gcc cgt atc cgc   1027
Ala Glu Leu Asp Thr Val Ala His Gly Phe Met Ile Ala Arg Ile Arg
    295                 300                 305

cag ggc gat tct gag gta gtg cct aaa cct gac acc gtg atc aac tac   1075
Gln Gly Asp Ser Glu Val Val Pro Lys Pro Asp Thr Val Ile Asn Tyr
310                 315                 320                 325

tct gac cgc atc cgc gtg gtg gtt gct cct ggt cgt gtg gct gaa gtg   1123
Ser Asp Arg Ile Arg Val Val Val Ala Pro Gly Arg Val Ala Glu Val
                330                 335                 340

cga cga ttc tta ggg gac tct gaa aag tcc ctt gct gat gtt aat ctg   1171
Arg Arg Phe Leu Gly Asp Ser Glu Lys Ser Leu Ala Asp Val Asn Leu
            345                 350                 355

ctg cct tta gcc atc gga tta tct ctt ggc ctg ttg ttg ggc gcg atc   1219
Leu Pro Leu Ala Ile Gly Leu Ser Leu Gly Leu Leu Leu Gly Ala Ile
        360                 365                 370

ccg att cct ctt cca ggc ggc acc acg atg tcc ctt ggc ttt ggt ggc   1267
Pro Ile Pro Leu Pro Gly Gly Thr Thr Met Ser Leu Gly Phe Gly Gly
    375                 380                 385

ggc ccg att att gcc ggc ctg att ttg gga gca ctc aag cac aca gga   1315
Gly Pro Ile Ile Ala Gly Leu Ile Leu Gly Ala Leu Lys His Thr Gly
390                 395                 400                 405

ccg ctg acg tgg cag atg ccg ttc cac gcc aac cgc acg atc tcc acc   1363
Pro Leu Thr Trp Gln Met Pro Phe His Ala Asn Arg Thr Ile Ser Thr
                410                 415                 420

ttg ggc ctg gcg ctg ttt ttg gct ggt gtg ggt acc tct gca ggt gca   1411
Leu Gly Leu Ala Leu Phe Leu Ala Gly Val Gly Thr Ser Ala Gly Ala
            425                 430                 435

gga ttt aga gct gcg ctt acc gat tcc tcc tcc ttg atc tac atg gcc   1459
Gly Phe Arg Ala Ala Leu Thr Asp Ser Ser Ser Leu Ile Tyr Met Ala
        440                 445                 450
```

```
ggt ggc ttg gtg atc acc ttg gcc tct gcg ctg ctg tgt gct gtg atc   1507
Gly Gly Leu Val Ile Thr Leu Ala Ser Ala Leu Leu Cys Ala Val Ile
    455                 460                 465

ggc atg tgg gta ctc agg ttg agg tgg gat gaa gcc atg ggt gtt gcc   1555
Gly Met Trp Val Leu Arg Leu Arg Trp Asp Glu Ala Met Gly Val Ala
470                 475                 480                 485

gct ggc acc acc aca aat cct gca att att tcc tat ctg aat ggg caa   1603
Ala Gly Thr Thr Thr Asn Pro Ala Ile Ile Ser Tyr Leu Asn Gly Gln
                490                 495                 500

acc gga acg gat ctt gcc aac agg gga tat gcc act gtg tac ccc acg   1651
Thr Gly Thr Asp Leu Ala Asn Arg Gly Tyr Ala Thr Val Tyr Pro Thr
            505                 510                 515

gcg atg atc ggt aaa atc ctc ggc gcg cag ata ttg ttc ttg ctg ctc   1699
Ala Met Ile Gly Lys Ile Leu Gly Ala Gln Ile Leu Phe Leu Leu Leu
        520                 525                 530

taaggtgatt tttgggcagt ggt                                        1722
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<210> 1480
<211> 533
<212> PRT
<213> Corynebacterium glutamicum

<400> 1480

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Val Leu Asp Phe Leu Ala Ala Asn Pro Leu Ile Ala Leu Val Val Ile
  1               5                  10                  15

Leu Ala Val Gly Leu Ala Ile Gly Gln Ile Arg Val Phe Gly Leu Ser
             20                  25                  30

Leu Gly Ala Ala Ala Val Leu Phe Val Ala Leu Val Val Ser Thr Ala
         35                  40                  45

Asn Thr Asp Ile Val Ile Pro Met Ile Val Tyr Gln Leu Gly Leu Ala
     50                  55                  60

Met Phe Val Tyr Val Ile Gly Leu Ser Ala Gly Pro Ala Phe Phe Ser
 65                  70                  75                  80

Glu Phe Ala Lys Lys Gly Trp Lys Leu Thr Ile Phe Met Leu Leu Leu
                 85                  90                  95

Leu Ala Thr Leu Ile Gly Leu Ala Trp Val Leu Ile Lys Ser Leu Gly
            100                 105                 110

Leu Asp Ala Ala Ile Gly Thr Gly Met Phe Thr Gly Ala Leu Thr Ser
        115                 120                 125

Thr Pro Gly Met Ala Ala Val Val Glu Leu Ile Glu Gly Ile Asp Pro
    130                 135                 140

Ser Leu Ala Ser Glu Pro Val Ile Gly Tyr Ser Leu Ala Tyr Pro Gly
145                 150                 155                 160

Ala Val Leu Gly Ser Ile Val Val Ala Ala Val Gly Ala Lys Leu Leu
```

```
                165                 170                 175

Lys Val Asn His Arg Glu Asp Ala Arg Lys Glu Gly Met Ile Thr Ala
            180                 185                 190

Pro Leu Val Trp Lys Gly Val Gln Leu Lys Pro Gly Ile Thr Gly Arg
        195                 200                 205

Val Gly Asp Leu Pro Arg Leu Ala Gly Glu Ser Ile Ile Ala Thr Arg
    210                 215                 220

Ile Val Asp Asp Pro His Thr His Arg Leu Ala Asp Pro Asp Leu Pro
225                 230                 235                 240

Ile Thr Glu Gly Met Glu Leu Leu Ile Asn Gly Thr Glu Glu Ala Val
                245                 250                 255

Asp Arg Ala Ile Lys Ala Leu Gly Glu Glu Arg Glu Thr Lys Ile Glu
            260                 265                 270

Asp Thr Glu Leu Ile Tyr Thr Arg Leu Thr Val Ser Ser Pro Glu Val
        275                 280                 285

Ala Gly Arg Thr Val Ala Glu Leu Asp Thr Val Ala His Gly Phe Met
    290                 295                 300

Ile Ala Arg Ile Arg Gln Gly Asp Ser Glu Val Val Pro Lys Pro Asp
305                 310                 315                 320

Thr Val Ile Asn Tyr Ser Asp Arg Ile Arg Val Val Val Ala Pro Gly
                325                 330                 335

Arg Val Ala Glu Val Arg Arg Phe Leu Gly Asp Ser Glu Lys Ser Leu
            340                 345                 350

Ala Asp Val Asn Leu Leu Pro Leu Ala Ile Gly Leu Ser Leu Gly Leu
        355                 360                 365

Leu Leu Gly Ala Ile Pro Ile Pro Leu Pro Gly Gly Thr Thr Met Ser
    370                 375                 380

Leu Gly Phe Gly Gly Gly Pro Ile Ile Ala Gly Leu Ile Leu Gly Ala
385                 390                 395                 400

Leu Lys His Thr Gly Pro Leu Thr Trp Gln Met Pro Phe His Ala Asn
                405                 410                 415

Arg Thr Ile Ser Thr Leu Gly Leu Ala Leu Phe Leu Ala Gly Val Gly
            420                 425                 430

Thr Ser Ala Gly Ala Gly Phe Arg Ala Ala Leu Thr Asp Ser Ser Ser
        435                 440                 445

Leu Ile Tyr Met Ala Gly Gly Leu Val Ile Thr Leu Ala Ser Ala Leu
    450                 455                 460

Leu Cys Ala Val Ile Gly Met Trp Val Leu Arg Leu Arg Trp Asp Glu
465                 470                 475                 480

Ala Met Gly Val Ala Ala Gly Thr Thr Thr Asn Pro Ala Ile Ile Ser
                485                 490                 495
```

```
Tyr Leu Asn Gly Gln Thr Gly Thr Asp Leu Ala Asn Arg Gly Tyr Ala
            500                 505                 510

Thr Val Tyr Pro Thr Ala Met Ile Gly Lys Ile Leu Gly Ala Gln Ile
        515                 520                 525

Leu Phe Leu Leu Leu
    530
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<210> 1481
<211> 1441
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1441)
<223> FRXA00506

<400> 1481

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gttggatctt gcattgaaaa aatgaaaacc tcgtcgggaa tgcaacttgg gatcacgtct 60

cgggcaagaa acgtccttaa aaaaagggga gtgattgtga gtg ctt gat ttc tta   115
                                            Val Leu Asp Phe Leu
                                              1               5

gct gcg aac ccg ctg att gcg ctg gtg gtt att ttg gcc gtt ggt tta   163
Ala Ala Asn Pro Leu Ile Ala Leu Val Val Ile Leu Ala Val Gly Leu
                10                  15                  20

gca att ggt cag att agg gtc ttt ggc ctt tct tta ggt gcc gcc gcg   211
Ala Ile Gly Gln Ile Arg Val Phe Gly Leu Ser Leu Gly Ala Ala Ala
            25                  30                  35

gtg ctg ttt gtg gcc ctg gtg gtt tca act gca aat acc gac atc gtc   259
Val Leu Phe Val Ala Leu Val Val Ser Thr Ala Asn Thr Asp Ile Val
        40                  45                  50

atc ccc atg att gtt tat cag ctg ggc ttg gcg atg ttc gtt tat gtc   307
Ile Pro Met Ile Val Tyr Gln Leu Gly Leu Ala Met Phe Val Tyr Val
    55                  60                  65

atc ggt ttg tcc gcc gga cca gca ttt ttc agt gag ttc gct aaa aag   355
Ile Gly Leu Ser Ala Gly Pro Ala Phe Phe Ser Glu Phe Ala Lys Lys
70                  75                  80                  85

ggc tgg aag ctc acc atc ttt atg ctc ctg ctg ctg gca aca ctg att   403
Gly Trp Lys Leu Thr Ile Phe Met Leu Leu Leu Leu Ala Thr Leu Ile
                90                  95                  100

ggt ttg gcg tgg gtg ctt att aag tca ctg ggg ctt gat gca gcg atc   451
Gly Leu Ala Trp Val Leu Ile Lys Ser Leu Gly Leu Asp Ala Ala Ile
            105                 110                 115

ggt acc ggt atg ttc acc ggc gcg ctg acc tcg act ccc ggt atg gca   499
Gly Thr Gly Met Phe Thr Gly Ala Leu Thr Ser Thr Pro Gly Met Ala
        120                 125                 130

gcg gtc gtg gaa ttg att gaa gga atc gat cca agc ctt gcc agt gaa   547
```

```
Ala Val Val Glu Leu Ile Glu Gly Ile Asp Pro Ser Leu Ala Ser Glu
    135                 140                 145

cct gtt att ggt tat tcc ttg gca tat ccg gga gcc gtg ctg gga tcc   595
Pro Val Ile Gly Tyr Ser Leu Ala Tyr Pro Gly Ala Val Leu Gly Ser
150                 155                 160                 165

att gtg gtg gcc gcg gtt gga gcg aaa ctg ctc aaa gta aat cac cgg   643
Ile Val Val Ala Ala Val Gly Ala Lys Leu Leu Lys Val Asn His Arg
                170                 175                 180

gaa gat gct cga aaa gaa ggc atg atc acc gca ccg ctg gtg tgg aag   691
Glu Asp Ala Arg Lys Glu Gly Met Ile Thr Ala Pro Leu Val Trp Lys
            185                 190                 195

ggt gtg cag ctc aaa cct gga atc aca ggc agg gtg gga gat ctt cca   739
Gly Val Gln Leu Lys Pro Gly Ile Thr Gly Arg Val Gly Asp Leu Pro
        200                 205                 210

cgc ctt gca ggt gaa agt atc atc gca acc cgc att gtg gat gat cca   787
Arg Leu Ala Gly Glu Ser Ile Ile Ala Thr Arg Ile Val Asp Asp Pro
    215                 220                 225

cat aca cac cgc ctc gcg gat cca gat ctg ccg att act gaa ggc atg   835
His Thr His Arg Leu Ala Asp Pro Asp Leu Pro Ile Thr Glu Gly Met
230                 235                 240                 245

gaa ctg ttg atc aac ggc act gaa gaa gcc gtg gat cgg gca att aag   883
Glu Leu Leu Ile Asn Gly Thr Glu Glu Ala Val Asp Arg Ala Ile Lys
                250                 255                 260

gcg ttg ggt gaa gaa cgc gaa acc aaa att gag gac aca gag ctg atc   931
Ala Leu Gly Glu Glu Arg Glu Thr Lys Ile Glu Asp Thr Glu Leu Ile
            265                 270                 275

tac acc cgc ctg acg gta tct agc cct gag gtt gca ggt aga acc gtt   979
Tyr Thr Arg Leu Thr Val Ser Ser Pro Glu Val Ala Gly Arg Thr Val
        280                 285                 290

gct gag ctt gat act gta gct cac gga ttc atg att gcc cgt atc cgc   1027
Ala Glu Leu Asp Thr Val Ala His Gly Phe Met Ile Ala Arg Ile Arg
    295                 300                 305

cag ggc gat tct gag gta gtg cct aaa cct gac acc gtg atc aac tac   1075
Gln Gly Asp Ser Glu Val Val Pro Lys Pro Asp Thr Val Ile Asn Tyr
310                 315                 320                 325

tct gac cgc atc cgc gtg gtg gtt gct cct ggt cgt gtg gct gaa gtg   1123
Ser Asp Arg Ile Arg Val Val Val Ala Pro Gly Arg Val Ala Glu Val
                330                 335                 340

cga cga ttc tta ggg gac tct gaa aag tcc ctt gct gat gtt aat ctg   1171
Arg Arg Phe Leu Gly Asp Ser Glu Lys Ser Leu Ala Asp Val Asn Leu
            345                 350                 355

ctg cct tta gcc atc gga tta tct ctt ggc ctg ttg ttg ggc gcg atc   1219
Leu Pro Leu Ala Ile Gly Leu Ser Leu Gly Leu Leu Leu Gly Ala Ile
        360                 365                 370

ccg att cct ctt cca ggc ggc acc acg atg tcc ctt ggc ttt ggt ggc   1267
Pro Ile Pro Leu Pro Gly Gly Thr Thr Met Ser Leu Gly Phe Gly Gly
```

```
    375                 380                 385

ggc ccg att att gcc ggc ctg att ttg gga gca ctc aag cac aca gga   1315
Gly Pro Ile Ile Ala Gly Leu Ile Leu Gly Ala Leu Lys His Thr Gly
390                 395                 400                 405

ccg ctg acg tgg cag atg ccg ttc cac gcc aac cgc acg atc tcc acc   1363
Pro Leu Thr Trp Gln Met Pro Phe His Ala Asn Arg Thr Ile Ser Thr
                410                 415                 420

ttg ggc ctg gcg ctg ttt ttg gct ggt gtg ggt acc tct gca ggt gca   1411
Leu Gly Leu Ala Leu Phe Leu Ala Gly Val Gly Thr Ser Ala Gly Ala
            425                 430                 435

gga ttt aga gct gcg ctt acc gat tcc tcc                           1441
Gly Phe Arg Ala Ala Leu Thr Asp Ser Ser
        440                 445
```

<210> 1482
<211> 447
<212> PRT
<213> Corynebacterium glutamicum

<400> 1482

```
Val Leu Asp Phe Leu Ala Ala Asn Pro Leu Ile Ala Leu Val Val Ile
  1               5                  10                  15

Leu Ala Val Gly Leu Ala Ile Gly Gln Ile Arg Val Phe Gly Leu Ser
             20                  25                  30

Leu Gly Ala Ala Ala Val Leu Phe Val Ala Leu Val Val Ser Thr Ala
         35                  40                  45

Asn Thr Asp Ile Val Ile Pro Met Ile Val Tyr Gln Leu Gly Leu Ala
     50                  55                  60

Met Phe Val Tyr Val Ile Gly Leu Ser Ala Gly Pro Ala Phe Phe Ser
 65                  70                  75                  80

Glu Phe Ala Lys Lys Gly Trp Lys Leu Thr Ile Phe Met Leu Leu Leu
                 85                  90                  95

Leu Ala Thr Leu Ile Gly Leu Ala Trp Val Leu Ile Lys Ser Leu Gly
            100                 105                 110

Leu Asp Ala Ala Ile Gly Thr Gly Met Phe Thr Gly Ala Leu Thr Ser
        115                 120                 125

Thr Pro Gly Met Ala Ala Val Val Glu Leu Ile Glu Gly Ile Asp Pro
    130                 135                 140

Ser Leu Ala Ser Glu Pro Val Ile Gly Tyr Ser Leu Ala Tyr Pro Gly
145                 150                 155                 160

Ala Val Leu Gly Ser Ile Val Val Ala Ala Val Gly Ala Lys Leu Leu
                165                 170                 175

Lys Val Asn His Arg Glu Asp Ala Arg Lys Glu Gly Met Ile Thr Ala
            180                 185                 190
```

```
Pro Leu Val Trp Lys Gly Val Gln Leu Lys Pro Gly Ile Thr Gly Arg
        195                 200                 205

Val Gly Asp Leu Pro Arg Leu Ala Gly Glu Ser Ile Ile Ala Thr Arg
    210                 215                 220

Ile Val Asp Asp Pro His Thr His Arg Leu Ala Asp Pro Asp Leu Pro
225                 230                 235                 240

Ile Thr Glu Gly Met Glu Leu Leu Ile Asn Gly Thr Glu Glu Ala Val
                245                 250                 255

Asp Arg Ala Ile Lys Ala Leu Gly Glu Glu Arg Glu Thr Lys Ile Glu
            260                 265                 270

Asp Thr Glu Leu Ile Tyr Thr Arg Leu Thr Val Ser Ser Pro Glu Val
        275                 280                 285

Ala Gly Arg Thr Val Ala Glu Leu Asp Thr Val Ala His Gly Phe Met
    290                 295                 300

Ile Ala Arg Ile Arg Gln Gly Asp Ser Glu Val Val Pro Lys Pro Asp
305                 310                 315                 320

Thr Val Ile Asn Tyr Ser Asp Arg Ile Arg Val Val Val Ala Pro Gly
                325                 330                 335

Arg Val Ala Glu Val Arg Arg Phe Leu Gly Asp Ser Glu Lys Ser Leu
            340                 345                 350

Ala Asp Val Asn Leu Leu Pro Leu Ala Ile Gly Leu Ser Leu Gly Leu
        355                 360                 365

Leu Leu Gly Ala Ile Pro Ile Pro Leu Pro Gly Gly Thr Thr Met Ser
    370                 375                 380

Leu Gly Phe Gly Gly Gly Pro Ile Ile Ala Gly Leu Ile Leu Gly Ala
385                 390                 395                 400

Leu Lys His Thr Gly Pro Leu Thr Trp Gln Met Pro Phe His Ala Asn
                405                 410                 415

Arg Thr Ile Ser Thr Leu Gly Leu Ala Leu Phe Leu Ala Gly Val Gly
            420                 425                 430

Thr Ser Ala Gly Ala Gly Phe Arg Ala Ala Leu Thr Asp Ser Ser
        435                 440                 445
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<210> 1483
<211> 522
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(499)
<223> RXN03115

<400> 1483
ggaactgctg gcaggcaacg tccgtgatgg cgatggtgtg cttgtcaacg tcgccgacgg 60

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cggccagaag ctcgacgttt ccagggcggt ctaacggctc gtg ggc aag cag gaa   115
                                            Val Gly Lys Gln Glu
                                              1               5

aag ctg cgc att cct ctc gat gtt ccg gga gtg gaa tca gaa gag gta   163
Lys Leu Arg Ile Pro Leu Asp Val Pro Gly Val Glu Ser Glu Glu Val
                 10                  15                  20

ggt gta gaa ctg ctt gcc gaa ggc tac tac ctg gta gcc act ttg ccg   211
Gly Val Glu Leu Leu Ala Glu Gly Tyr Tyr Leu Val Ala Thr Leu Pro
             25                  30                  35

gct gtc gcc cag gac tgt gcc ctg ggt gac gtc gtg cgg gca cat cat   259
Ala Val Ala Gln Asp Cys Ala Leu Gly Asp Val Val Arg Ala His His
         40                  45                  50

gtt gat gag gtc ttg gaa ttt caa gaa gtg gca gtt gct ggc gga aac   307
Val Asp Glu Val Leu Glu Phe Gln Glu Val Ala Val Ala Gly Gly Asn
     55                  60                  65

aaa acc ctc cgg gtg ctc gtt gat gcc atc gct gct gac cac gtg cga   355
Lys Thr Leu Arg Val Leu Val Asp Ala Ile Ala Ala Asp His Val Arg
 70                  75                  80                  85

gcc caa cta gaa aca ctt ggg cta cac gtg gaa gct ccc atg tca gaa   403
Ala Gln Leu Glu Thr Leu Gly Leu His Val Glu Ala Pro Met Ser Glu
                 90                  95                 100

atg cta act gtc aat att gcc ccc gat tca ccg tcg cac ggt ttg gag   451
Met Leu Thr Val Asn Ile Ala Pro Asp Ser Pro Ser His Gly Leu Glu
            105                 110                 115

atc ctg ctc gat gat ctg cat gct cag ggg gta att ttc agg gcg tta   499
Ile Leu Leu Asp Asp Leu His Ala Gln Gly Val Ile Phe Arg Ala Leu
        120                 125                 130

tagagcgcct aattgtagag agc                                        522
```

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<210> 1484
<211> 133
<212> PRT
<213> Corynebacterium glutamicum

<400> 1484

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Val Gly Lys Gln Glu Lys Leu Arg Ile Pro Leu Asp Val Pro Gly Val
  1               5                  10                  15

Glu Ser Glu Glu Val Gly Val Glu Leu Leu Ala Glu Gly Tyr Tyr Leu
             20                  25                  30

Val Ala Thr Leu Pro Ala Val Ala Gln Asp Cys Ala Leu Gly Asp Val
         35                  40                  45

Val Arg Ala His His Val Asp Glu Val Leu Glu Phe Gln Glu Val Ala
     50                  55                  60

Val Ala Gly Gly Asn Lys Thr Leu Arg Val Leu Val Asp Ala Ile Ala
 65                  70                  75                  80
```

```
Ala Asp His Val Arg Ala Gln Leu Glu Thr Leu Gly Leu His Val Glu
                85                  90                  95

Ala Pro Met Ser Glu Met Leu Thr Val Asn Ile Ala Pro Asp Ser Pro
            100                 105                 110

Ser His Gly Leu Glu Ile Leu Leu Asp Asp Leu His Ala Gln Gly Val
        115                 120                 125

Ile Phe Arg Ala Leu
    130
```

<210> 1485
<211> 270
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(247)
<223> RXN03122

<400> 1485

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atggaccatg gcgggatgag tggaatgatg agcgaggagg acatgacagc cctcgaggac 60

gcccagggca cccgaggctg cccggctcta ccttgagcag atg acc gcc cac cat   115
                                            Met Thr Ala His His
                                              1               5

gag ggc gcg gtc gat atg gcc cgc gat gag gtc act gat ggc cag aac   163
Glu Gly Ala Val Asp Met Ala Arg Asp Glu Val Thr Asp Gly Gln Asn
                10                  15                  20

ccg cag gcc atc gct ctg gct gag cag gtc att gaa gat cag gag gcc   211
Pro Gln Ala Ile Ala Leu Ala Glu Gln Val Ile Glu Asp Gln Glu Ala
            25                  30                  35

gag atc gcc gag atg gag cat atg ctc aac gag ctc tgaacaagga        257
Glu Ile Ala Glu Met Glu His Met Leu Asn Glu Leu
        40                  45

cattccccga cca                                                    270
```

<210> 1486
<211> 49
<212> PRT
<213> Corynebacterium glutamicum

<400> 1486

```
Met Thr Ala His His Glu Gly Ala Val Asp Met Ala Arg Asp Glu Val
  1               5                  10                  15

Thr Asp Gly Gln Asn Pro Gln Ala Ile Ala Leu Ala Glu Gln Val Ile
            20                  25                  30

Glu Asp Gln Glu Ala Glu Ile Ala Glu Met Glu His Met Leu Asn Glu
        35                  40                  45

Leu
```

<210> 1487
<211> 474
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(451)
<223> RXN03134

<400> 1487
atgctgtttc atcgctggcg ttggcttttt cgagccattc gagctcttct ccggggagat 60

ccagtttgct gatcagcggg tttgtttcgc gtggggcgtg gtg gct tgg cgc gtc 115
Val Ala Trp Arg Val
1 5

ggc cca ggt tcc cat gag cat gac ata gtt ggg tcc tcc ggc ttt gga 163
Gly Pro Gly Ser His Glu His Asp Ile Val Gly Ser Ser Gly Phe Gly
10 15 20

tcc gag gcc gac gga gga ttt ttt cca gcc tcc gaa gga ttg gcg ttg 211
Ser Glu Ala Asp Gly Gly Phe Phe Pro Ala Ser Glu Gly Leu Ala Leu
25 30 35

gac aat ggc gcc ggt gat gcc gcg gtt gac gta ggc gtt tcc gac atc 259
Asp Asn Gly Ala Gly Asp Ala Ala Val Asp Val Gly Val Ser Asp Ile
40 45 50

gac gtg gtc aag cca ggt gcg gac ttc gtc ggc gtc gag gga ttg gag 307
Asp Val Val Lys Pro Gly Ala Asp Phe Val Gly Val Glu Gly Leu Glu
55 60 65

tcc gcc ggt gag tcc gaa gtc gtt gcc gtt ttg gaa ttc gat ggc ttc 355
Ser Ala Gly Glu Ser Glu Val Val Ala Val Leu Glu Phe Asp Gly Phe
70 75 80 85

att gag gtc ggt ggc ttt cat cag gcc gag gac tgg tcc gaa tac ttc 403
Ile Glu Val Gly Gly Phe His Gln Ala Glu Asp Trp Ser Glu Tyr Phe
90 95 100

tgt gag gtg gaa gaa ggt tcc tgg ttt gac gcc ttc ttt gat gcc ggg 451
Cys Glu Val Glu Glu Gly Ser Trp Phe Asp Ala Phe Phe Asp Ala Gly
105 110 115

tgaccagagt cggccggtgt cgt 474

<210> 1488
<211> 117
<212> PRT
<213> Corynebacterium glutamicum

<400> 1488
Val Ala Trp Arg Val Gly Pro Gly Ser His Glu His Asp Ile Val Gly
1 5 10 15

Ser Ser Gly Phe Gly Ser Glu Ala Asp Gly Gly Phe Phe Pro Ala Ser

```
            20                  25                  30

Glu Gly Leu Ala Leu Asp Asn Gly Ala Gly Asp Ala Ala Val Asp Val
         35                  40                  45

Gly Val Ser Asp Ile Asp Val Val Lys Pro Gly Ala Asp Phe Val Gly
     50                  55                  60

Val Glu Gly Leu Glu Ser Ala Gly Glu Ser Glu Val Val Ala Val Leu
 65                  70                  75                  80

Glu Phe Asp Gly Phe Ile Glu Val Gly Gly Phe His Gln Ala Glu Asp
                 85                  90                  95

Trp Ser Glu Tyr Phe Cys Glu Val Glu Glu Gly Ser Trp Phe Asp Ala
            100                 105                 110

Phe Phe Asp Ala Gly
        115


<210> 1489
<211> 852
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(829)
<223> RXN03135

<400> 1489
ttagcttgtc gacgtccccc tcttccaaca cctccggctt tgtttgtttt tccaaccaac 60

cgggctctgc tgcggtggcg acggcttttg tggcccactg ttg gtt ttg gat gag   115
                                            Leu Val Leu Asp Glu
                                              1               5

cgc tgg gtt ggt gtc ggg ctc gtt gat aaa tgg gac gag ggg ggc gtc   163
Arg Trp Val Gly Val Gly Leu Val Asp Lys Trp Asp Glu Gly Gly Val
                 10                  15                  20

gag aag cgt ctc ttt gct gcg gtc ttg tgt gtg gtt ggg gcc ggg cgc   211
Glu Lys Arg Leu Phe Ala Ala Val Leu Cys Val Val Gly Ala Gly Arg
             25                  30                  35

ggg cac gtc gat gag cgt ggc gag gtc aga tat gga ggc gcg gaa gcg   259
Gly His Val Asp Glu Arg Gly Glu Val Arg Tyr Gly Gly Ala Glu Ala
         40                  45                  50

gct ctc ctc tcg ctt gaa gga cgg gtt gtc ggc gtc gag gtc gaa gat   307
Ala Leu Leu Ser Leu Glu Gly Arg Val Val Gly Val Glu Val Glu Asp
     55                  60                  65

ggc gga cat gaa gtt ttc gct cgc ggc gtt ttc ctc gag gcg gcg cac   355
Gly Gly His Glu Val Phe Ala Arg Gly Val Phe Leu Glu Ala Ala His
 70                  75                  80                  85

gag gta aga aat ggc cac gtc gaa ttc ttg tgg gcg cac ggc tgg tac   403
Glu Val Arg Asn Gly His Val Glu Phe Leu Trp Ala His Gly Trp Tyr
                 90                  95                 100
```

```
gta aag cag cag ctc acc gac gtc aac gct gac ggc gcg cgc ctg atc   451
Val Lys Gln Gln Leu Thr Asp Val Asn Ala Asp Gly Ala Arg Leu Ile
            105                 110                 115

gga cgc cat gcc ctg cag cat ttc gaa ctc cac acg gtc cgc tac ccc   499
Gly Arg His Ala Leu Gln His Phe Glu Leu His Thr Val Arg Tyr Pro
        120                 125                 130

acg ctc cac aga gag caa atg tgc gaa tgc tat gtc gaa aag gtt gtg   547
Thr Leu His Arg Glu Gln Met Cys Glu Cys Tyr Val Glu Lys Val Val
    135                 140                 145

gcc ggc aac gcc cag gcg cag gcc ctc cat gtt ttc ttt gcg cat cgt   595
Ala Gly Asn Ala Gln Ala Gln Ala Leu His Val Phe Phe Ala His Arg
150                 155                 160                 165

cca ata gag gac gcg ctt gta att ggc atc ggt ggc ttg ttt gga agg   643
Pro Ile Glu Asp Ala Leu Val Ile Gly Ile Gly Gly Leu Phe Gly Arg
                170                 175                 180

ttc tgt ggc aac tgg cca gcc ggt gat ctg cgc gtg gac gtg ctc cat   691
Phe Cys Gly Asn Trp Pro Ala Gly Asp Leu Arg Val Asp Val Leu His
            185                 190                 195

agg caa att agc acc ctt gac cag gcg aac ctt aac gcc cgc ccc gcc   739
Arg Gln Ile Ser Thr Leu Asp Gln Ala Asn Leu Asn Ala Arg Pro Ala
        200                 205                 210

tgt gtt gac gcg ctc gcg gcc gaa ctg cgc caa gtc ctg gat tgc acc   787
Cys Val Asp Ala Leu Ala Ala Glu Leu Arg Gln Val Leu Asp Cys Thr
    215                 220                 225

gag ggc atc ggg aag gta cgc ctg caa cac aat tcc ggc ttc           829
Glu Gly Ile Gly Lys Val Arg Leu Gln His Asn Ser Gly Phe
230                 235                 240

tagttcatgc agctctggat tgg                                        852
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<210> 1490
<211> 243
<212> PRT
<213> Corynebacterium glutamicum

<400> 1490

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Leu Val Leu Asp Glu Arg Trp Val Gly Val Gly Leu Val Asp Lys Trp
  1               5                  10                  15

Asp Glu Gly Gly Val Glu Lys Arg Leu Phe Ala Ala Val Leu Cys Val
             20                  25                  30

Val Gly Ala Gly Arg Gly His Val Asp Glu Arg Gly Glu Val Arg Tyr
         35                  40                  45

Gly Gly Ala Glu Ala Ala Leu Leu Ser Leu Glu Gly Arg Val Val Gly
     50                  55                  60

Val Glu Val Glu Asp Gly Gly His Glu Val Phe Ala Arg Gly Val Phe
 65                  70                  75                  80
```

```
Leu Glu Ala Ala His Glu Val Arg Asn Gly His Val Glu Phe Leu Trp
                85                  90                  95

Ala His Gly Trp Tyr Val Lys Gln Gln Leu Thr Asp Val Asn Ala Asp
            100                 105                 110

Gly Ala Arg Leu Ile Gly Arg His Ala Leu Gln His Phe Glu Leu His
        115                 120                 125

Thr Val Arg Tyr Pro Thr Leu His Arg Glu Gln Met Cys Glu Cys Tyr
    130                 135                 140

Val Glu Lys Val Val Ala Gly Asn Ala Gln Ala Gln Ala Leu His Val
145                 150                 155                 160

Phe Phe Ala His Arg Pro Ile Glu Asp Ala Leu Val Ile Gly Ile Gly
                165                 170                 175

Gly Leu Phe Gly Arg Phe Cys Gly Asn Trp Pro Ala Gly Asp Leu Arg
            180                 185                 190

Val Asp Val Leu His Arg Gln Ile Ser Thr Leu Asp Gln Ala Asn Leu
        195                 200                 205

Asn Ala Arg Pro Ala Cys Val Asp Ala Leu Ala Ala Glu Leu Arg Gln
    210                 215                 220

Val Leu Asp Cys Thr Glu Gly Ile Gly Lys Val Arg Leu Gln His Asn
225                 230                 235                 240

Ser Gly Phe
```

Sequence Listing

<210> 1491
<211> 852
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(829)
<223> FRXA02285

<400> 1491

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ttagcttgtc gacgtccccc tcttccaaca cctccggctt tgtttgtttt tccaaccaac 60

cgggctctgc tgcggtggcg acggcttttg tggcccactg ttg gtt ttg gat gag   115
                                              Leu Val Leu Asp Glu
                                                1               5

cgc tgg gtt ggt gtc ggg ctc gtt gat aaa tgg gac gag ggg ggc gtc   163
Arg Trp Val Gly Val Gly Leu Val Asp Lys Trp Asp Glu Gly Gly Val
                10                  15                  20

gag aag cgt ctc ttt gct gcg gtc ttg tgt gtg gtt ggg gcc ggg cgc   211
Glu Lys Arg Leu Phe Ala Ala Val Leu Cys Val Val Gly Ala Gly Arg
            25                  30                  35

ggg cac gtc gat gag cgt ggc gag gtc aga tat gga ggc gcg gaa gcg   259
Gly His Val Asp Glu Arg Gly Glu Val Arg Tyr Gly Gly Ala Glu Ala
```

```
         40                  45                  50

gct ctc ctc tcg ctt gaa gga cgg gtt gtc ggc gtc gag gtc gaa gat   307
Ala Leu Leu Ser Leu Glu Gly Arg Val Val Gly Val Glu Val Glu Asp
     55                  60                  65

ggc gga cat gaa gtt ttc gct cgc ggc gtt ttc ctc gag gcg gcg cac   355
Gly Gly His Glu Val Phe Ala Arg Gly Val Phe Leu Glu Ala Ala His
 70                  75                  80                  85

gag gta aga aat ggc cac gtc gaa ttc ttg tgg gcg cac ggc tgg tac   403
Glu Val Arg Asn Gly His Val Glu Phe Leu Trp Ala His Gly Trp Tyr
                 90                  95                 100

gta aag cag cag ctc acc gac gtc aac gct gac ggc gcg cgc ctg atc   451
Val Lys Gln Gln Leu Thr Asp Val Asn Ala Asp Gly Ala Arg Leu Ile
            105                 110                 115

gga cgc cat gcc ctg cag cat ttc gaa ctc cac acg gtc cgc tac ccc   499
Gly Arg His Ala Leu Gln His Phe Glu Leu His Thr Val Arg Tyr Pro
        120                 125                 130

acg ctc cac aga gag caa atg tgc gaa tgc tat gtc gaa aag gtt gtg   547
Thr Leu His Arg Glu Gln Met Cys Glu Cys Tyr Val Glu Lys Val Val
    135                 140                 145

gcc ggc aac gcc cag gcg cag gcc ctc cat gtt ttc ttt gcg cat cgt   595
Ala Gly Asn Ala Gln Ala Gln Ala Leu His Val Phe Phe Ala His Arg
150                 155                 160                 165

cca ata gag gac gcg ctt gta att ggc atc ggt ggc ttg ttt gga agg   643
Pro Ile Glu Asp Ala Leu Val Ile Gly Ile Gly Gly Leu Phe Gly Arg
                170                 175                 180

ttc tgt ggc aac tgg cca gcc ggt gat ctg cgc gtg gac gtg ctc cat   691
Phe Cys Gly Asn Trp Pro Ala Gly Asp Leu Arg Val Asp Val Leu His
            185                 190                 195

agg caa att agc acc ctt gac cag gcg aac ctt aac gcc cgc ccc gcc   739
Arg Gln Ile Ser Thr Leu Asp Gln Ala Asn Leu Asn Ala Arg Pro Ala
        200                 205                 210

tgt gtt gac gcg ctc gcg gcc gaa ctg cgc caa gtc ctg gat tgc acc   787
Cys Val Asp Ala Leu Ala Ala Glu Leu Arg Gln Val Leu Asp Cys Thr
    215                 220                 225

gag ggc atc ggg aag gta cgc ctg caa cac aat tcc ggc ttc           829
Glu Gly Ile Gly Lys Val Arg Leu Gln His Asn Ser Gly Phe
230                 235                 240

tagttcatgc agctctggat tgg                                        852


<210> 1492
<211> 243
<212> PRT
<213> Corynebacterium glutamicum

<400> 1492
Leu Val Leu Asp Glu Arg Trp Val Gly Val Gly Leu Val Asp Lys Trp
  1               5                  10                  15
```

```
Asp Glu Gly Gly Val Glu Lys Arg Leu Phe Ala Ala Val Leu Cys Val
            20                  25                  30

Val Gly Ala Gly Arg Gly His Val Asp Glu Arg Gly Glu Val Arg Tyr
        35                  40                  45

Gly Gly Ala Glu Ala Ala Leu Leu Ser Leu Glu Gly Arg Val Val Gly
    50                  55                  60

Val Glu Val Glu Asp Gly Gly His Glu Val Phe Ala Arg Gly Val Phe
65                  70                  75                  80

Leu Glu Ala Ala His Glu Val Arg Asn Gly His Val Glu Phe Leu Trp
                85                  90                  95

Ala His Gly Trp Tyr Val Lys Gln Gln Leu Thr Asp Val Asn Ala Asp
            100                 105                 110

Gly Ala Arg Leu Ile Gly Arg His Ala Leu Gln His Phe Glu Leu His
        115                 120                 125

Thr Val Arg Tyr Pro Thr Leu His Arg Glu Gln Met Cys Glu Cys Tyr
    130                 135                 140

Val Glu Lys Val Val Ala Gly Asn Ala Gln Ala Gln Ala Leu His Val
145                 150                 155                 160

Phe Phe Ala His Arg Pro Ile Glu Asp Ala Leu Val Ile Gly Ile Gly
                165                 170                 175

Gly Leu Phe Gly Arg Phe Cys Gly Asn Trp Pro Ala Gly Asp Leu Arg
            180                 185                 190

Val Asp Val Leu His Arg Gln Ile Ser Thr Leu Asp Gln Ala Asn Leu
        195                 200                 205

Asn Ala Arg Pro Ala Cys Val Asp Ala Leu Ala Ala Glu Leu Arg Gln
    210                 215                 220

Val Leu Asp Cys Thr Glu Gly Ile Gly Lys Val Arg Leu Gln His Asn
225                 230                 235                 240

Ser Gly Phe
```

<210> 1493
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(571)
<223> RXN03138

<400> 1493
agaatgttcc agtcttggca tccaaccagc cgattccgct ggcccacact ggggcgttgg 60

cgaggtcttt ggcggtgtac aagttgagga ctaccttgac ttg gat att gtt ccg 115

```
                                                Leu Asp Ile Val Pro
                                                  1               5

aag gat gtc gct gaa agc ttc gcc gta ggt gag gtc gtt ttt ctt cgc   163
Lys Asp Val Ala Glu Ser Phe Ala Val Gly Glu Val Val Phe Leu Arg
                10                  15                  20

gtg ttg ggt gac ggc gtc gtt gat gat gtg ccc gtc cac agc atc gac   211
Val Leu Gly Asp Gly Val Val Asp Asp Val Pro Val His Ser Ile Asp
            25                  30                  35

gga ggc tcc gat ttc ggc ggt tcc gtc tgg gga gaa ggt cac tcc gaa   259
Gly Gly Ser Asp Phe Gly Gly Ser Val Trp Gly Glu Gly His Ser Glu
        40                  45                  50

aga gct gtc gtc ttg ggt acc gcg cga acc ggt ggc tct tgc gtc gtc   307
Arg Ala Val Val Leu Gly Thr Ala Arg Thr Gly Gly Ser Cys Val Val
    55                  60                  65

aag caa atc tct tat ttc ttt tat ctt gcg tcc tat gga cgc cgg gct   355
Lys Gln Ile Ser Tyr Phe Phe Tyr Leu Ala Ser Tyr Gly Arg Arg Ala
70                  75                  80                  85

tgg cag aat ctg gtt ggg gct ggt ggc ggt gag gta ttc ggt gag gat   403
Trp Gln Asn Leu Val Gly Ala Gly Gly Gly Glu Val Phe Gly Glu Asp
                90                  95                  100

tgc gtc ggc gcc ggc gag gtt gtc ggg gtt gat gcc ggc gag ttc gtt   451
Cys Val Gly Ala Gly Glu Val Val Gly Val Asp Ala Gly Glu Phe Val
            105                 110                 115

gct aat ggt gat cag tcg gga gag gtc gag gtg gta cag ctt ttg ttg   499
Ala Asn Gly Asp Gln Ser Gly Glu Val Glu Val Val Gln Leu Leu Leu
        120                 125                 130

cag ggc ttt gag ttc ggg caa gtc ggc gag cgt ggc aaa cgc gat gga   547
Gln Gly Phe Glu Phe Gly Gln Val Gly Glu Arg Gly Lys Arg Asp Gly
    135                 140                 145

tat gcg gga gac ctg cgc ttt tgt tagacctgtg acgatggcga ggc         594
Tyr Ala Gly Asp Leu Arg Phe Cys
150                 155
```

<210> 1494
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 1494

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Leu Asp Ile Val Pro Lys Asp Val Ala Glu Ser Phe Ala Val Gly Glu
  1               5                  10                  15

Val Val Phe Leu Arg Val Leu Gly Asp Gly Val Val Asp Asp Val Pro
            20                  25                  30

Val His Ser Ile Asp Gly Gly Ser Asp Phe Gly Gly Ser Val Trp Gly
        35                  40                  45

Glu Gly His Ser Glu Arg Ala Val Val Leu Gly Thr Ala Arg Thr Gly
    50                  55                  60
```

```
Gly Ser Cys Val Val Lys Gln Ile Ser Tyr Phe Phe Tyr Leu Ala Ser
 65                  70                  75                  80

Tyr Gly Arg Arg Ala Trp Gln Asn Leu Val Gly Ala Gly Gly Gly Glu
                 85                  90                  95

Val Phe Gly Glu Asp Cys Val Gly Ala Gly Glu Val Val Gly Val Asp
            100                 105                 110

Ala Gly Glu Phe Val Ala Asn Gly Asp Gln Ser Gly Glu Val Glu Val
        115                 120                 125

Val Gln Leu Leu Leu Gln Gly Phe Glu Phe Gly Gln Val Gly Glu Arg
    130                 135                 140

Gly Lys Arg Asp Gly Tyr Ala Gly Asp Leu Arg Phe Cys
145                 150                 155


<210> 1495
<211> 372
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(349)
<223> RXN03140

<400> 1495
ctcaagcgat cggtggaaca tccactaacg gggttaccaa aaatccttcg cggacactcc 60

cgaaggaaca cttcttgcga gaaggaaagg aagaagcact gtg aag ggc att cat   115
                                              Val Lys Gly Ile His
                                                1               5

cag gaa att agc cgt atc gag cgt agc cac gat tat ctg tgg agc gtc   163
Gln Glu Ile Ser Arg Ile Glu Arg Ser His Asp Tyr Leu Trp Ser Val
                10                  15                  20

cga gaa gac ctg cat gca cga ttc gac aac caa ctg aag gca cac ttt   211
Arg Glu Asp Leu His Ala Arg Phe Asp Asn Gln Leu Lys Ala His Phe
            25                  30                  35

gta gac agt gtc ctg gat agc att gca gaa gga tat gaa ggc cga atc   259
Val Asp Ser Val Leu Asp Ser Ile Ala Glu Gly Tyr Glu Gly Arg Ile
        40                  45                  50

aac cga ttc cgc aaa atc ttc att gaa atg aaa gcg gtt gaa gag ctg   307
Asn Arg Phe Arg Lys Ile Phe Ile Glu Met Lys Ala Val Glu Glu Leu
    55                  60                  65

cgc acc atc gcc gcc acc cgc cca agc cac ctc ttg gct gca           349
Arg Thr Ile Ala Ala Thr Arg Pro Ser His Leu Leu Ala Ala
 70                  75                  80

taagacactt aaaagttaaa taa                                        372


<210> 1496
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<211> 83
<212> PRT
<213> Corynebacterium glutamicum

<400> 1496
Val Lys Gly Ile His Gln Glu Ile Ser Arg Ile Glu Arg Ser His Asp
1 5 10 15

Tyr Leu Trp Ser Val Arg Glu Asp Leu His Ala Arg Phe Asp Asn Gln
20 25 30

Leu Lys Ala His Phe Val Asp Ser Val Leu Asp Ser Ile Ala Glu Gly
35 40 45

Tyr Glu Gly Arg Ile Asn Arg Phe Arg Lys Ile Phe Ile Glu Met Lys
50 55 60

Ala Val Glu Glu Leu Arg Thr Ile Ala Ala Thr Arg Pro Ser His Leu
65 70 75 80

Leu Ala Ala

<210> 1497
<211> 453
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(430)
<223> RXN03141

<400> 1497
ggccctgctg cttcatgcgg tgagctgcgc gaccgaaagc gatctgtgag gaagcggtga 60

aatctgggtt tcggtccagc ttgaggatgt attccacggt gtg gtt gaa gcc acc 115
Val Val Glu Ala Thr
1 5

ggt gtc gcc ggt ggt aat cac gtg gcc acc gtg tgg cat gcc ggt gtg 163
Gly Val Ala Gly Gly Asn His Val Ala Thr Val Trp His Ala Gly Val
10 15 20

ctc gga gtc gaa ggt tgc ttc gtc gat gaa gtt gac ttc gac ttc gta 211
Leu Gly Val Glu Gly Cys Phe Val Asp Glu Val Asp Phe Asp Phe Val
25 30 35

gcc aac gaa gta atc agg cat ggt gcg gat gtc gtt ttc gat gcg ctc 259
Ala Asn Glu Val Ile Arg His Gly Ala Asp Val Val Phe Asp Ala Leu
40 45 50

gtg atc ggc cgc gtc ggc aac cac gaa gca ttg gcg ctt gtg ggt ttg 307
Val Ile Gly Arg Val Gly Asn His Glu Ala Leu Ala Leu Val Gly Leu
55 60 65

ctt tcc ggt aag gtc gcc ggc ttc gcc gcg gcg ggc ctt ttc cag ggc 355
Leu Ser Gly Lys Val Ala Gly Phe Ala Ala Ala Gly Leu Phe Gln Gly
70 75 80 85

```
gtc ttc gga tgg gag ggt gta ctg gac tgc ctt ttg aac gcc agg gat   403
Val Phe Gly Trp Glu Gly Val Leu Asp Cys Leu Leu Asn Ala Arg Asp
                 90                  95                 100

gcg tcg caa agc atc gga gtg gcc ctg tgacaaacct gggccccaga         450
Ala Ser Gln Ser Ile Gly Val Ala Leu
            105                 110

agg                                                               453


<210> 1498
<211> 110
<212> PRT
<213> Corynebacterium glutamicum

<400> 1498
Val Val Glu Ala Thr Gly Val Ala Gly Gly Asn His Val Ala Thr Val
  1               5                  10                  15

Trp His Ala Gly Val Leu Gly Val Glu Gly Cys Phe Val Asp Glu Val
             20                  25                  30

Asp Phe Asp Phe Val Ala Asn Glu Val Ile Arg His Gly Ala Asp Val
         35                  40                  45

Val Phe Asp Ala Leu Val Ile Gly Arg Val Gly Asn His Glu Ala Leu
     50                  55                  60

Ala Leu Val Gly Leu Leu Ser Gly Lys Val Ala Gly Phe Ala Ala Ala
 65                  70                  75                  80

Gly Leu Phe Gln Gly Val Phe Gly Trp Glu Gly Val Leu Asp Cys Leu
                 85                  90                  95

Leu Asn Ala Arg Asp Ala Ser Gln Ser Ile Gly Val Ala Leu
            100                 105                 110


<210> 1499
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(571)
<223> RXN03146

<400> 1499
taacgtgggg gttttaagct tgcgtagaca tatcgttttt cgatagattt acatcttgaa 60

acgatacgcc catccacggc gcatgtctga aaggttcccc atg aat ccc cgc atc   115
                                              Met Asn Pro Arg Ile
                                                1               5

ctc atg ctg ctt cgc atc att ttc ggc gcg gcc ttc ctc gca ctg ttg   163
Leu Met Leu Leu Arg Ile Ile Phe Gly Ala Ala Phe Leu Ala Leu Leu
                10                  15                  20

gtg ctg caa gtc ctg ctc gcc atc aaa atc gtg cgc gat ggc ctc aac   211
```

```
Val Leu Gln Val Leu Leu Ala Ile Lys Ile Val Arg Asp Gly Leu Asn
            25                  30                  35

tcc ggc gag ctc tcc ccc atc ccg ctc acc att ctc gcg agc ttc gtg   259
Ser Gly Glu Leu Ser Pro Ile Pro Leu Thr Ile Leu Ala Ser Phe Val
        40                  45                  50

atc atc ggt ttc ggg ctc gtg cag ttc atc atc gtc tgt ctg ttc gcg   307
Ile Ile Gly Phe Gly Leu Val Gln Phe Ile Ile Val Cys Leu Phe Ala
    55                  60                  65

cta ctg cgt ctc gtg gaa gac gat gaa atc ttc gac gcc cac tcg ctc   355
Leu Leu Arg Leu Val Glu Asp Asp Glu Ile Phe Asp Ala His Ser Leu
70                  75                  80                  85

gcc tgg gtt gat cga att gcc atc acc atc gca gcc ggc gcc gtt tta   403
Ala Trp Val Asp Arg Ile Ala Ile Thr Ile Ala Ala Gly Ala Val Leu
                90                  95                  100

ctc ctc cca atg gcc tac atc gtc gca gaa gtc gac gac gcc ccc gga   451
Leu Leu Pro Met Ala Tyr Ile Val Ala Glu Val Asp Asp Ala Pro Gly
            105                 110                 115

gcc atc gtc ttc ggt ctc atc ctc gcg atg ctc atc acg ggc gta tcc   499
Ala Ile Val Phe Gly Leu Ile Leu Ala Met Leu Ile Thr Gly Val Ser
        120                 125                 130

ctg ctg gta aaa atc atg cgc gca ctc ctg gcc cgc gcc atc gga ttc   547
Leu Leu Val Lys Ile Met Arg Ala Leu Leu Ala Arg Ala Ile Gly Phe
    135                 140                 145

tcc acg gaa ctg gaa tcg gtg atc taaatggcca tcatcgtcga cat         594
Ser Thr Glu Leu Glu Ser Val Ile
150                 155
```

Sequence Listing.ST25.txt

<210> 1500
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 1500

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Met Asn Pro Arg Ile Leu Met Leu Leu Arg Ile Ile Phe Gly Ala Ala
  1               5                  10                  15

Phe Leu Ala Leu Leu Val Leu Gln Val Leu Leu Ala Ile Lys Ile Val
            20                  25                  30

Arg Asp Gly Leu Asn Ser Gly Glu Leu Ser Pro Ile Pro Leu Thr Ile
        35                  40                  45

Leu Ala Ser Phe Val Ile Ile Gly Phe Gly Leu Val Gln Phe Ile Ile
    50                  55                  60

Val Cys Leu Phe Ala Leu Leu Arg Leu Val Glu Asp Asp Glu Ile Phe
65                  70                  75                  80

Asp Ala His Ser Leu Ala Trp Val Asp Arg Ile Ala Ile Thr Ile Ala
                85                  90                  95

Ala Gly Ala Val Leu Leu Leu Pro Met Ala Tyr Ile Val Ala Glu Val
```

```
            100                 105                 110

Asp Asp Ala Pro Gly Ala Ile Val Phe Gly Leu Ile Leu Ala Met Leu
        115                 120                 125

Ile Thr Gly Val Ser Leu Leu Val Lys Ile Met Arg Ala Leu Leu Ala
    130                 135                 140

Arg Ala Ile Gly Phe Ser Thr Glu Leu Glu Ser Val Ile
145                 150                 155


<210> 1501
<211> 375
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(352)
<223> RXN03147

<400> 1501
ccctgatccc gaggacgatg accgccaaag cgatggcgcc tccaatcagg atgtactgca 60

gtgggattgg gcgggcgtca tcgatggcat cgatgcagtt ttg gaa atc ctc ttt   115
                                              Leu Glu Ile Leu Phe
                                                1               5

aag agc ggt ttg gga ttc gtt gta atc atc ggt gcg gtc ggc gaa tac   163
Lys Ser Gly Leu Gly Phe Val Val Ile Ile Gly Ala Val Gly Glu Tyr
                10                  15                  20

ttc ggc gcg gat ttc tgc ggt gcg ggt gcc ggt ggt ggc ggc ttg ttg   211
Phe Gly Ala Asp Phe Cys Gly Ala Gly Ala Gly Gly Gly Gly Leu Leu
            25                  30                  35

aag ttg gct gag tac atc gct ggc tgg atc gct gga gaa tcc gct gat   259
Lys Leu Ala Glu Tyr Ile Ala Gly Trp Ile Ala Gly Glu Ser Ala Asp
        40                  45                  50

gat gtc ttt ggc ttc gtc gta tgt gta ctc cgt ttt gaa act ttc ctc   307
Asp Val Phe Gly Phe Val Val Cys Val Leu Arg Phe Glu Thr Phe Leu
    55                  60                  65

ggc gtt ggg gtc tgc cag cgt ggg atc gtc tgg gag gag cat ggc       352
Gly Val Gly Val Cys Gln Arg Gly Ile Val Trp Glu Glu His Gly
70                  75                  80

taggccttcg ccggattcga tgg                                        375


<210> 1502
<211> 84
<212> PRT
<213> Corynebacterium glutamicum

<400> 1502
Leu Glu Ile Leu Phe Lys Ser Gly Leu Gly Phe Val Val Ile Ile Gly
  1               5                  10                  15
```

```
Ala Val Gly Glu Tyr Phe Gly Ala Asp Phe Cys Gly Ala Gly Ala Gly
            20                  25                  30

Gly Gly Gly Leu Leu Lys Leu Ala Glu Tyr Ile Ala Gly Trp Ile Ala
        35                  40                  45

Gly Glu Ser Ala Asp Asp Val Phe Gly Phe Val Val Cys Val Leu Arg
    50                  55                  60

Phe Glu Thr Phe Leu Gly Val Gly Val Cys Gln Arg Gly Ile Val Trp
65                  70                  75                  80

Glu Glu His Gly
```

<210> 1503
<211> 390
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(367)
<223> RXN03149

<400> 1503

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gctttactag aaccagtgat cggtaaacta ccttttagtt cggctattag cagtacaatc 60

tctgtggcgc tgggatttat tttagttacc gtatatcgat gtg gtt att ggc gaa   115
                                            Val Val Ile Gly Glu
                                              1               5

ctg ctt cct aag agc tat agt atc gtc aat acg gag aag gtc gtc ttg   163
Leu Leu Pro Lys Ser Tyr Ser Ile Val Asn Thr Glu Lys Val Val Leu
                10                  15                  20

ttc gta gtt aaa cca ctt cat tat ttt tat aaa gta atg ttt cct ttt   211
Phe Val Val Lys Pro Leu His Tyr Phe Tyr Lys Val Met Phe Pro Phe
            25                  30                  35

att tgg gta ttg aat cat tca gct gca ggg cta ggg aag cta tta ggt   259
Ile Trp Val Leu Asn His Ser Ala Ala Gly Leu Gly Lys Leu Leu Gly
        40                  45                  50

gtg cgt ctc gta tct gaa gga gaa gag aca ttg tct caa gaa gag ctg   307
Val Arg Leu Val Ser Glu Gly Glu Glu Thr Leu Ser Gln Glu Glu Leu
    55                  60                  65

aca tta gtc gca ttg aat tct tat gaa aaa gga gag ttg cca aag aag   355
Thr Leu Val Ala Leu Asn Ser Tyr Glu Lys Gly Glu Leu Pro Lys Lys
70                  75                  80                  85

aat atc att att tgaaaacgtg tttgaatttg atg                        390
Asn Ile Ile Ile
```

<210> 1504
<211> 89
<212> PRT

<213> Corynebacterium glutamicum

<400> 1504

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Val Val Ile Gly Glu Leu Leu Pro Lys Ser Tyr Ser Ile Val Asn Thr
  1               5                  10                  15

Glu Lys Val Val Leu Phe Val Val Lys Pro Leu His Tyr Phe Tyr Lys
             20                  25                  30

Val Met Phe Pro Phe Ile Trp Val Leu Asn His Ser Ala Ala Gly Leu
         35                  40                  45

Gly Lys Leu Leu Gly Val Arg Leu Val Ser Glu Gly Glu Glu Thr Leu
     50                  55                  60

Ser Gln Glu Glu Leu Thr Leu Val Ala Leu Asn Ser Tyr Glu Lys Gly
 65                  70                  75                  80

Glu Leu Pro Lys Lys Asn Ile Ile Ile
                 85
```

<210> 1505
<211> 396
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(373)
<223> RXN03152

<400> 1505

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gcaaaatatc agctttgacc tgcacatata gttgcacaat ggtgaaagtg cacataaagt 60

aactttcgta ttcgaatatt taaacctaag gggtttagca atg aag cta ttt tct   115
                                          Met Lys Leu Phe Ser
                                            1               5

cgt act ccc ctc gtc gca ctc ggc aca gct gct gca atg gca gca acc   163
Arg Thr Pro Leu Val Ala Leu Gly Thr Ala Ala Ala Met Ala Ala Thr
                10                  15                  20

tcc atc tcc gtt cct gca cag gct gaa gaa gtc gca cca gca cag gtt   211
Ser Ile Ser Val Pro Ala Gln Ala Glu Glu Val Ala Pro Ala Gln Val
            25                  30                  35

gtg tac gtg gct gac acc gta gaa gaa gaa acg ggt agc tcc aac gga   259
Val Tyr Val Ala Asp Thr Val Glu Glu Glu Thr Gly Ser Ser Asn Gly
        40                  45                  50

tct tct gac att gac tct gac acc att ttg gat tac gtc gtc gtt att   307
Ser Ser Asp Ile Asp Ser Asp Thr Ile Leu Asp Tyr Val Val Val Ile
    55                  60                  65

act ggc atc gtt ggc gtc ctc agc gct ggt ttg acc ttc gct act gct   355
Thr Gly Ile Val Gly Val Leu Ser Ala Gly Leu Thr Phe Ala Thr Ala
70                  75                  80                  85

ttc cag cgt tca ttg cag taaatttcag cgttaatcac caa                 396
Phe Gln Arg Ser Leu Gln
```

90

<210> 1506
<211> 91
<212> PRT
<213> Corynebacterium glutamicum

<400> 1506
Met Lys Leu Phe Ser Arg Thr Pro Leu Val Ala Leu Gly Thr Ala Ala
1 5 10 15

Ala Met Ala Ala Thr Ser Ile Ser Val Pro Ala Gln Ala Glu Glu Val
20 25 30

Ala Pro Ala Gln Val Val Tyr Val Ala Asp Thr Val Glu Glu Glu Thr
35 40 45

Gly Ser Ser Asn Gly Ser Ser Asp Ile Asp Ser Asp Thr Ile Leu Asp
50 55 60

Tyr Val Val Val Ile Thr Gly Ile Val Gly Val Leu Ser Ala Gly Leu
65 70 75 80

Thr Phe Ala Thr Ala Phe Gln Arg Ser Leu Gln
85 90

<210> 1507
<211> 687
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(664)
<223> RXN03153

<400> 1507
taatttgaat tttagggaac ctaccccgag cttttgcagt ctaacgctta tgagtgcctt 60

ttcacggccc tcgttacgac tacaaagatc ggggtatttt atg cga cga atc tgg 115
Met Arg Arg Ile Trp
1 5

ctg ctc gta tgc ggc atc gca ttg act gtc gcc ggc tgc acg agt gga 163
Leu Leu Val Cys Gly Ile Ala Leu Thr Val Ala Gly Cys Thr Ser Gly
10 15 20

tcc acc act ccc aca acc gtc acg gta acc gca acg cca acg tcg gag 211
Ser Thr Thr Pro Thr Thr Val Thr Val Thr Ala Thr Pro Thr Ser Glu
25 30 35

gag gct gca tcc acg gag ccg acc aac gac ata ctt gcc agc caa ttt 259
Glu Ala Ala Ser Thr Glu Pro Thr Asn Asp Ile Leu Ala Ser Gln Phe
40 45 50

cat ccg tgt gaa gta ctc acg cag gaa cag ttc gaa gaa gtc gga ttg 307
His Pro Cys Glu Val Leu Thr Gln Glu Gln Phe Glu Glu Val Gly Leu
55 60 65

```
gga gtc ttg att gtt gaa gac gct tac ctc ggc tcg aca ggt tta ggt   355
Gly Val Leu Ile Val Glu Asp Ala Tyr Leu Gly Ser Thr Gly Leu Gly
 70                  75                  80                  85

tgc agt ttc ggg aaa gca gac aga gag gat ttt tca ggt acg tgg ctc   403
Cys Ser Phe Gly Lys Ala Asp Arg Glu Asp Phe Ser Gly Thr Trp Leu
                90                  95                 100

att tca act gac caa gca aac cga caa ttt gtt gaa aac caa gat cta   451
Ile Ser Thr Asp Gln Ala Asn Arg Gln Phe Val Glu Asn Gln Asp Leu
            105                 110                 115

gag aca ttg gat tgg gga tcc aat gac aat cca gat ctg tat gtg cat   499
Glu Thr Leu Asp Trp Gly Ser Asn Asp Asn Pro Asp Leu Tyr Val His
        120                 125                 130

caa atg tcc gag acg ggt cgt caa tgt gag gca gca gtt gac tat gac   547
Gln Met Ser Glu Thr Gly Arg Gln Cys Glu Ala Ala Val Asp Tyr Asp
    135                 140                 145

tgg ggc cgg ctt acg gtt gac tat ctc gaa tta ggt gag ggc tgg gag   595
Trp Gly Arg Leu Thr Val Asp Tyr Leu Glu Leu Gly Glu Gly Trp Glu
150                 155                 160                 165

cca gaa att ttg tgc tct gat gct gtt gaa att tta gaa aat ctc atc   643
Pro Glu Ile Leu Cys Ser Asp Ala Val Glu Ile Leu Glu Asn Leu Ile
                170                 175                 180

aag gaa cta agg gga att cca tgacattgaa aattgatccc tcg             687
Lys Glu Leu Arg Gly Ile Pro
            185
```

<210> 1508
<211> 188
<212> PRT
<213> Corynebacterium glutamicum

<400> 1508

```
Met Arg Arg Ile Trp Leu Leu Val Cys Gly Ile Ala Leu Thr Val Ala
  1               5                  10                  15

Gly Cys Thr Ser Gly Ser Thr Thr Pro Thr Thr Val Thr Val Thr Ala
             20                  25                  30

Thr Pro Thr Ser Glu Glu Ala Ala Ser Thr Glu Pro Thr Asn Asp Ile
         35                  40                  45

Leu Ala Ser Gln Phe His Pro Cys Glu Val Leu Thr Gln Glu Gln Phe
     50                  55                  60

Glu Glu Val Gly Leu Gly Val Leu Ile Val Glu Asp Ala Tyr Leu Gly
 65                  70                  75                  80

Ser Thr Gly Leu Gly Cys Ser Phe Gly Lys Ala Asp Arg Glu Asp Phe
                 85                  90                  95

Ser Gly Thr Trp Leu Ile Ser Thr Asp Gln Ala Asn Arg Gln Phe Val
            100                 105                 110

Glu Asn Gln Asp Leu Glu Thr Leu Asp Trp Gly Ser Asn Asp Asn Pro
```

```
        115                 120                 125

Asp Leu Tyr Val His Gln Met Ser Glu Thr Gly Arg Gln Cys Glu Ala
    130                 135                 140

Ala Val Asp Tyr Asp Trp Gly Arg Leu Thr Val Asp Tyr Leu Glu Leu
145                 150                 155                 160

Gly Glu Gly Trp Glu Pro Glu Ile Leu Cys Ser Asp Ala Val Glu Ile
                165                 170                 175

Leu Glu Asn Leu Ile Lys Glu Leu Arg Gly Ile Pro
            180                 185


<210> 1509
<211> 1035
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1012)
<223> RXN03154

<400> 1509
aaagtgccct ctcctaaatc gtttctaagg gctcgtcaga ccccagttga tacaaacata 60

cattctgaaa attcagtcgc ttaaatgggc gcagcgggaa atg ctg aaa act aca   115
                                              Met Leu Lys Thr Thr
                                                1               5

tta atc acc gat acc cta ggg cac gtg acc tct act gaa ccc acc acc   163
Leu Ile Thr Asp Thr Leu Gly His Val Thr Ser Thr Glu Pro Thr Thr
                10                  15                  20

aca gcc cat gtt cca cta cct gat gga tct tcc act cca gtc caa att   211
Thr Ala His Val Pro Leu Pro Asp Gly Ser Ser Thr Pro Val Gln Ile
            25                  30                  35

tgg gcg tca gat aac aaa gac tcc caa ctg gtg atg ctg tgg cca ggt   259
Trp Ala Ser Asp Asn Lys Asp Ser Gln Leu Val Met Leu Trp Pro Gly
        40                  45                  50

ttc ggc atg ggt ggc tat tac tat cgt ccg ctt gcg gca gcg cta aat   307
Phe Gly Met Gly Gly Tyr Tyr Tyr Arg Pro Leu Ala Ala Ala Leu Asn
    55                  60                  65

aaa gct gga ttc cat gtg gcg att ggt gaa ctt cgt ggt cag ggg caa   355
Lys Ala Gly Phe His Val Ala Ile Gly Glu Leu Arg Gly Gln Gly Gln
70                  75                  80                  85

agt tcc gcg aag gct tct cgg aaa agt cag tgg gga tac cat gat ctc   403
Ser Ser Ala Lys Ala Ser Arg Lys Ser Gln Trp Gly Tyr His Asp Leu
                90                  95                  100

gca tcg gta gat ttt ccg ctg cag att gcc gct gcg aaa aag gcg ctt   451
Ala Ser Val Asp Phe Pro Leu Gln Ile Ala Ala Ala Lys Lys Ala Leu
            105                 110                 115

gac ctg gag gaa ggc cat ccc atg agg ttt ttg tcg cat tcg atg ggt   499
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Asp Leu Glu Glu Gly His Pro Met Arg Phe Leu Ser His Ser Met Gly
        120                 125                 130

ggg cag att tct tgt ctt ttc gca gcg agg ccg gag gct gag aaa tat   547
Gly Gln Ile Ser Cys Leu Phe Ala Ala Arg Pro Glu Ala Glu Lys Tyr
    135                 140                 145

aat ctt cgg gcg att ttc ggg gtg ggt gca ggg tcg ccg ttt agg cct   595
Asn Leu Arg Ala Ile Phe Gly Val Gly Ala Gly Ser Pro Phe Arg Pro
150                 155                 160                 165

acg ttt agt ccg aaa atg ggg aag cgt ttg gga ttg ggt gcg gtg ctg   643
Thr Phe Ser Pro Lys Met Gly Lys Arg Leu Gly Leu Gly Ala Val Leu
                170                 175                 180

ctt ggt ggg att ggt ggc cac att gtg gga ttt tgg ccc ggc aaa gtt   691
Leu Gly Gly Ile Gly Gly His Ile Val Gly Phe Trp Pro Gly Lys Val
            185                 190                 195

tta gga aaa gac ctg gtg ggt tat ggc cga caa tcg gga act cac atg   739
Leu Gly Lys Asp Leu Val Gly Tyr Gly Arg Gln Ser Gly Thr His Met
        200                 205                 210

agg gaa tgg cgt cga ttc cat aag cac aat tct ttg gac gat ctc acc   787
Arg Glu Trp Arg Arg Phe His Lys His Asn Ser Leu Asp Asp Leu Thr
    215                 220                 225

gcg cag gac atc aac tat gtg gag gtg atg aag aag gtg agc att cct   835
Ala Gln Asp Ile Asn Tyr Val Glu Val Met Lys Lys Val Ser Ile Pro
230                 235                 240                 245

att act ttt agt cgt tgt cct gat gat gag gac tgc ccg cag gca tcg   883
Ile Thr Phe Ser Arg Cys Pro Asp Asp Glu Asp Cys Pro Gln Ala Ser
                250                 255                 260

att gat ggg ttg gcg agt ttt gtt ccc gca gcg cag atc aaa atg ata   931
Ile Asp Gly Leu Ala Ser Phe Val Pro Ala Ala Gln Ile Lys Met Ile
            265                 270                 275

gaa att cca gaa gcc ctg gga cat aac cgg tgg gct cgg gaa cct gaa   979
Glu Ile Pro Glu Ala Leu Gly His Asn Arg Trp Ala Arg Glu Pro Glu
        280                 285                 290

tca aca gtg aaa ctc ttc ctg gaa caa gct ctt tagtgaccga tggagcggag 1032
Ser Thr Val Lys Leu Phe Leu Glu Gln Ala Leu
    295                 300

gta                                                               1035


<210> 1510
<211> 304
<212> PRT
<213> Corynebacterium glutamicum

<400> 1510
Met Leu Lys Thr Thr Leu Ile Thr Asp Thr Leu Gly His Val Thr Ser
  1               5                  10                  15

Thr Glu Pro Thr Thr Thr Ala His Val Pro Leu Pro Asp Gly Ser Ser
             20                  25                  30
```

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Thr Pro Val Gln Ile Trp Ala Ser Asp Asn Lys Asp Ser Gln Leu Val
         35                  40                  45

Met Leu Trp Pro Gly Phe Gly Met Gly Gly Tyr Tyr Tyr Arg Pro Leu
     50                  55                  60

Ala Ala Ala Leu Asn Lys Ala Gly Phe His Val Ala Ile Gly Glu Leu
 65                  70                  75                  80

Arg Gly Gln Gly Gln Ser Ser Ala Lys Ala Ser Arg Lys Ser Gln Trp
                 85                  90                  95

Gly Tyr His Asp Leu Ala Ser Val Asp Phe Pro Leu Gln Ile Ala Ala
            100                 105                 110

Ala Lys Lys Ala Leu Asp Leu Glu Glu Gly His Pro Met Arg Phe Leu
        115                 120                 125

Ser His Ser Met Gly Gly Gln Ile Ser Cys Leu Phe Ala Ala Arg Pro
    130                 135                 140

Glu Ala Glu Lys Tyr Asn Leu Arg Ala Ile Phe Gly Val Gly Ala Gly
145                 150                 155                 160

Ser Pro Phe Arg Pro Thr Phe Ser Pro Lys Met Gly Lys Arg Leu Gly
                165                 170                 175

Leu Gly Ala Val Leu Leu Gly Gly Ile Gly Gly His Ile Val Gly Phe
            180                 185                 190

Trp Pro Gly Lys Val Leu Gly Lys Asp Leu Val Gly Tyr Gly Arg Gln
        195                 200                 205

Ser Gly Thr His Met Arg Glu Trp Arg Arg Phe His Lys His Asn Ser
    210                 215                 220

Leu Asp Asp Leu Thr Ala Gln Asp Ile Asn Tyr Val Glu Val Met Lys
225                 230                 235                 240

Lys Val Ser Ile Pro Ile Thr Phe Ser Arg Cys Pro Asp Asp Glu Asp
                245                 250                 255

Cys Pro Gln Ala Ser Ile Asp Gly Leu Ala Ser Phe Val Pro Ala Ala
            260                 265                 270

Gln Ile Lys Met Ile Glu Ile Pro Glu Ala Leu Gly His Asn Arg Trp
        275                 280                 285

Ala Arg Glu Pro Glu Ser Thr Val Lys Leu Phe Leu Glu Gln Ala Leu
    290                 295                 300
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<210> 1511
<211> 303
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(280)
<223> RXN03156

<400> 1511
gtatcgacct cgatgatcgc gttgctgcag agatgaccat tttaggtcgc cctgtgccta 60

aagaaggata accaccacac cagaaaagaa gtacctcatt atg gct cga acc aca 115
Met Ala Arg Thr Thr
1 5

cct cca cca gct gat gta ctc gac atc atc att tcc acc gtg aag cag 163
Pro Pro Pro Ala Asp Val Leu Asp Ile Ile Ile Ser Thr Val Lys Gln
10 15 20

acc atc ggc att gat ctt gct gaa ctg att cag ggc cgt gca ctc ggc 211
Thr Ile Gly Ile Asp Leu Ala Glu Leu Ile Gln Gly Arg Ala Leu Gly
25 30 35

cag gct caa ggt gag gca caa ggc aaa gct agt gca gca gcc ctt gag 259
Gln Ala Gln Gly Glu Ala Gln Gly Lys Ala Ser Ala Ala Ala Leu Glu
40 45 50

cag gca cct cat aat gag cag taaataacac acaccacatg tgc 303
Gln Ala Pro His Asn Glu Gln
55 60

<210> 1512
<211> 60
<212> PRT
<213> Corynebacterium glutamicum

<400> 1512
Met Ala Arg Thr Thr Pro Pro Pro Ala Asp Val Leu Asp Ile Ile Ile
1 5 10 15

Ser Thr Val Lys Gln Thr Ile Gly Ile Asp Leu Ala Glu Leu Ile Gln
20 25 30

Gly Arg Ala Leu Gly Gln Ala Gln Gly Glu Ala Gln Gly Lys Ala Ser
35 40 45

Ala Ala Ala Leu Glu Gln Ala Pro His Asn Glu Gln
50 55 60

<210> 1513
<211> 182
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(159)
<223> FRXA00176

<400> 1513
cag ctg atg tac tcg aca tca tca ttt acc acc gtg aag cag acc atc 48
Gln Leu Met Tyr Ser Thr Ser Ser Phe Thr Thr Val Lys Gln Thr Ile

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  1               5                  10                  15

ggc att gat ctt gct gaa ctg att cag ggc cgt gca ctc ggc cag gct   96
Gly Ile Asp Leu Ala Glu Leu Ile Gln Gly Arg Ala Leu Gly Gln Ala
             20                  25                  30

caa ggt gag gca caa ggc aaa gct agt gca gca gcc ctt gag cag gca   144
Gln Gly Glu Ala Gln Gly Lys Ala Ser Ala Ala Ala Leu Glu Gln Ala
         35                  40                  45

cct cat aat gag cag taaataacac acaccacatg tgc                     182
Pro His Asn Glu Gln
     50


<210> 1514
<211> 53
<212> PRT
<213> Corynebacterium glutamicum

<400> 1514
Gln Leu Met Tyr Ser Thr Ser Ser Phe Thr Thr Val Lys Gln Thr Ile
  1               5                  10                  15

Gly Ile Asp Leu Ala Glu Leu Ile Gln Gly Arg Ala Leu Gly Gln Ala
             20                  25                  30

Gln Gly Glu Ala Gln Gly Lys Ala Ser Ala Ala Ala Leu Glu Gln Ala
         35                  40                  45

Pro His Asn Glu Gln
     50


<210> 1515
<211> 519
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(496)
<223> RXN03162

<400> 1515
ggtcaatcag ttcctgccac tgctctggct tgtcgtaggt gtacttcgcg ccggagaaca 60

gggttgcgga gaagttgtcg ccgccttctg ctggcttctt gtg cac gac gaa cac   115
                                              Val His Asp Glu His
                                                1               5

tgg gtg tgg tcc gac gag aag gat gcg gat ttc gcc ttc gac gat gcg   163
Trp Val Trp Ser Asp Glu Lys Asp Ala Asp Phe Ala Phe Asp Asp Ala
                10                  15                  20

tgg cat gaa acg cat atc aac gag cat gcc gtt gtc gcc gat gat gta   211
Trp His Glu Thr His Ile Asn Glu His Ala Val Val Ala Asp Asp Val
             25                  30                  35

ctg gtc aca gaa atc cat gaa ctc gcc gag ctt gcg gac ttc agt gtg   259
Leu Val Thr Glu Ile His Glu Leu Ala Glu Leu Ala Asp Phe Ser Val
```

```
        40                  45                  50

gtt gtc gac tgc ttc ggt gca ctt gat ttc agt gtc caa tgg cag tgc   307
Val Val Asp Cys Phe Gly Ala Leu Asp Phe Ser Val Gln Trp Gln Cys
     55                  60                  65

ggt gcc tgg ctc gat gga tgc agc cag ttc ctt gtc tac caa ctg gac   355
Gly Ala Trp Leu Asp Gly Cys Ser Gln Phe Leu Val Tyr Gln Leu Asp
 70                  75                  80                  85

gcg cca aat gcc gga gcc ggt gga gcc acg gtt ttg ctt gag cac gcg   403
Ala Pro Asn Ala Gly Ala Gly Gly Ala Thr Val Leu Leu Glu His Ala
                 90                  95                 100

ctc acc gaa gga cag gga ggt tgg gaa aac ctt gtg gaa ggt ctc cac   451
Leu Thr Glu Gly Gln Gly Gly Trp Glu Asn Leu Val Glu Gly Leu His
            105                 110                 115

gtc gta gta cgc ctc ggt gtc gga tgg cac cag gtc ggt ttg gga        496
Val Val Val Arg Leu Gly Val Gly Trp His Gln Val Gly Leu Gly
        120                 125                 130

tagcttgacc agcgcatctt tcg                                         519


<210> 1516
<211> 132
<212> PRT
<213> Corynebacterium glutamicum

<400> 1516
Val His Asp Glu His Trp Val Trp Ser Asp Glu Lys Asp Ala Asp Phe
  1               5                  10                  15

Ala Phe Asp Asp Ala Trp His Glu Thr His Ile Asn Glu His Ala Val
             20                  25                  30

Val Ala Asp Asp Val Leu Val Thr Glu Ile His Glu Leu Ala Glu Leu
         35                  40                  45

Ala Asp Phe Ser Val Val Val Asp Cys Phe Gly Ala Leu Asp Phe Ser
     50                  55                  60

Val Gln Trp Gln Cys Gly Ala Trp Leu Asp Gly Cys Ser Gln Phe Leu
 65                  70                  75                  80

Val Tyr Gln Leu Asp Ala Pro Asn Ala Gly Ala Gly Gly Ala Thr Val
                 85                  90                  95

Leu Leu Glu His Ala Leu Thr Glu Gly Gln Gly Gly Trp Glu Asn Leu
            100                 105                 110

Val Glu Gly Leu His Val Val Val Arg Leu Gly Val Gly Trp His Gln
        115                 120                 125

Val Gly Leu Gly
    130


<210> 1517
<211> 730
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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(730)
<223> RXN03167

<400> 1517
gccgcgactg cgggtgcttt tgcgctgttg cgtaaaaaat agtttttatt aagggcattc 60

cctgattccc aggtggtgcc acattgttta tggtggagat atg aac acg aac ttg 115
Met Asn Thr Asn Leu
1 5

ccg aac cta tac acc gca ttt gac ctt gat cga agt gaa tcc tcc gaa 163
Pro Asn Leu Tyr Thr Ala Phe Asp Leu Asp Arg Ser Glu Ser Ser Glu
10 15 20

gct tta ggt gtt tcc ctt tct gcc cgc gat ctt cgc tta gaa caa atg 211
Ala Leu Gly Val Ser Leu Ser Ala Arg Asp Leu Arg Leu Glu Gln Met
25 30 35

gga att gcc cag gac gat cct cga cgt gcc caa acc gtc caa gct ttc 259
Gly Ile Ala Gln Asp Asp Pro Arg Arg Ala Gln Thr Val Gln Ala Phe
40 45 50

gca gtg ctt gca gac cca gca aaa cgc gcc acc tac gat gct caa tta 307
Ala Val Leu Ala Asp Pro Ala Lys Arg Ala Thr Tyr Asp Ala Gln Leu
55 60 65

gaa gct gga gtt cca ctc acc tgg gcg cag att cag cat tta gga aac 355
Glu Ala Gly Val Pro Leu Thr Trp Ala Gln Ile Gln His Leu Gly Asn
70 75 80 85

ttc ggc acc ttg cct tcc acc cct act gcg cag ccg ttt gcg gca cct 403
Phe Gly Thr Leu Pro Ser Thr Pro Thr Ala Gln Pro Phe Ala Ala Pro
90 95 100

cag ccg gag ccg tcg ccg gaa ccg caa cag cag tgg aat agc gga caa 451
Gln Pro Glu Pro Ser Pro Glu Pro Gln Gln Gln Trp Asn Ser Gly Gln
105 110 115

aac tat gcg tat ggc aat ccg acc atg gat tac caa act cag cag agc 499
Asn Tyr Ala Tyr Gly Asn Pro Thr Met Asp Tyr Gln Thr Gln Gln Ser
120 125 130

tac aac ccg atg cag gac caa acc caa gcg tcg atg tat gcg caa cct 547
Tyr Asn Pro Met Gln Asp Gln Thr Gln Ala Ser Met Tyr Ala Gln Pro
135 140 145

ttc gcg aac acc cct gca ccg atg tac aac agc aat cag gtt ttt aac 595
Phe Ala Asn Thr Pro Ala Pro Met Tyr Asn Ser Asn Gln Val Phe Asn
150 155 160 165

agg cct act gcg ggt acg cgt ttg tgg atg gcg atc ctc gac agt att 643
Arg Pro Thr Ala Gly Thr Arg Leu Trp Met Ala Ile Leu Asp Ser Ile
170 175 180

ttt gcc ggc atc gct ggt gga att gtc tcc ggt att ttc ggc ttt gga 691
Phe Ala Gly Ile Ala Gly Gly Ile Val Ser Gly Ile Phe Gly Phe Gly

```
            185                 190                 195

tct gaa ttc ctc acc agt gtc atc atg att ttg gtg ctg                 730
Ser Glu Phe Leu Thr Ser Val Ile Met Ile Leu Val Leu
        200                 205                 210


<210> 1518
<211> 210
<212> PRT
<213> Corynebacterium glutamicum

<400> 1518
Met Asn Thr Asn Leu Pro Asn Leu Tyr Thr Ala Phe Asp Leu Asp Arg
  1               5                  10                  15

Ser Glu Ser Ser Glu Ala Leu Gly Val Ser Leu Ser Ala Arg Asp Leu
             20                  25                  30

Arg Leu Glu Gln Met Gly Ile Ala Gln Asp Asp Pro Arg Arg Ala Gln
         35                  40                  45

Thr Val Gln Ala Phe Ala Val Leu Ala Asp Pro Ala Lys Arg Ala Thr
     50                  55                  60

Tyr Asp Ala Gln Leu Glu Ala Gly Val Pro Leu Thr Trp Ala Gln Ile
 65                  70                  75                  80

Gln His Leu Gly Asn Phe Gly Thr Leu Pro Ser Thr Pro Thr Ala Gln
                 85                  90                  95

Pro Phe Ala Ala Pro Gln Pro Glu Pro Ser Pro Glu Pro Gln Gln Gln
            100                 105                 110

Trp Asn Ser Gly Gln Asn Tyr Ala Tyr Gly Asn Pro Thr Met Asp Tyr
        115                 120                 125

Gln Thr Gln Gln Ser Tyr Asn Pro Met Gln Asp Gln Thr Gln Ala Ser
    130                 135                 140

Met Tyr Ala Gln Pro Phe Ala Asn Thr Pro Ala Pro Met Tyr Asn Ser
145                 150                 155                 160

Asn Gln Val Phe Asn Arg Pro Thr Ala Gly Thr Arg Leu Trp Met Ala
                165                 170                 175

Ile Leu Asp Ser Ile Phe Ala Gly Ile Ala Gly Gly Ile Val Ser Gly
            180                 185                 190

Ile Phe Gly Phe Gly Ser Glu Phe Leu Thr Ser Val Ile Met Ile Leu
        195                 200                 205

Val Leu
    210


<210> 1519
<211> 736
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(736)
<223> FRXA02862

<400> 1519
gccgcgactg cgggtgcttt tgcgctgttg cgtaaaaaat agtttttatt aagggcattc 60

cctgattccc aggtggtgcc acattgttta tggtggagat atg aac acg aac ttg 115
Met Asn Thr Asn Leu
1 5

ccg aac cta tac acc gca ttt gac ctt gat cga agt gaa tcc tcc gaa 163
Pro Asn Leu Tyr Thr Ala Phe Asp Leu Asp Arg Ser Glu Ser Ser Glu
10 15 20

gct tta ggt gtt tcc ctt tct gcc cgc gat ctt cgc tta gaa caa atg 211
Ala Leu Gly Val Ser Leu Ser Ala Arg Asp Leu Arg Leu Glu Gln Met
25 30 35

gga att gcc cag gac gat cct cga cgt gcc caa acc gtc caa gct ttc 259
Gly Ile Ala Gln Asp Asp Pro Arg Arg Ala Gln Thr Val Gln Ala Phe
40 45 50

gca gtg ctt gca gac cca gca aaa cgc gcc acc tac gat gct caa tta 307
Ala Val Leu Ala Asp Pro Ala Lys Arg Ala Thr Tyr Asp Ala Gln Leu
55 60 65

gaa gct gga gtt cca ctc acc tgg gcg cag att cag cat tta gga aac 355
Glu Ala Gly Val Pro Leu Thr Trp Ala Gln Ile Gln His Leu Gly Asn
70 75 80 85

ttc ggc acc ttg cct tcc acc cct act gcg cag ccg ttt gcg gca cct 403
Phe Gly Thr Leu Pro Ser Thr Pro Thr Ala Gln Pro Phe Ala Ala Pro
90 95 100

cag ccg gag ccg tcg ccg gaa ccg caa cag cag tgg aat agc gga caa 451
Gln Pro Glu Pro Ser Pro Glu Pro Gln Gln Gln Trp Asn Ser Gly Gln
105 110 115

aac tat gcg tat ggc aat ccg acc atg gat tac caa act cag cag agc 499
Asn Tyr Ala Tyr Gly Asn Pro Thr Met Asp Tyr Gln Thr Gln Gln Ser
120 125 130

tac aac ccg atg cag gac caa acc caa gcg tcg atg tat gcg caa cct 547
Tyr Asn Pro Met Gln Asp Gln Thr Gln Ala Ser Met Tyr Ala Gln Pro
135 140 145

ttc gcg aac acc cct gca ccg atg tac aac agc aat cag gtt ttt aac 595
Phe Ala Asn Thr Pro Ala Pro Met Tyr Asn Ser Asn Gln Val Phe Asn
150 155 160 165

agg cct act gcg ggt acg cgt ttg tgg atg gcg atc ctc gac agt att 643
Arg Pro Thr Ala Gly Thr Arg Leu Trp Met Ala Ile Leu Asp Ser Ile
170 175 180

ttt gcc ggc atc gct ggt gga att gtc tcc ggt att ttc ggc ttt gga 691
Phe Ala Gly Ile Ala Gly Gly Ile Val Ser Gly Ile Phe Gly Phe Gly
185 190 195

tct gaa ttc ctc acc agt gtc atc atg att ttg gtg ctg atc gtc 736

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Ser Glu Phe Leu Thr Ser Val Ile Met Ile Leu Val Leu Ile Val
        200                 205                 210


<210> 1520
<211> 212
<212> PRT
<213> Corynebacterium glutamicum

<400> 1520
Met Asn Thr Asn Leu Pro Asn Leu Tyr Thr Ala Phe Asp Leu Asp Arg
  1               5                  10                  15

Ser Glu Ser Ser Glu Ala Leu Gly Val Ser Leu Ser Ala Arg Asp Leu
             20                  25                  30

Arg Leu Glu Gln Met Gly Ile Ala Gln Asp Asp Pro Arg Arg Ala Gln
         35                  40                  45

Thr Val Gln Ala Phe Ala Val Leu Ala Asp Pro Ala Lys Arg Ala Thr
     50                  55                  60

Tyr Asp Ala Gln Leu Glu Ala Gly Val Pro Leu Thr Trp Ala Gln Ile
 65                  70                  75                  80

Gln His Leu Gly Asn Phe Gly Thr Leu Pro Ser Thr Pro Thr Ala Gln
                 85                  90                  95

Pro Phe Ala Ala Pro Gln Pro Glu Pro Ser Pro Glu Pro Gln Gln Gln
            100                 105                 110

Trp Asn Ser Gly Gln Asn Tyr Ala Tyr Gly Asn Pro Thr Met Asp Tyr
        115                 120                 125

Gln Thr Gln Gln Ser Tyr Asn Pro Met Gln Asp Gln Thr Gln Ala Ser
    130                 135                 140

Met Tyr Ala Gln Pro Phe Ala Asn Thr Pro Ala Pro Met Tyr Asn Ser
145                 150                 155                 160

Asn Gln Val Phe Asn Arg Pro Thr Ala Gly Thr Arg Leu Trp Met Ala
                165                 170                 175

Ile Leu Asp Ser Ile Phe Ala Gly Ile Ala Gly Gly Ile Val Ser Gly
            180                 185                 190

Ile Phe Gly Phe Gly Ser Glu Phe Leu Thr Ser Val Ile Met Ile Leu
        195                 200                 205

Val Leu Ile Val
    210


<210> 1521
<211> 372
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(349)
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<223> RXN03170

<400> 1521
gttaaatcat tgccgcccag aagaagaccg cgcgggcgaa tttgggcttg gagggaacca 60

aacggccact tttccagtcc aacaaagtat gaggattaat ttg ccc cac gcc aaa 115
Leu Pro His Ala Lys
1 5

gag ctc gcc cac gag ctg tgt ttg ttg ccc acc cct gct gtg ccc gcg 163
Glu Leu Ala His Glu Leu Cys Leu Leu Pro Thr Pro Ala Val Pro Ala
10 15 20

ctt ccc act gat tct ggc gcg cag ttt gat atc cac cag gca cta tcc 211
Leu Pro Thr Asp Ser Gly Ala Gln Phe Asp Ile His Gln Ala Leu Ser
25 30 35

gcc tcc ctt gcc acc tat gcc cgc aac ctc acc ttg ctg tcc cac acc 259
Ala Ser Leu Ala Thr Tyr Ala Arg Asn Leu Thr Leu Leu Ser His Thr
40 45 50

gcc gag aat tta gga aac cgc gcg ctg acg ggc ctc gct gaa atc gaa 307
Ala Glu Asn Leu Gly Asn Arg Ala Leu Thr Gly Leu Ala Glu Ile Glu
55 60 65

gac acc gac gac caa ctc gca cac gca ttg gag cgc ctg aca 349
Asp Thr Asp Asp Gln Leu Ala His Ala Leu Glu Arg Leu Thr
70 75 80

tgatcggtct gatcagcgcc ctt 372

<210> 1522
<211> 83
<212> PRT
<213> Corynebacterium glutamicum

<400> 1522
Leu Pro His Ala Lys Glu Leu Ala His Glu Leu Cys Leu Leu Pro Thr
1 5 10 15

Pro Ala Val Pro Ala Leu Pro Thr Asp Ser Gly Ala Gln Phe Asp Ile
20 25 30

His Gln Ala Leu Ser Ala Ser Leu Ala Thr Tyr Ala Arg Asn Leu Thr
35 40 45

Leu Leu Ser His Thr Ala Glu Asn Leu Gly Asn Arg Ala Leu Thr Gly
50 55 60

Leu Ala Glu Ile Glu Asp Thr Asp Asp Gln Leu Ala His Ala Leu Glu
65 70 75 80

Arg Leu Thr

<210> 1523
<211> 372
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(349)
<223> FRXA02856

<400> 1523
gttaaatcat tgccgcccag aagaagaccg cgcgggcgaa tttgggcttg gagggaacca 60

aacggccact tttccagtcc aacaaagtat gaggattaat ttg ccc cac gcc aaa 115
Leu Pro His Ala Lys
1 5

gag ctc gcc cac gag ctg tgt ttg ttg ccc acc cct gct gtg ccc gcg 163
Glu Leu Ala His Glu Leu Cys Leu Leu Pro Thr Pro Ala Val Pro Ala
10 15 20

ctt ccc act gat tct ggc gcg cag ttt gat atc cac cag gca cta tcc 211
Leu Pro Thr Asp Ser Gly Ala Gln Phe Asp Ile His Gln Ala Leu Ser
25 30 35

gcc tcc ctt gcc acc tat gcc cgc aac ctc acc ttg ctg tcc cac acc 259
Ala Ser Leu Ala Thr Tyr Ala Arg Asn Leu Thr Leu Leu Ser His Thr
40 45 50

gcc gag aat tta gga aac cgc gcg ctg acg ggc ctc gct gaa atc gaa 307
Ala Glu Asn Leu Gly Asn Arg Ala Leu Thr Gly Leu Ala Glu Ile Glu
55 60 65

gac acc gac gac caa ctc gca cac gca ttg gag cgc ctg aca 349
Asp Thr Asp Asp Gln Leu Ala His Ala Leu Glu Arg Leu Thr
70 75 80

tgatcggtct gatcagcgcc ctt 372

<210> 1524
<211> 83
<212> PRT
<213> Corynebacterium glutamicum

<400> 1524
Leu Pro His Ala Lys Glu Leu Ala His Glu Leu Cys Leu Leu Pro Thr
1 5 10 15

Pro Ala Val Pro Ala Leu Pro Thr Asp Ser Gly Ala Gln Phe Asp Ile
20 25 30

His Gln Ala Leu Ser Ala Ser Leu Ala Thr Tyr Ala Arg Asn Leu Thr
35 40 45

Leu Leu Ser His Thr Ala Glu Asn Leu Gly Asn Arg Ala Leu Thr Gly
50 55 60

Leu Ala Glu Ile Glu Asp Thr Asp Asp Gln Leu Ala His Ala Leu Glu
65 70 75 80

Arg Leu Thr

<210> 1525
<211> 1049
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1026)
<223> RXN03172

<400> 1525

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cca gag tgg aag aaa ttc aac tcc ggc gac gca gcc cgc gtt gtc cca   48
Pro Glu Trp Lys Lys Phe Asn Ser Gly Asp Ala Ala Arg Val Val Pro
  1               5                  10                  15

gac gcc aac gca gag ctc gac atc atc ggc gca cca gca ctt ctt gcc   96
Asp Ala Asn Ala Glu Leu Asp Ile Ile Gly Ala Pro Ala Leu Leu Ala
             20                  25                  30

gat cgc ccc tcc tac gca aac gtc aaa acc ctc tcc cgc atc ttc gct   144
Asp Arg Pro Ser Tyr Ala Asn Val Lys Thr Leu Ser Arg Ile Phe Ala
         35                  40                  45

gtc atg cgc agc ctc ggc cac gtc acc gct gcc tcc cca gtc acc gtg   192
Val Met Arg Ser Leu Gly His Val Thr Ala Ala Ser Pro Val Thr Val
     50                  55                  60

ttc ttc tcc tcc cac tcc gtg ctc agc aac gtt gac cgc gga tcc gag   240
Phe Phe Ser Ser His Ser Val Leu Ser Asn Val Asp Arg Gly Ser Glu
 65                  70                  75                  80

cac tac tcc gga ccc aac ggc ctg ggc gaa tgg acc tcc gtt ggt cgc   288
His Tyr Ser Gly Pro Asn Gly Leu Gly Glu Trp Thr Ser Val Gly Arg
                 85                  90                  95

gca gta gcc acc aac tgg aac ggc gtt gtc gac gcc ctc gac gaa gcc   336
Ala Val Ala Thr Asn Trp Asn Gly Val Val Asp Ala Leu Asp Glu Ala
            100                 105                 110

atc acc gtc aag gaa gta aac agc ctc ttt acc gaa gac gcc gca acc   384
Ile Thr Val Lys Glu Val Asn Ser Leu Phe Thr Glu Asp Ala Ala Thr
        115                 120                 125

cgc att caa gaa gca caa gca gct gtt cag gca gct cgc gag gct gaa   432
Arg Ile Gln Glu Ala Gln Ala Ala Val Gln Ala Ala Arg Glu Ala Glu
    130                 135                 140

gag caa atc gcc aag gaa gaa gcc gaa aag gtc gac cct tac gac aac   480
Glu Gln Ile Ala Lys Glu Glu Ala Glu Lys Val Asp Pro Tyr Asp Asn
145                 150                 155                 160

tcc cca tgg gct gca gca ggc atc gac ccc atc aag gtc tcc atc gac   528
Ser Pro Trp Ala Ala Ala Gly Ile Asp Pro Ile Lys Val Ser Ile Asp
                165                 170                 175

gga cgc acc atc tac acc ctg cgc acc tac ctc ggc gga cag cca gta   576
Gly Arg Thr Ile Tyr Thr Leu Arg Thr Tyr Leu Gly Gly Gln Pro Val
            180                 185                 190

ttc ctc gga aaa ttc ggc gaa atc tcc acc ttc aac agc caa aaa tcc   624
Phe Leu Gly Lys Phe Gly Glu Ile Ser Thr Phe Asn Ser Gln Lys Ser
```

```
        195                 200                 205

ctc ctg cgc tgg ctc gtc gaa cac gat gac cac gac ctc gcc cgc gcc   672
Leu Leu Arg Trp Leu Val Glu His Asp Asp His Asp Leu Ala Arg Ala
    210                 215                 220

tcc acc tgg agc gac ctc atg ctc ggc atc aac gcc ggt gaa acc gaa   720
Ser Thr Trp Ser Asp Leu Met Leu Gly Ile Asn Ala Gly Glu Thr Glu
225                 230                 235                 240

ctc ctc gtc cac agc gac aac gtc tac tcc ttc aac ggc ctg gtc aaa   768
Leu Leu Val His Ser Asp Asn Val Tyr Ser Phe Asn Gly Leu Val Lys
                245                 250                 255

gac atc aac acc tcc gtc gac gcc gta gac acc caa caa atg gcc cgc   816
Asp Ile Asn Thr Ser Val Asp Ala Val Asp Thr Gln Gln Met Ala Arg
            260                 265                 270

gcc tac gaa ctc atg gca gac acc gcc gac tgg gcc gac gac gac tcc   864
Ala Tyr Glu Leu Met Ala Asp Thr Ala Asp Trp Ala Asp Asp Asp Ser
        275                 280                 285

atg aat tcc tac ttc ctg gcc aac cca cgc atg cag gac tac atc tcc   912
Met Asn Ser Tyr Phe Leu Ala Asn Pro Arg Met Gln Asp Tyr Ile Ser
    290                 295                 300

tac atg ctc ggc ggc agc gac acc tcc gga tat gtc cct cac gca cca   960
Tyr Met Leu Gly Gly Ser Asp Thr Ser Gly Tyr Val Pro His Ala Pro
305                 310                 315                 320

ttc aac gac cac tct gag agc tgg cgc gag ctg gag gag atg ctg atc  1008
Phe Asn Asp His Ser Glu Ser Trp Arg Glu Leu Glu Glu Met Leu Ile
                325                 330                 335

aag cga ttc agc aag ttc taggtcgcct atttggggtt cgt                1049
Lys Arg Phe Ser Lys Phe
            340
```

<210> 1526
<211> 342
<212> PRT
<213> Corynebacterium glutamicum

<400> 1526

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Pro Glu Trp Lys Lys Phe Asn Ser Gly Asp Ala Ala Arg Val Val Pro
  1               5                  10                  15

Asp Ala Asn Ala Glu Leu Asp Ile Ile Gly Ala Pro Ala Leu Leu Ala
             20                  25                  30

Asp Arg Pro Ser Tyr Ala Asn Val Lys Thr Leu Ser Arg Ile Phe Ala
         35                  40                  45

Val Met Arg Ser Leu Gly His Val Thr Ala Ala Ser Pro Val Thr Val
     50                  55                  60

Phe Phe Ser Ser His Ser Val Leu Ser Asn Val Asp Arg Gly Ser Glu
 65                  70                  75                  80

His Tyr Ser Gly Pro Asn Gly Leu Gly Glu Trp Thr Ser Val Gly Arg
```

```
                85                  90                  95

Ala Val Ala Thr Asn Trp Asn Gly Val Val Asp Ala Leu Asp Glu Ala
            100                 105                 110

Ile Thr Val Lys Glu Val Asn Ser Leu Phe Thr Glu Asp Ala Ala Thr
        115                 120                 125

Arg Ile Gln Glu Ala Gln Ala Ala Val Gln Ala Ala Arg Glu Ala Glu
    130                 135                 140

Glu Gln Ile Ala Lys Glu Glu Ala Glu Lys Val Asp Pro Tyr Asp Asn
145                 150                 155                 160

Ser Pro Trp Ala Ala Ala Gly Ile Asp Pro Ile Lys Val Ser Ile Asp
                165                 170                 175

Gly Arg Thr Ile Tyr Thr Leu Arg Thr Tyr Leu Gly Gly Gln Pro Val
            180                 185                 190

Phe Leu Gly Lys Phe Gly Glu Ile Ser Thr Phe Asn Ser Gln Lys Ser
        195                 200                 205

Leu Leu Arg Trp Leu Val Glu His Asp Asp His Asp Leu Ala Arg Ala
    210                 215                 220

Ser Thr Trp Ser Asp Leu Met Leu Gly Ile Asn Ala Gly Glu Thr Glu
225                 230                 235                 240

Leu Leu Val His Ser Asp Asn Val Tyr Ser Phe Asn Gly Leu Val Lys
                245                 250                 255

Asp Ile Asn Thr Ser Val Asp Ala Val Asp Thr Gln Gln Met Ala Arg
            260                 265                 270

Ala Tyr Glu Leu Met Ala Asp Thr Ala Asp Trp Ala Asp Asp Asp Ser
        275                 280                 285

Met Asn Ser Tyr Phe Leu Ala Asn Pro Arg Met Gln Asp Tyr Ile Ser
    290                 295                 300

Tyr Met Leu Gly Gly Ser Asp Thr Ser Gly Tyr Val Pro His Ala Pro
305                 310                 315                 320

Phe Asn Asp His Ser Glu Ser Trp Arg Glu Leu Glu Glu Met Leu Ile
                325                 330                 335

Lys Arg Phe Ser Lys Phe
            340
```

<210> 1527
<211> 1049
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1026)
<223> FRXA02858

<400> 1527

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cca gag tgg aag aaa ttc aac tcc ggc gac gca gcc cgc gtt gtc cca   48
Pro Glu Trp Lys Lys Phe Asn Ser Gly Asp Ala Ala Arg Val Val Pro
  1               5                  10                  15

gac gcc aac gca gag ctc gac atc atc ggc gca cca gca ctt ctt gcc   96
Asp Ala Asn Ala Glu Leu Asp Ile Ile Gly Ala Pro Ala Leu Leu Ala
             20                  25                  30

gat cgc ccc tcc tac gca aac gtc aaa acc ctc tcc cgc atc ttc gct   144
Asp Arg Pro Ser Tyr Ala Asn Val Lys Thr Leu Ser Arg Ile Phe Ala
         35                  40                  45

gtc atg cgc agc ctc ggc cac gtc acc gct gcc tcc cca gtc acc gtg   192
Val Met Arg Ser Leu Gly His Val Thr Ala Ala Ser Pro Val Thr Val
     50                  55                  60

ttc ttc tcc tcc cac tcc gtg ctc agc aac gtt gac cgc gga tcc gag   240
Phe Phe Ser Ser His Ser Val Leu Ser Asn Val Asp Arg Gly Ser Glu
 65                  70                  75                  80

cac tac tcc gga ccc aac ggc ctg ggc gaa tgg acc tcc gtt ggt cgc   288
His Tyr Ser Gly Pro Asn Gly Leu Gly Glu Trp Thr Ser Val Gly Arg
                 85                  90                  95

gca gta gcc acc aac tgg aac ggc gtt gtc gac gcc ctc gac gaa gcc   336
Ala Val Ala Thr Asn Trp Asn Gly Val Val Asp Ala Leu Asp Glu Ala
            100                 105                 110

atc acc gtc aag gaa gta aac agc ctc ttt acc gaa gac gcc gca acc   384
Ile Thr Val Lys Glu Val Asn Ser Leu Phe Thr Glu Asp Ala Ala Thr
        115                 120                 125

cgc att caa gaa gca caa gca gct gtt cag gca gct cgc gag gct gaa   432
Arg Ile Gln Glu Ala Gln Ala Ala Val Gln Ala Ala Arg Glu Ala Glu
    130                 135                 140

gag caa atc gcc aag gaa gaa gcc gaa aag gtc gac cct tac gac aac   480
Glu Gln Ile Ala Lys Glu Glu Ala Glu Lys Val Asp Pro Tyr Asp Asn
145                 150                 155                 160

tcc cca tgg gct gca gca ggc atc gac ccc atc aag gtc tcc atc gac   528
Ser Pro Trp Ala Ala Ala Gly Ile Asp Pro Ile Lys Val Ser Ile Asp
                165                 170                 175

gga cgc acc atc tac acc ctg cgc acc tac ctc ggc gga cag cca gta   576
Gly Arg Thr Ile Tyr Thr Leu Arg Thr Tyr Leu Gly Gly Gln Pro Val
            180                 185                 190

ttc ctc gga aaa ttc ggc gaa atc ttc acc ttc aac agc caa aaa tcc   624
Phe Leu Gly Lys Phe Gly Glu Ile Phe Thr Phe Asn Ser Gln Lys Ser
        195                 200                 205

ctc ctg cgc tgg ctc gtc gaa cac gat gac cac gac ctc gcc cgc gcc   672
Leu Leu Arg Trp Leu Val Glu His Asp Asp His Asp Leu Ala Arg Ala
    210                 215                 220

tcc acc tgg agc gac ctc atg ctc ggc atc aac gcc ggt gaa acc gaa   720
Ser Thr Trp Ser Asp Leu Met Leu Gly Ile Asn Ala Gly Glu Thr Glu
225                 230                 235                 240
```

```
ctc ctc gtc cac agc gac aac gtc tac tcc ttc aac ggc ctg gtc aaa   768
Leu Leu Val His Ser Asp Asn Val Tyr Ser Phe Asn Gly Leu Val Lys
                245                 250                 255

gac atc aac acc tcc gtc gac gcc gta gac acc caa caa atg gcc cgc   816
Asp Ile Asn Thr Ser Val Asp Ala Val Asp Thr Gln Gln Met Ala Arg
            260                 265                 270

gcc tac gaa ctc atg gca gac acc gcc gac tgg gcc gac gac gac tcc   864
Ala Tyr Glu Leu Met Ala Asp Thr Ala Asp Trp Ala Asp Asp Asp Ser
        275                 280                 285

atg aat tcc tac ttc ctg gcc aac cca cgc atg cag gac tac atc tcc   912
Met Asn Ser Tyr Phe Leu Ala Asn Pro Arg Met Gln Asp Tyr Ile Ser
    290                 295                 300

tac atg ctc ggc ggc agc gac acc tcc gga tat gtc cct cac gca cca   960
Tyr Met Leu Gly Gly Ser Asp Thr Ser Gly Tyr Val Pro His Ala Pro
305                 310                 315                 320

ttc aac gac cac tct gag agc tgg cgc gag ctg gag gag atg ctg atc  1008
Phe Asn Asp His Ser Glu Ser Trp Arg Glu Leu Glu Glu Met Leu Ile
                325                 330                 335

aag cga ttc agc aag ttc taggtcgcct atttggggtt cgt                1049
Lys Arg Phe Ser Lys Phe
            340
```

<210> 1528
<211> 342
<212> PRT
<213> Corynebacterium glutamicum

<400> 1528

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Pro Glu Trp Lys Lys Phe Asn Ser Gly Asp Ala Ala Arg Val Val Pro
  1               5                  10                  15

Asp Ala Asn Ala Glu Leu Asp Ile Ile Gly Ala Pro Ala Leu Leu Ala
             20                  25                  30

Asp Arg Pro Ser Tyr Ala Asn Val Lys Thr Leu Ser Arg Ile Phe Ala
         35                  40                  45

Val Met Arg Ser Leu Gly His Val Thr Ala Ala Ser Pro Val Thr Val
     50                  55                  60

Phe Phe Ser Ser His Ser Val Leu Ser Asn Val Asp Arg Gly Ser Glu
 65                  70                  75                  80

His Tyr Ser Gly Pro Asn Gly Leu Gly Glu Trp Thr Ser Val Gly Arg
                85                  90                  95

Ala Val Ala Thr Asn Trp Asn Gly Val Val Asp Ala Leu Asp Glu Ala
            100                 105                 110

Ile Thr Val Lys Glu Val Asn Ser Leu Phe Thr Glu Asp Ala Ala Thr
        115                 120                 125

Arg Ile Gln Glu Ala Gln Ala Ala Val Gln Ala Ala Arg Glu Ala Glu
    130                 135                 140
```

```
Glu Gln Ile Ala Lys Glu Glu Ala Glu Lys Val Asp Pro Tyr Asp Asn
145                 150                 155                 160

Ser Pro Trp Ala Ala Ala Gly Ile Asp Pro Ile Lys Val Ser Ile Asp
                165                 170                 175

Gly Arg Thr Ile Tyr Thr Leu Arg Thr Tyr Leu Gly Gly Gln Pro Val
            180                 185                 190

Phe Leu Gly Lys Phe Gly Glu Ile Phe Thr Phe Asn Ser Gln Lys Ser
        195                 200                 205

Leu Leu Arg Trp Leu Val Glu His Asp Asp His Asp Leu Ala Arg Ala
    210                 215                 220

Ser Thr Trp Ser Asp Leu Met Leu Gly Ile Asn Ala Gly Glu Thr Glu
225                 230                 235                 240

Leu Leu Val His Ser Asp Asn Val Tyr Ser Phe Asn Gly Leu Val Lys
                245                 250                 255

Asp Ile Asn Thr Ser Val Asp Ala Val Asp Thr Gln Gln Met Ala Arg
            260                 265                 270

Ala Tyr Glu Leu Met Ala Asp Thr Ala Asp Trp Ala Asp Asp Asp Ser
        275                 280                 285

Met Asn Ser Tyr Phe Leu Ala Asn Pro Arg Met Gln Asp Tyr Ile Ser
    290                 295                 300

Tyr Met Leu Gly Gly Ser Asp Thr Ser Gly Tyr Val Pro His Ala Pro
305                 310                 315                 320

Phe Asn Asp His Ser Glu Ser Trp Arg Glu Leu Glu Glu Met Leu Ile
                325                 330                 335

Lys Arg Phe Ser Lys Phe
            340
```

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<210> 1529
<211> 1121
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1098)
<223> RXN03173

<400> 1529

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ctc aac cgc gac acc cat cac ctg tgg gtc gtc tta acc acc gac tcc   48
Leu Asn Arg Asp Thr His His Leu Trp Val Val Leu Thr Thr Asp Ser
  1               5                  10                  15

gac gac ttc gac gca gac tcc ttt acc acc gaa gtc atc cgg atc acc   96
Asp Asp Phe Asp Ala Asp Ser Phe Thr Thr Glu Val Ile Arg Ile Thr
             20                  25                  30

ggc tac tcc cgc cac gaa gtc aac aac ggc ctt aac gcc atg gcc gcg   144
```

```
Gly Tyr Ser Arg His Glu Val Asn Asn Gly Leu Asn Ala Met Ala Ala
         35                  40                  45

atg acc aac ctc cca cac ctg cgc gcc atc caa gaa cgc tac tac ttc   192
Met Thr Asn Leu Pro His Leu Arg Ala Ile Gln Glu Arg Tyr Tyr Phe
     50                  55                  60

ctg agc atc cgc tac ctc gcc tcc atc atg atc gcc gtg gcc aaa gca   240
Leu Ser Ile Arg Tyr Leu Ala Ser Ile Met Ile Ala Val Ala Lys Ala
 65                  70                  75                  80

gac ccc acc ctg tgg gaa gaa ctc gac ctg cgc atc acc gac gcc tta   288
Asp Pro Thr Leu Trp Glu Glu Leu Asp Leu Arg Ile Thr Asp Ala Leu
                 85                  90                  95

aca cca gtc acc gca ggg gaa gtc atg atc caa tcc tcc acc ctg tcc   336
Thr Pro Val Thr Ala Gly Glu Val Met Ile Gln Ser Ser Thr Leu Ser
            100                 105                 110

aaa cgc atc gcc gcc tgg atc aaa gaa ctc gac ccc gaa ccc aca cca   384
Lys Arg Ile Ala Ala Trp Ile Lys Glu Leu Asp Pro Glu Pro Thr Pro
        115                 120                 125

gag ccc aca ccg aaa gag gac tat gtt cac gtc cac acc act gat gag   432
Glu Pro Thr Pro Lys Glu Asp Tyr Val His Val His Thr Thr Asp Glu
    130                 135                 140

gcg acc tat gtc cgc atc aaa atc agc ggc ccc aac cgc ctg atc ctc   480
Ala Thr Tyr Val Arg Ile Lys Ile Ser Gly Pro Asn Arg Leu Ile Leu
145                 150                 155                 160

aat gac atc atc acc caa ctc aaa gac aca gac acc gag gac agc ctg   528
Asn Asp Ile Ile Thr Gln Leu Lys Asp Thr Asp Thr Glu Asp Ser Leu
                165                 170                 175

cct gaa gcg ctc atg gcg ttc ctg aca gag aaa atc cag tta aag atc   576
Pro Glu Ala Leu Met Ala Phe Leu Thr Glu Lys Ile Gln Leu Lys Ile
            180                 185                 190

acc aaa tac ctc ttc acc cca cat aag cac cct gag cag gtg tgg tca   624
Thr Lys Tyr Leu Phe Thr Pro His Lys His Pro Glu Gln Val Trp Ser
        195                 200                 205

ccg gac tac ggt gac att gat ccc gaa gcc tat gcc aac gcc acc ctc   672
Pro Asp Tyr Gly Asp Ile Asp Pro Glu Ala Tyr Ala Asn Ala Thr Leu
    210                 215                 220

gtg tgc gcc aag gac tta gat gag ctc gct gga gcc acg gag aag agc   720
Val Cys Ala Lys Asp Leu Asp Glu Leu Ala Gly Ala Thr Glu Lys Ser
225                 230                 235                 240

tac acc ccg agt gag aag atg aaa gcc ctg atc aga gct cgg gat ggg   768
Tyr Thr Pro Ser Glu Lys Met Lys Ala Leu Ile Arg Ala Arg Asp Gly
                245                 250                 255

cat tgc cgc ttc cca ggg tgt tgc gtt ccg gcg agt aag tgc cag gtc   816
His Cys Arg Phe Pro Gly Cys Cys Val Pro Ala Ser Lys Cys Gln Val
            260                 265                 270

gat cac att atc ccg tgg gcg gag ggc ggc ccg aca gcg gcg tgg aac   864
Asp His Ile Ile Pro Trp Ala Glu Gly Gly Pro Thr Ala Ala Trp Asn
```

```
        275                 280                 285

ctg cag ttg ttg tgc cag cgg cat cac aat atg aaa acc gat ggt cgc   912
Leu Gln Leu Leu Cys Gln Arg His His Asn Met Lys Thr Asp Gly Arg
    290                 295                 300

ttt act gct gat gct aat gga ttg gcg gag att aga tgg att ggg ccg   960
Phe Thr Ala Asp Ala Asn Gly Leu Ala Glu Ile Arg Trp Ile Gly Pro
305                 310                 315                 320

atg gat gta cca gcg gtg acc agg ccg acg ggt ccg ttg gtg aaa gcg   1008
Met Asp Val Pro Ala Val Thr Arg Pro Thr Gly Pro Leu Val Lys Ala
                325                 330                 335

atg ccg cgg ggg att tgg ggt cag gtg ttg agg gat cgg atc cag gct   1056
Met Pro Arg Gly Ile Trp Gly Gln Val Leu Arg Asp Arg Ile Gln Ala
            340                 345                 350

agg ttt gag cgg atc cgc gac cgc gcc ctc aac aaa gaa gac           1098
Arg Phe Glu Arg Ile Arg Asp Arg Ala Leu Asn Lys Glu Asp
        355                 360                 365

tagaagcgca caggtttttg cat                                        1121


<210> 1530
<211> 366
<212> PRT
<213> Corynebacterium glutamicum

<400> 1530
Leu Asn Arg Asp Thr His His Leu Trp Val Val Leu Thr Thr Asp Ser
  1               5                  10                  15

Asp Asp Phe Asp Ala Asp Ser Phe Thr Thr Glu Val Ile Arg Ile Thr
             20                  25                  30

Gly Tyr Ser Arg His Glu Val Asn Asn Gly Leu Asn Ala Met Ala Ala
         35                  40                  45

Met Thr Asn Leu Pro His Leu Arg Ala Ile Gln Glu Arg Tyr Tyr Phe
     50                  55                  60

Leu Ser Ile Arg Tyr Leu Ala Ser Ile Met Ile Ala Val Ala Lys Ala
 65                  70                  75                  80

Asp Pro Thr Leu Trp Glu Glu Leu Asp Leu Arg Ile Thr Asp Ala Leu
                 85                  90                  95

Thr Pro Val Thr Ala Gly Glu Val Met Ile Gln Ser Ser Thr Leu Ser
            100                 105                 110

Lys Arg Ile Ala Ala Trp Ile Lys Glu Leu Asp Pro Glu Pro Thr Pro
        115                 120                 125

Glu Pro Thr Pro Lys Glu Asp Tyr Val His Val His Thr Thr Asp Glu
    130                 135                 140

Ala Thr Tyr Val Arg Ile Lys Ile Ser Gly Pro Asn Arg Leu Ile Leu
145                 150                 155                 160
```

```
Asn Asp Ile Ile Thr Gln Leu Lys Asp Thr Asp Thr Glu Asp Ser Leu
                165                 170                 175

Pro Glu Ala Leu Met Ala Phe Leu Thr Glu Lys Ile Gln Leu Lys Ile
            180                 185                 190

Thr Lys Tyr Leu Phe Thr Pro His Lys His Pro Glu Gln Val Trp Ser
        195                 200                 205

Pro Asp Tyr Gly Asp Ile Asp Pro Glu Ala Tyr Ala Asn Ala Thr Leu
    210                 215                 220

Val Cys Ala Lys Asp Leu Asp Glu Leu Ala Gly Ala Thr Glu Lys Ser
225                 230                 235                 240

Tyr Thr Pro Ser Glu Lys Met Lys Ala Leu Ile Arg Ala Arg Asp Gly
                245                 250                 255

His Cys Arg Phe Pro Gly Cys Cys Val Pro Ala Ser Lys Cys Gln Val
            260                 265                 270

Asp His Ile Ile Pro Trp Ala Glu Gly Gly Pro Thr Ala Ala Trp Asn
        275                 280                 285

Leu Gln Leu Leu Cys Gln Arg His His Asn Met Lys Thr Asp Gly Arg
    290                 295                 300

Phe Thr Ala Asp Ala Asn Gly Leu Ala Glu Ile Arg Trp Ile Gly Pro
305                 310                 315                 320

Met Asp Val Pro Ala Val Thr Arg Pro Thr Gly Pro Leu Val Lys Ala
                325                 330                 335

Met Pro Arg Gly Ile Trp Gly Gln Val Leu Arg Asp Arg Ile Gln Ala
            340                 345                 350

Arg Phe Glu Arg Ile Arg Asp Arg Ala Leu Asn Lys Glu Asp
        355                 360                 365
```

<210> 1531
<211> 503
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(480)
<223> FRXA02874

<400> 1531

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acc gaa ctc aac cgc gac acc cat cac ctg tgg gtc gtc tta acc acc   48
Thr Glu Leu Asn Arg Asp Thr His His Leu Trp Val Val Leu Thr Thr
  1               5                  10                  15

gac tcc gac gac ttc gac gca gac tcc ttt acc acc gaa gtc atc cgg   96
Asp Ser Asp Asp Phe Asp Ala Asp Ser Phe Thr Thr Glu Val Ile Arg
             20                  25                  30

atc acc ggc tac tcc cgc cac gaa gtc aac aac ggc ctt aac gcc atg   144
Ile Thr Gly Tyr Ser Arg His Glu Val Asn Asn Gly Leu Asn Ala Met
```

```
         35                  40                  45

gcc gcg atg acc aac ctc cca cac ctg cgc gcc atc caa gaa cgc tac   192
Ala Ala Met Thr Asn Leu Pro His Leu Arg Ala Ile Gln Glu Arg Tyr
     50                  55                  60

tac ttc ctg agc atc cgc tac ctc gcc tcc atc atg atc gcc gtg gcc   240
Tyr Phe Leu Ser Ile Arg Tyr Leu Ala Ser Ile Met Ile Ala Val Ala
 65                  70                  75                  80

aaa gca gac ccc acc ctg tgg gaa gaa ctc gac ctg cgc atc acc gac   288
Lys Ala Asp Pro Thr Leu Trp Glu Glu Leu Asp Leu Arg Ile Thr Asp
                 85                  90                  95

gcc tta aca cca gtc acc gca ggg gaa gtc atg atc caa tcc tcc acc   336
Ala Leu Thr Pro Val Thr Ala Gly Glu Val Met Ile Gln Ser Ser Thr
            100                 105                 110

ctg tcc aaa cng cat cgc cng cct gga tca aag aac tcg acc ccg aac   384
Leu Ser Lys Xaa His Arg Xaa Pro Gly Ser Lys Asn Ser Thr Pro Asn
        115                 120                 125

cca cac cag agc cca cac cga aag agg act atg ttc acg tcc aca cca   432
Pro His Gln Ser Pro His Arg Lys Arg Thr Met Phe Thr Ser Thr Pro
    130                 135                 140

ctg atg agg cga cct atg tcc gca tca aaa tca gcg gcc cca acc gcc   480
Leu Met Arg Arg Pro Met Ser Ala Ser Lys Ser Ala Ala Pro Thr Ala
145                 150                 155                 160

tgatcctcaa tgacatcatc acc                                        503


<210> 1532
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 1532
Thr Glu Leu Asn Arg Asp Thr His His Leu Trp Val Val Leu Thr Thr
  1               5                  10                  15

Asp Ser Asp Asp Phe Asp Ala Asp Ser Phe Thr Thr Glu Val Ile Arg
             20                  25                  30

Ile Thr Gly Tyr Ser Arg His Glu Val Asn Asn Gly Leu Asn Ala Met
         35                  40                  45

Ala Ala Met Thr Asn Leu Pro His Leu Arg Ala Ile Gln Glu Arg Tyr
     50                  55                  60

Tyr Phe Leu Ser Ile Arg Tyr Leu Ala Ser Ile Met Ile Ala Val Ala
 65                  70                  75                  80

Lys Ala Asp Pro Thr Leu Trp Glu Glu Leu Asp Leu Arg Ile Thr Asp
                 85                  90                  95

Ala Leu Thr Pro Val Thr Ala Gly Glu Val Met Ile Gln Ser Ser Thr
            100                 105                 110

Leu Ser Lys Xaa His Arg Xaa Pro Gly Ser Lys Asn Ser Thr Pro Asn
```

```
        115                 120                 125

Pro His Gln Ser Pro His Arg Lys Arg Thr Met Phe Thr Ser Thr Pro
    130                 135                 140

Leu Met Arg Arg Pro Met Ser Ala Ser Lys Ser Ala Ala Pro Thr Ala
145                 150                 155                 160
```

<210> 1533
<211> 556
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> RXN03174

<400> 1533

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gcgatgctcg aacgcgcaga acgctcctgg gtagacaaag ccgctgcata cgatttgcgc 60

tggtcagatc actcaccact gaacgtgatc tactcctaaa atg ctg ctg aca att   115
                                                Met Leu Leu Thr Ile
                                                  1               5

cta tgg gcc atc ggc atc acc gcc gaa ggc atg aca ggc gcg ctg gcc   163
Leu Trp Ala Ile Gly Ile Thr Ala Glu Gly Met Thr Gly Ala Leu Ala
                10                  15                  20

gca ggc cga caa aaa atg gat ctc ttc gga gta tcc gtc atc gca tgc   211
Ala Gly Arg Gln Lys Met Asp Leu Phe Gly Val Ser Val Ile Ala Cys
            25                  30                  35

gtt acc gcg atc ggc ggc gga tcc atc cgc gac atg ctg ctg gga cat   259
Val Thr Ala Ile Gly Gly Gly Ser Ile Arg Asp Met Leu Leu Gly His
        40                  45                  50

tac ccg ctg gtg tgg gtg gaa aag cca ctg tat cta ctg ctg atc att   307
Tyr Pro Leu Val Trp Val Glu Lys Pro Leu Tyr Leu Leu Leu Ile Ile
    55                  60                  65

ggc gca gcc att ttg aca gtg tcc att tcc ttc ctg atg gag cac ttc   355
Gly Ala Ala Ile Leu Thr Val Ser Ile Ser Phe Leu Met Glu His Phe
70                  75                  80                  85

cgt gtg ttg ttc ctc gtg ctc gac gcc gtg ggt ctt tct gca ttc gct   403
Arg Val Leu Phe Leu Val Leu Asp Ala Val Gly Leu Ser Ala Phe Ala
                90                  95                  100

gtg atc ggc aca caa atc gca ctg gaa atg ggc tac gga ttc atc atc   451
Val Ile Gly Thr Gln Ile Ala Leu Glu Met Gly Tyr Gly Phe Ile Ile
            105                 110                 115

gca gta gtg gca tca gtg ctc aca ggt gta ttc ggc ggc gtc atg cgt   499
Ala Val Val Ala Ser Val Leu Thr Gly Val Phe Gly Gly Val Met Arg
        120                 125                 130
```

```
gac ctt ttg tgt gac cgc atc cca ctg gta ttt caa aaa gag ctc tac   547
Asp Leu Leu Cys Asp Arg Ile Pro Leu Val Phe Gln Lys Glu Leu Tyr
    135                 140                 145

gca tca atc                                                       556
Ala Ser Ile
150
```

<210> 1534
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 1534

```
Met Leu Leu Thr Ile Leu Trp Ala Ile Gly Ile Thr Ala Glu Gly Met
  1               5                  10                  15

Thr Gly Ala Leu Ala Ala Gly Arg Gln Lys Met Asp Leu Phe Gly Val
             20                  25                  30

Ser Val Ile Ala Cys Val Thr Ala Ile Gly Gly Gly Ser Ile Arg Asp
         35                  40                  45

Met Leu Leu Gly His Tyr Pro Leu Val Trp Val Glu Lys Pro Leu Tyr
     50                  55                  60

Leu Leu Leu Ile Ile Gly Ala Ala Ile Leu Thr Val Ser Ile Ser Phe
 65                  70                  75                  80

Leu Met Glu His Phe Arg Val Leu Phe Leu Val Leu Asp Ala Val Gly
                 85                  90                  95

Leu Ser Ala Phe Ala Val Ile Gly Thr Gln Ile Ala Leu Glu Met Gly
            100                 105                 110

Tyr Gly Phe Ile Ile Ala Val Val Ala Ser Val Leu Thr Gly Val Phe
        115                 120                 125

Gly Gly Val Met Arg Asp Leu Leu Cys Asp Arg Ile Pro Leu Val Phe
    130                 135                 140

Gln Lys Glu Leu Tyr Ala Ser Ile
145                 150
```

<210> 1535
<211> 562
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(562)
<223> FRXA02884

<400> 1535

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gcgatgctcg aacgcgcaga acgctcctgg gtagacaaag ccgctgcata cgatttgcgc 60

tggtcagatc actcaccact gaacgtgatc tactcctaaa atg ctg ctg aca att   115
                                                Met Leu Leu Thr Ile
```

```
                                                    1               5

cta tgg gcc atc ggc atc acc gcc gaa ggc atg aca ggc gcg ctg gcc   163
Leu Trp Ala Ile Gly Ile Thr Ala Glu Gly Met Thr Gly Ala Leu Ala
                10                  15                  20

gca ggc cga caa aaa atg gat ctc ttc gga gta tcc gtc atc gca tgc   211
Ala Gly Arg Gln Lys Met Asp Leu Phe Gly Val Ser Val Ile Ala Cys
            25                  30                  35

gtt acc gcg atc ggc ggc gga tcc atc cgc gac atg ctg ctg gga cat   259
Val Thr Ala Ile Gly Gly Gly Ser Ile Arg Asp Met Leu Leu Gly His
        40                  45                  50

tac ccg ctg gtg tgg gtg gaa aag cca ctg tat cta ctg ctg atc att   307
Tyr Pro Leu Val Trp Val Glu Lys Pro Leu Tyr Leu Leu Leu Ile Ile
    55                  60                  65

ggc gca gcc att ttg aca gtg tcc att tcc ttc ctg atg gag cac ttc   355
Gly Ala Ala Ile Leu Thr Val Ser Ile Ser Phe Leu Met Glu His Phe
70                  75                  80                  85

cgt gtg ttg ttc ctc gtg ctc gac gcc gtg ggt ctt tct gca ttc gct   403
Arg Val Leu Phe Leu Val Leu Asp Ala Val Gly Leu Ser Ala Phe Ala
                90                  95                  100

gtg atc ggc aca caa atc gca ctg gaa atg ggc tac gga ttc atc atc   451
Val Ile Gly Thr Gln Ile Ala Leu Glu Met Gly Tyr Gly Phe Ile Ile
            105                 110                 115

gca gta gtg gca tca gtg ctc aca ggt gta ttc ggc ggc gtc atg cgt   499
Ala Val Val Ala Ser Val Leu Thr Gly Val Phe Gly Gly Val Met Arg
        120                 125                 130

gac ctt ttg tgt gac cgc atc cca ctg gta ttt caa aaa gag ctc tac   547
Asp Leu Leu Cys Asp Arg Ile Pro Leu Val Phe Gln Lys Glu Leu Tyr
    135                 140                 145

gca tca atc gca ttc                                               562
Ala Ser Ile Ala Phe
150
```

<210> 1536
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 1536

```
Met Leu Leu Thr Ile Leu Trp Ala Ile Gly Ile Thr Ala Glu Gly Met
  1               5                  10                  15

Thr Gly Ala Leu Ala Ala Gly Arg Gln Lys Met Asp Leu Phe Gly Val
            20                  25                  30

Ser Val Ile Ala Cys Val Thr Ala Ile Gly Gly Gly Ser Ile Arg Asp
        35                  40                  45

Met Leu Leu Gly His Tyr Pro Leu Val Trp Val Glu Lys Pro Leu Tyr
    50                  55                  60
```

```
Leu Leu Leu Ile Ile Gly Ala Ala Ile Leu Thr Val Ser Ile Ser Phe
 65                  70                  75                  80

Leu Met Glu His Phe Arg Val Leu Phe Leu Val Leu Asp Ala Val Gly
                 85                  90                  95

Leu Ser Ala Phe Ala Val Ile Gly Thr Gln Ile Ala Leu Glu Met Gly
            100                 105                 110

Tyr Gly Phe Ile Ile Ala Val Val Ala Ser Val Leu Thr Gly Val Phe
        115                 120                 125

Gly Gly Val Met Arg Asp Leu Leu Cys Asp Arg Ile Pro Leu Val Phe
    130                 135                 140

Gln Lys Glu Leu Tyr Ala Ser Ile Ala Phe
145                 150
```

<210> 1537
<211> 781
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (93)..(758)
<223> RXN03177

<400> 1537

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ctgcccgatt tatgttttcc gacggcacca tctgcaaaga acgagtgtga ccggtagctt 60

tatgggctga acaattctaa ggagaattat ccgtg aaa aag aag ctt atg ttg    113
                                  Val Lys Lys Lys Leu Met Leu
                                    1               5

cct ttg att gtt gca gct ttg ggg tta agt gcc tgc agc tcc gaa cct   161
Pro Leu Ile Val Ala Ala Leu Gly Leu Ser Ala Cys Ser Ser Glu Pro
         10                  15                  20

gca gca gcc cca ctc gaa gca gag cca tta cat aac ctg ctc att gat   209
Ala Ala Ala Pro Leu Glu Ala Glu Pro Leu His Asn Leu Leu Ile Asp
     25                  30                  35

ggt tca gag tcc ggc ttg gac aat gcc act gaa gga aac gac acc tca   257
Gly Ser Glu Ser Gly Leu Asp Asn Ala Thr Glu Gly Asn Asp Thr Ser
 40                  45                  50                  55

tta agt ggc caa ccc atc aat ctt aca gtg gtc aac ggt gcc tta gat   305
Leu Ser Gly Gln Pro Ile Asn Leu Thr Val Val Asn Gly Ala Leu Asp
                 60                  65                  70

atc gat ggc tcc tgc gga aaa gcc ctc caa gct gta gag gac gtc aat   353
Ile Asp Gly Ser Cys Gly Lys Ala Leu Gln Ala Val Glu Asp Val Asn
            75                  80                  85

ctg gac agc gta gct agc gca tcc agg gca ctg gca tcc ggc gac aaa   401
Leu Asp Ser Val Ala Ser Ala Ser Arg Ala Leu Ala Ser Gly Asp Lys
         90                  95                  100

caa gta ggc atc gcc atg tac tca acc gcc gaa gac aac gac atc tca   449
```

```
Gln Val Gly Ile Ala Met Tyr Ser Thr Ala Glu Asp Asn Asp Ile Ser
    105                 110                 115

cca atg gac ctc tac gca gac atc gcg aat gct tgc gaa gac ccc gtc   497
Pro Met Asp Leu Tyr Ala Asp Ile Ala Asn Ala Cys Glu Asp Pro Val
120                 125                 130                 135

gtc gat tct tcc gac acc acc tac acc ttc ggc aaa ctc gat gat gct   545
Val Asp Ser Ser Asp Thr Thr Tyr Thr Phe Gly Lys Leu Asp Asp Ala
                140                 145                 150

ccc gac ggc gcc gtt gga ttc acc ctc gac att gaa gtc acc cct gac   593
Pro Asp Gly Ala Val Gly Phe Thr Leu Asp Ile Glu Val Thr Pro Asp
            155                 160                 165

aat caa ggc tcc acc gtg atg atg atc caa gaa tta gga aac cac cac   641
Asn Gln Gly Ser Thr Val Met Met Ile Gln Glu Leu Gly Asn His His
        170                 175                 180

atc atc gtc gca gga ctt gaa acc acc cca gaa gaa acc gcc act gtc   689
Ile Ile Val Ala Gly Leu Glu Thr Thr Pro Glu Glu Thr Ala Thr Val
    185                 190                 195

ttc gaa gca caa cgc acc aaa ctc gaa gaa ggc ttg cag ctt aaa cag   737
Phe Glu Ala Gln Arg Thr Lys Leu Glu Glu Gly Leu Gln Leu Lys Gln
200                 205                 210                 215

aat tgg cag ctt ggg tgg gtt taaatgcgcc caacctaaga aaa             781
Asn Trp Gln Leu Gly Trp Val
                220
```

<210> 1538
<211> 222
<212> PRT
<213> Corynebacterium glutamicum

<400> 1538

```
Val Lys Lys Lys Leu Met Leu Pro Leu Ile Val Ala Ala Leu Gly Leu
  1               5                  10                  15

Ser Ala Cys Ser Ser Glu Pro Ala Ala Ala Pro Leu Glu Ala Glu Pro
             20                  25                  30

Leu His Asn Leu Leu Ile Asp Gly Ser Glu Ser Gly Leu Asp Asn Ala
         35                  40                  45

Thr Glu Gly Asn Asp Thr Ser Leu Ser Gly Gln Pro Ile Asn Leu Thr
     50                  55                  60

Val Val Asn Gly Ala Leu Asp Ile Asp Gly Ser Cys Gly Lys Ala Leu
 65                  70                  75                  80

Gln Ala Val Glu Asp Val Asn Leu Asp Ser Val Ala Ser Ala Ser Arg
                 85                  90                  95

Ala Leu Ala Ser Gly Asp Lys Gln Val Gly Ile Ala Met Tyr Ser Thr
            100                 105                 110

Ala Glu Asp Asn Asp Ile Ser Pro Met Asp Leu Tyr Ala Asp Ile Ala
        115                 120                 125
```

```
Asn Ala Cys Glu Asp Pro Val Val Asp Ser Ser Asp Thr Thr Tyr Thr
    130                 135                 140

Phe Gly Lys Leu Asp Asp Ala Pro Asp Gly Ala Val Gly Phe Thr Leu
145                 150                 155                 160

Asp Ile Glu Val Thr Pro Asp Asn Gln Gly Ser Thr Val Met Met Ile
                165                 170                 175

Gln Glu Leu Gly Asn His His Ile Ile Val Ala Gly Leu Glu Thr Thr
            180                 185                 190

Pro Glu Glu Thr Ala Thr Val Phe Glu Ala Gln Arg Thr Lys Leu Glu
        195                 200                 205

Glu Gly Leu Gln Leu Lys Gln Asn Trp Gln Leu Gly Trp Val
    210                 215                 220


<210> 1539
<211> 782
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (94)..(759)
<223> FRXA02881

<400> 1539
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ttatgggctg aacaattcta aggagaatta tccgtg aaa aag aag ctt atg ttg   114
                                    Val Lys Lys Lys Leu Met Leu
                                      1               5

cct ttg att gtt gca gct ttg ggg tta agt gcc tgc agc tcc gaa cct   162
Pro Leu Ile Val Ala Ala Leu Gly Leu Ser Ala Cys Ser Ser Glu Pro
         10                  15                  20

gca gca gcc cca ctc gaa gca gag cca tta cat aac ctg ctc att gat   210
Ala Ala Ala Pro Leu Glu Ala Glu Pro Leu His Asn Leu Leu Ile Asp
     25                  30                  35

ggt tca gag tcc ggc ttg gac aat gcc act gaa gga aac gac acc tca   258
Gly Ser Glu Ser Gly Leu Asp Asn Ala Thr Glu Gly Asn Asp Thr Ser
 40                  45                  50                  55

tta agt ggc caa ccc atc aat ctt aca gtg gtc aac ggt gcc tta gat   306
Leu Ser Gly Gln Pro Ile Asn Leu Thr Val Val Asn Gly Ala Leu Asp
                 60                  65                  70

atc gat ggc tcc tgc gga aaa gcc ctc caa gct gta gag gac gtc aat   354
Ile Asp Gly Ser Cys Gly Lys Ala Leu Gln Ala Val Glu Asp Val Asn
             75                  80                  85

ctg gac agc gta gct agc gca tcc agg gca ctg gca tcc ggc gac aaa   402
Leu Asp Ser Val Ala Ser Ala Ser Arg Ala Leu Ala Ser Gly Asp Lys
         90                  95                  100
```

```
caa gta ggc atc gcc atg tac tca acc gcc gaa gac aac gac atc tca   450
Gln Val Gly Ile Ala Met Tyr Ser Thr Ala Glu Asp Asn Asp Ile Ser
    105                 110                 115

cca atg gac ctc tac gca gac atc gcg aat gct tgc gaa gac ccc gtc   498
Pro Met Asp Leu Tyr Ala Asp Ile Ala Asn Ala Cys Glu Asp Pro Val
120                 125                 130                 135

gtc gat tct tcc gac acc acc tac acc ttc ggc aaa ctc gat gat gct   546
Val Asp Ser Ser Asp Thr Thr Tyr Thr Phe Gly Lys Leu Asp Asp Ala
                140                 145                 150

ccc gac ggc gcc gtt gga ttc acc ctc gac att gaa gtc acc cct gac   594
Pro Asp Gly Ala Val Gly Phe Thr Leu Asp Ile Glu Val Thr Pro Asp
            155                 160                 165

aat caa ggc tcc acc gtg atg atg atc caa gaa tta gga aac cac cac   642
Asn Gln Gly Ser Thr Val Met Met Ile Gln Glu Leu Gly Asn His His
        170                 175                 180

atc atc gtc gca gga ctt gaa acc acc cca gaa gaa acc gcc act gtc   690
Ile Ile Val Ala Gly Leu Glu Thr Thr Pro Glu Glu Thr Ala Thr Val
    185                 190                 195

ttc gaa gca caa cgc acc aaa ctc gaa gaa ggc ttg cag ctt aaa cag   738
Phe Glu Ala Gln Arg Thr Lys Leu Glu Glu Gly Leu Gln Leu Lys Gln
200                 205                 210                 215

aat tgg cag ctt ggg tgg gtt taaatgcgcc caacctaaga aaa             782
Asn Trp Gln Leu Gly Trp Val
                220
```

Do not add new matter

<210> 1540
<211> 222
<212> PRT
<213> Corynebacterium glutamicum

<400> 1540

```
Val Lys Lys Lys Leu Met Leu Pro Leu Ile Val Ala Ala Leu Gly Leu
  1               5                  10                  15

Ser Ala Cys Ser Ser Glu Pro Ala Ala Ala Pro Leu Glu Ala Glu Pro
             20                  25                  30

Leu His Asn Leu Leu Ile Asp Gly Ser Glu Ser Gly Leu Asp Asn Ala
         35                  40                  45

Thr Glu Gly Asn Asp Thr Ser Leu Ser Gly Gln Pro Ile Asn Leu Thr
     50                  55                  60

Val Val Asn Gly Ala Leu Asp Ile Asp Gly Ser Cys Gly Lys Ala Leu
 65                  70                  75                  80

Gln Ala Val Glu Asp Val Asn Leu Asp Ser Val Ala Ser Ala Ser Arg
                 85                  90                  95

Ala Leu Ala Ser Gly Asp Lys Gln Val Gly Ile Ala Met Tyr Ser Thr
            100                 105                 110

Ala Glu Asp Asn Asp Ile Ser Pro Met Asp Leu Tyr Ala Asp Ile Ala
```

```
        115                 120                 125

Asn Ala Cys Glu Asp Pro Val Val Asp Ser Ser Asp Thr Thr Tyr Thr
    130                 135                 140

Phe Gly Lys Leu Asp Asp Ala Pro Asp Gly Ala Val Gly Phe Thr Leu
145                 150                 155                 160

Asp Ile Glu Val Thr Pro Asp Asn Gln Gly Ser Thr Val Met Met Ile
                165                 170                 175

Gln Glu Leu Gly Asn His His Ile Ile Val Ala Gly Leu Glu Thr Thr
            180                 185                 190

Pro Glu Glu Thr Ala Thr Val Phe Glu Ala Gln Arg Thr Lys Leu Glu
        195                 200                 205

Glu Gly Leu Gln Leu Lys Gln Asn Trp Gln Leu Gly Trp Val
    210                 215                 220
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<210> 1541
<211> 373
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(373)
<223> RXN03182

<400> 1541
actcgacacc accgtcacca acttcatgat ggtcatcgca ctcttaggat tcatcagctc 60

tgtatccgta gcccgcttcc gcaagaggga tggtgcctaa atg acc ctg caa cta 115
                                                Met Thr Leu Gln Leu
                                                  1   5

ttc acc gac atc gtg tct ctg gtg ttc att ctc agc ggc gca ttc ttg 163
Phe Thr Asp Ile Val Ser Leu Val Phe Ile Leu Ser Gly Ala Phe Leu
                10   15   20

tca ttc tcc gca tcc atc ggc ctc ata cga ttc aaa gac acc atg tcc 211
Ser Phe Ser Ala Ser Ile Gly Leu Ile Arg Phe Lys Asp Thr Met Ser
            25   30   35

aga gtc cac gcc atg acc aaa ccc caa aca acc ggc ctt atc ctc acc 259
Arg Val His Ala Met Thr Lys Pro Gln Thr Thr Gly Leu Ile Leu Thr
        40   45   50

gtt gta ggc gca atc atc cgc atc tta ggc cac gaa cac ttc gat caa 307
Val Val Gly Ala Ile Ile Arg Ile Leu Gly His Glu His Phe Asp Gln
    55   60   65

tca caa cgc agt gac ctc gga gtc ctt gtt ctc ctc gta ctg ttt gca 355
Ser Gln Arg Ser Asp Leu Gly Val Leu Val Leu Leu Val Leu Phe Ala
70   75   80   85

ctg ctc acc agc cca gtg   373
Leu Leu Thr Ser Pro Val
                90
```
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<210> 1542
<211> 91
<212> PRT
<213> Corynebacterium glutamicum

<400> 1542
Met Thr Leu Gln Leu Phe Thr Asp Ile Val Ser Leu Val Phe Ile Leu
1 5 10 15

Ser Gly Ala Phe Leu Ser Phe Ser Ala Ser Ile Gly Leu Ile Arg Phe
20 25 30

Lys Asp Thr Met Ser Arg Val His Ala Met Thr Lys Pro Gln Thr Thr
35 40 45

Gly Leu Ile Leu Thr Val Val Gly Ala Ile Ile Arg Ile Leu Gly His
50 55 60

Glu His Phe Asp Gln Ser Gln Arg Ser Asp Leu Gly Val Leu Val Leu
65 70 75 80

Leu Val Leu Phe Ala Leu Leu Thr Ser Pro Val
85 90

<210> 1543
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (87)..(584)
<223> RXN03184

<400> 1543
gcacaacgtc gctggtcagt gccattagtc acgcaagaaa tgggcgggtc cggtggaaga 60

ctggcctgct gtttggtgcc gcgggcatg gtt ggc gcg ttt ggc ggt ggc gtt 113
Met Val Gly Ala Phe Gly Gly Gly Val
1 5

ctc ggg ggc tac att cct ggc acg att ttg atg atc gcg ttt gcg ctc 161
Leu Gly Gly Tyr Ile Pro Gly Thr Ile Leu Met Ile Ala Phe Ala Leu
10 15 20 25

atg atg atc gcc acg tcg act gcg atg ttg cgg ggg cgt aag cag aag 209
Met Met Ile Ala Thr Ser Thr Ala Met Leu Arg Gly Arg Lys Gln Lys
30 35 40

aag ggg gcg tcg aaa agc tct ctt tgg cgc gtc ctt gtt gat ggc ctg 257
Lys Gly Ala Ser Lys Ser Ser Leu Trp Arg Val Leu Val Asp Gly Leu
45 50 55

gtg gtc ggc gcg gtg acc ggg ctt gtt ggt gcg ggc ggc ggc ttt ttg 305
Val Val Gly Ala Val Thr Gly Leu Val Gly Ala Gly Gly Gly Phe Leu
60 65 70

gtg gtg ccg gcg ctg gcg ctg ctc ggc ggg ctg tcg atg ccg gtg gct 353

```
Val Val Pro Ala Leu Ala Leu Leu Gly Gly Leu Ser Met Pro Val Ala
     75                  80                  85

gtg ggc acg tcg ttg gtg gtg atc acg atg aag tcg ttt gcg ggg ctt   401
Val Gly Thr Ser Leu Val Val Ile Thr Met Lys Ser Phe Ala Gly Leu
 90                  95                 100                 105

gcc ggg tat ctg acc agc gtg cag ctg gat tgg ggg ctg gtg ctg atg   449
Ala Gly Tyr Leu Thr Ser Val Gln Leu Asp Trp Gly Leu Val Leu Met
                110                 115                 120

gtg act gcg gcc gcc atc gtc ggt tcg ctt gcc ggt tcg cgc ctt gcg   497
Val Thr Ala Ala Ala Ile Val Gly Ser Leu Ala Gly Ser Arg Leu Ala
            125                 130                 135

ggg cgc gtg cct gag act ttg ctc cgc aaa ggg ttc ggg gtg ttc gtg   545
Gly Arg Val Pro Glu Thr Leu Leu Arg Lys Gly Phe Gly Val Phe Val
        140                 145                 150

ctg gtc atg ggc gtg ttc gtg ctc ggc ttg gag ctt tta taagcttttc    594
Leu Val Met Gly Val Phe Val Leu Gly Leu Glu Leu Leu
    155                 160                 165

gacgtctcc                                                         603


<210> 1544
<211> 166
<212> PRT
<213> Corynebacterium glutamicum

<400> 1544
Met Val Gly Ala Phe Gly Gly Gly Val Leu Gly Gly Tyr Ile Pro Gly
  1               5                  10                  15

Thr Ile Leu Met Ile Ala Phe Ala Leu Met Met Ile Ala Thr Ser Thr
             20                  25                  30

Ala Met Leu Arg Gly Arg Lys Gln Lys Lys Gly Ala Ser Lys Ser Ser
         35                  40                  45

Leu Trp Arg Val Leu Val Asp Gly Leu Val Val Gly Ala Val Thr Gly
     50                  55                  60

Leu Val Gly Ala Gly Gly Gly Phe Leu Val Val Pro Ala Leu Ala Leu
 65                  70                  75                  80

Leu Gly Gly Leu Ser Met Pro Val Ala Val Gly Thr Ser Leu Val Val
                85                  90                  95

Ile Thr Met Lys Ser Phe Ala Gly Leu Ala Gly Tyr Leu Thr Ser Val
            100                 105                 110

Gln Leu Asp Trp Gly Leu Val Leu Met Val Thr Ala Ala Ala Ile Val
        115                 120                 125

Gly Ser Leu Ala Gly Ser Arg Leu Ala Gly Arg Val Pro Glu Thr Leu
    130                 135                 140

Leu Arg Lys Gly Phe Gly Val Phe Val Leu Val Met Gly Val Phe Val
145                 150                 155                 160
```

Leu Gly Leu Glu Leu Leu
165

<210> 1545
<211> 295
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (84)..(272)
<223> RXN03185

<400> 1545
agcgcccaac cgttcagacc agcggtttct ctgaggatgc aaagtccatg atgggtnagg 60

tcactgagct gtccgaaacc accatg aat gat ctt gca gct gaa ggt gaa aac 113
Met Asn Asp Leu Ala Ala Glu Gly Glu Asn
1 5 10

gat cct tac cgc atg gtt cag cag ctg cgc cgc aag ctc tct cgc ttc 161
Asp Pro Tyr Arg Met Val Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe
15 20 25

gtc gag cag aag tgg aag cgc cag ccg gtc atc atg cca acc gtc att 209
Val Glu Gln Lys Trp Lys Arg Gln Pro Val Ile Met Pro Thr Val Ile
30 35 40

ccg atg act gcg gaa acc acg cac atc ggt gac gat gag gtt cgc gct 257
Pro Met Thr Ala Glu Thr Thr His Ile Gly Asp Asp Glu Val Arg Ala
45 50 55

tca cgc gag tcc ctg taaaagcatt tcgcttttcg acg 295
Ser Arg Glu Ser Leu
60

<210> 1546
<211> 63
<212> PRT
<213> Corynebacterium glutamicum

<400> 1546
Met Asn Asp Leu Ala Ala Glu Gly Glu Asn Asp Pro Tyr Arg Met Val
1 5 10 15

Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe Val Glu Gln Lys Trp Lys
20 25 30

Arg Gln Pro Val Ile Met Pro Thr Val Ile Pro Met Thr Ala Glu Thr
35 40 45

Thr His Ile Gly Asp Asp Glu Val Arg Ala Ser Arg Glu Ser Leu
50 55 60

<210> 1547
<211> 864
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(841)
<223> RXA00003

<400> 1547
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aagcgccaag aaggccaccc ttgccttcgc ggtgcagcac gtg cag gtg aga atc 115
Val Gln Val Arg Ile
1 5

ctc agc agc gag ctt gtc tgc agc ctc tcc ggt gcc atc cgg ggc gtg 163
Leu Ser Ser Glu Leu Val Cys Ser Leu Ser Gly Ala Ile Arg Gly Val
10 15 20

aac cta gat att gca gca ccg aag ccc aag aag tca ggc cgc cgc aca 211
Asn Leu Asp Ile Ala Ala Pro Lys Pro Lys Lys Ser Gly Arg Arg Thr
25 30 35

ctc aca aaa ccc gaa tgg gat gcc gtc att aag cat ctg tta acg cgg 259
Leu Thr Lys Pro Glu Trp Asp Ala Val Ile Lys His Leu Leu Thr Arg
40 45 50

gat acc gag cca ctg tta acc ccc acc aag cac aag aac atc cga caa 307
Asp Thr Glu Pro Leu Leu Thr Pro Thr Lys His Lys Asn Ile Arg Gln
55 60 65

agc acc aag aac atc cat gcc cgc att gtg cgg ctc act ctc ctc caa 355
Ser Thr Lys Asn Ile His Ala Arg Ile Val Arg Leu Thr Leu Leu Gln
70 75 80 85

gcc gtt tca ggg ctg aga att gcc gaa gcc aat caa ttg cag tgg aag 403
Ala Val Ser Gly Leu Arg Ile Ala Glu Ala Asn Gln Leu Gln Trp Lys
90 95 100

cac atc atc gac ggt gac gat ggc atg ctc att aat gcc agc gcc gat 451
His Ile Ile Asp Gly Asp Asp Gly Met Leu Ile Asn Ala Ser Ala Asp
105 110 115

att gtc aag ggg cga aaa ggc aag gaa aga ggg cgg tat atc cct atc 499
Ile Val Lys Gly Arg Lys Gly Lys Glu Arg Gly Arg Tyr Ile Pro Ile
120 125 130

ctg agg gcc gac gta gcg gaa tac ctg cgt aca cac cgc gag gac gac 547
Leu Arg Ala Asp Val Ala Glu Tyr Leu Arg Thr His Arg Glu Asp Asp
135 140 145

gag cat ttc atc gta ggc tca ccg acg acg acc gcg agg ccc tgg gac 595
Glu His Phe Ile Val Gly Ser Pro Thr Thr Thr Ala Arg Pro Trp Asp
150 155 160 165

gcg acg aac gca gat gac aag gtg ccc gag cta tac cgg caa att gca 643
Ala Thr Asn Ala Asp Asp Lys Val Pro Glu Leu Tyr Arg Gln Ile Ala
170 175 180

gaa gct aca ggc gtg aag act ctt caa gac ctc cga agc cac tcc tgg 691
Glu Ala Thr Gly Val Lys Thr Leu Gln Asp Leu Arg Ser His Ser Trp
185 190 195

```
cgt gcg acg ctg cac ggt gtg tac gcg gac gtg atg gac cca gct aca   739
Arg Ala Thr Leu His Gly Val Tyr Ala Asp Val Met Asp Pro Ala Thr
        200                 205                 210

cgc gcc gcc att ttc ggc cac acc gag cag gta gct gag gag tac tac   787
Arg Ala Ala Ile Phe Gly His Thr Glu Gln Val Ala Glu Glu Tyr Tyr
    215                 220                 225

aac gac cgc caa aat att gaa tca ctc atg aga caa gtc aag cgc gcc   835
Asn Asp Arg Gln Asn Ile Glu Ser Leu Met Arg Gln Val Lys Arg Ala
230                 235                 240                 245

tac gcg taactacgct taagactacg cgt                                 864
Tyr Ala
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<210> 1548
<211> 247
<212> PRT
<213> Corynebacterium glutamicum

<400> 1548

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Val Gln Val Arg Ile Leu Ser Ser Glu Leu Val Cys Ser Leu Ser Gly
  1               5                  10                  15

Ala Ile Arg Gly Val Asn Leu Asp Ile Ala Ala Pro Lys Pro Lys Lys
            20                  25                  30

Ser Gly Arg Arg Thr Leu Thr Lys Pro Glu Trp Asp Ala Val Ile Lys
        35                  40                  45

His Leu Leu Thr Arg Asp Thr Glu Pro Leu Leu Thr Pro Thr Lys His
    50                  55                  60

Lys Asn Ile Arg Gln Ser Thr Lys Asn Ile His Ala Arg Ile Val Arg
65                  70                  75                  80

Leu Thr Leu Leu Gln Ala Val Ser Gly Leu Arg Ile Ala Glu Ala Asn
                85                  90                  95

Gln Leu Gln Trp Lys His Ile Ile Asp Gly Asp Asp Gly Met Leu Ile
            100                 105                 110

Asn Ala Ser Ala Asp Ile Val Lys Gly Arg Lys Gly Lys Glu Arg Gly
        115                 120                 125

Arg Tyr Ile Pro Ile Leu Arg Ala Asp Val Ala Glu Tyr Leu Arg Thr
    130                 135                 140

His Arg Glu Asp Asp Glu His Phe Ile Val Gly Ser Pro Thr Thr Thr
145                 150                 155                 160

Ala Arg Pro Trp Asp Ala Thr Asn Ala Asp Asp Lys Val Pro Glu Leu
                165                 170                 175

Tyr Arg Gln Ile Ala Glu Ala Thr Gly Val Lys Thr Leu Gln Asp Leu
            180                 185                 190

Arg Ser His Ser Trp Arg Ala Thr Leu His Gly Val Tyr Ala Asp Val
```

```
        195                 200                 205

Met Asp Pro Ala Thr Arg Ala Ala Ile Phe Gly His Thr Glu Gln Val
    210                 215                 220

Ala Glu Glu Tyr Tyr Asn Asp Arg Gln Asn Ile Glu Ser Leu Met Arg
225                 230                 235                 240

Gln Val Lys Arg Ala Tyr Ala
                245
```

<210> 1549
<211> 615
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(592)
<223> RXA00008

<400> 1549

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cattggcgtg gtgatcgccg gcattatcgc acaactcacc ctgcgcttct acgtgaggaa 60

ataagactat tgaactcctt gccgtagact tagaaagact atg gcc aag aag aaa   115
                                            Met Ala Lys Lys Lys
                                              1               5

aag aaa gtc gac gaa aac aac tca gtt ctc gcg acc aat cgc aag gcc   163
Lys Lys Val Asp Glu Asn Asn Ser Val Leu Ala Thr Asn Arg Lys Ala
                10                  15                  20

cgc cat gac tac cac atc att gat acg tgg gag gcg ggc gtg gtg ctc   211
Arg His Asp Tyr His Ile Ile Asp Thr Trp Glu Ala Gly Val Val Leu
            25                  30                  35

tta ggc acc gaa atc aaa tca ctg cgc gaa ggt aag gta tcc ctc gtg   259
Leu Gly Thr Glu Ile Lys Ser Leu Arg Glu Gly Lys Val Ser Leu Val
        40                  45                  50

gat tcc ttt gcc acc att gat aac gga gaa atc tgg ctt cag cat ctc   307
Asp Ser Phe Ala Thr Ile Asp Asn Gly Glu Ile Trp Leu Gln His Leu
    55                  60                  65

cac atc ccg cag tat tcc atg ggc tcc tgg aca aac cac acg ccc aag   355
His Ile Pro Gln Tyr Ser Met Gly Ser Trp Thr Asn His Thr Pro Lys
70                  75                  80                  85

cgc acc cgc aaa ctt ttg ctg cac cgc aac gag att gat tcc ctg atg   403
Arg Thr Arg Lys Leu Leu Leu His Arg Asn Glu Ile Asp Ser Leu Met
                90                  95                  100

ggt aaa gtc cgc gac ggc aac cgc acg ttg gtt ccg ctc aag ctt tac   451
Gly Lys Val Arg Asp Gly Asn Arg Thr Leu Val Pro Leu Lys Leu Tyr
            105                 110                 115

ctc aaa aac ggt cgc gtc aaa ctc gaa ctc gga ctc gca caa ggt aag   499
Leu Lys Asn Gly Arg Val Lys Leu Glu Leu Gly Leu Ala Gln Gly Lys
        120                 125                 130
```

```
cag gat tac gac aag cgc caa gat atc aag cgt cgc acc gaa gaa cgc   547
Gln Asp Tyr Asp Lys Arg Gln Asp Ile Lys Arg Arg Thr Glu Glu Arg
    135                 140                 145

gaa gtc acc cgt gag ctc ggc cgt cgc att aag gga atc aac gcg       592
Glu Val Thr Arg Glu Leu Gly Arg Arg Ile Lys Gly Ile Asn Ala
150                 155                 160

taaatgagta ttcacatcgc aaa                                        615
```

<210> 1550
<211> 164
<212> PRT
<213> Corynebacterium glutamicum

<400> 1550

```
Met Ala Lys Lys Lys Lys Lys Val Asp Glu Asn Asn Ser Val Leu Ala
  1               5                  10                  15

Thr Asn Arg Lys Ala Arg His Asp Tyr His Ile Ile Asp Thr Trp Glu
             20                  25                  30

Ala Gly Val Val Leu Leu Gly Thr Glu Ile Lys Ser Leu Arg Glu Gly
         35                  40                  45

Lys Val Ser Leu Val Asp Ser Phe Ala Thr Ile Asp Asn Gly Glu Ile
     50                  55                  60

Trp Leu Gln His Leu His Ile Pro Gln Tyr Ser Met Gly Ser Trp Thr
 65                  70                  75                  80

Asn His Thr Pro Lys Arg Thr Arg Lys Leu Leu Leu His Arg Asn Glu
                 85                  90                  95

Ile Asp Ser Leu Met Gly Lys Val Arg Asp Gly Asn Arg Thr Leu Val
            100                 105                 110

Pro Leu Lys Leu Tyr Leu Lys Asn Gly Arg Val Lys Leu Glu Leu Gly
        115                 120                 125

Leu Ala Gln Gly Lys Gln Asp Tyr Asp Lys Arg Gln Asp Ile Lys Arg
    130                 135                 140

Arg Thr Glu Glu Arg Glu Val Thr Arg Glu Leu Gly Arg Arg Ile Lys
145                 150                 155                 160

Gly Ile Asn Ala
```

<210> 1551
<211> 432
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(409)
<223> RXA00015

<400> 1551
aagacgcaca gaagctacac acatagctac atcgtcagca ccaaagccgg aacaagaact 60

acagcaaccg acgacactca acgagcgcga cctccaagac atg att gat atg tgc 115
Met Ile Asp Met Cys
1 5

acc act cct cga caa gag atc atg atc cgc gag caa ttt aag gag atc 163
Thr Thr Pro Arg Gln Glu Ile Met Ile Arg Glu Gln Phe Lys Glu Ile
10 15 20

aac aac ggt agg gtt gta cct cat tac gat cag ctt gaa cag ctc gca 211
Asn Asn Gly Arg Val Val Pro His Tyr Asp Gln Leu Glu Gln Leu Ala
25 30 35

gag att ttt tca act aaa gac tca atc gac atg gtc aac gag ata ctc 259
Glu Ile Phe Ser Thr Lys Asp Ser Ile Asp Met Val Asn Glu Ile Leu
40 45 50

aat cgc gat acg gat ttt ctc agt aat gaa ggc aca att ttt atg gaa 307
Asn Arg Asp Thr Asp Phe Leu Ser Asn Glu Gly Thr Ile Phe Met Glu
55 60 65

tac att ttc aac ggt gga ttc cat acg gac aac ggc tat caa ccg ttg 355
Tyr Ile Phe Asn Gly Gly Phe His Thr Asp Asn Gly Tyr Gln Pro Leu
70 75 80 85

tcc tat gca tat gtt gaa cga ggc tta gcg atc cgc cct cca cgc ata 403
Ser Tyr Ala Tyr Val Glu Arg Gly Leu Ala Ile Arg Pro Pro Arg Ile
90 95 100

gtg ctc tagatatgac acaaatcggt att 432
Val Leu

<210> 1552
<211> 103
<212> PRT
<213> Corynebacterium glutamicum

<400> 1552
Met Ile Asp Met Cys Thr Thr Pro Arg Gln Glu Ile Met Ile Arg Glu
1 5 10 15

Gln Phe Lys Glu Ile Asn Asn Gly Arg Val Val Pro His Tyr Asp Gln
20 25 30

Leu Glu Gln Leu Ala Glu Ile Phe Ser Thr Lys Asp Ser Ile Asp Met
35 40 45

Val Asn Glu Ile Leu Asn Arg Asp Thr Asp Phe Leu Ser Asn Glu Gly
50 55 60

Thr Ile Phe Met Glu Tyr Ile Phe Asn Gly Gly Phe His Thr Asp Asn
65 70 75 80

Gly Tyr Gln Pro Leu Ser Tyr Ala Tyr Val Glu Arg Gly Leu Ala Ile
85 90 95

Arg Pro Pro Arg Ile Val Leu

100

<210> 1553
<211> 1422
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1399)
<223> RXA00018

<400> 1553
caacccgccc cacaaacaca tacaattaac ttctatattt agtaaataaa taactagtat 60

ttttaatgac ttacaaatat caagaaagaa tctattcctt atg tcc gca tta tct 115
Met Ser Ala Leu Ser
1 5

aga ccg cac aag atc gcc acc ggc gtt gct gtc gca act ctt acc ctc 163
Arg Pro His Lys Ile Ala Thr Gly Val Ala Val Ala Thr Leu Thr Leu
10 15 20

acc ttg tgt acc tct gct gcc ggc gtt gtc cat gca gcg caa caa tcc 211
Thr Leu Cys Thr Ser Ala Ala Gly Val Val His Ala Ala Gln Gln Ser
25 30 35

atc agc ggt cca gaa tcc tcc tgt gct ttt aat caa cag cgt tgg gat 259
Ile Ser Gly Pro Glu Ser Ser Cys Ala Phe Asn Gln Gln Arg Trp Asp
40 45 50

gac agc aaa gtt aag ctt gac gac acc atc gct acg gcc aaa aac tca 307
Asp Ser Lys Val Lys Leu Asp Asp Thr Ile Ala Thr Ala Lys Asn Ser
55 60 65

ttg gta caa aca ggc gaa ctg cac cgc aac gaa cag gat cta ctt act 355
Leu Val Gln Thr Gly Glu Leu His Arg Asn Glu Gln Asp Leu Leu Thr
70 75 80 85

ggc tat ctt ttc cag caa ccg cac agc agc aat tac ctt gca ctc aac 403
Gly Tyr Leu Phe Gln Gln Pro His Ser Ser Asn Tyr Leu Ala Leu Asn
90 95 100

aac gct tat gcc gat gcc gta gca atc aaa gac agc ttt gtc cgc cca 451
Asn Ala Tyr Ala Asp Ala Val Ala Ile Lys Asp Ser Phe Val Arg Pro
105 110 115

aca tgt gac ggt tct aaa gag tcc aag att gcc agc gaa cac gcc gtg 499
Thr Cys Asp Gly Ser Lys Glu Ser Lys Ile Ala Ser Glu His Ala Val
120 125 130

tct gag gtt gtg ggt gca gtg aat gta ctc gcc cga gca caa aaa gcg 547
Ser Glu Val Val Gly Ala Val Asn Val Leu Ala Arg Ala Gln Lys Ala
135 140 145

ctg cag att aac tcc gac acc tac gaa cag caa cgt cgt tgt gat gcc 595
Leu Gln Ile Asn Ser Asp Thr Tyr Glu Gln Gln Arg Arg Cys Asp Ala
150 155 160 165

ctt cgt cta gca agc cga gat gaa tca gat gtt ctt atg cgc att gat 643

```
Leu Arg Leu Ala Ser Arg Asp Glu Ser Asp Val Leu Met Arg Ile Asp
                170                 175                 180

cgc acc atg ctg cag ctt cgt cgc aca cta gct gac att gac cag gcg   691
Arg Thr Met Leu Gln Leu Arg Arg Thr Leu Ala Asp Ile Asp Gln Ala
            185                 190                 195

tcc aca gac att cgc gat att cgg gct caa aca aca agc ttt gaa cgt   739
Ser Thr Asp Ile Arg Asp Ile Arg Ala Gln Thr Thr Ser Phe Glu Arg
        200                 205                 210

gat ctt gcc cgc gag caa aaa gag gcc gac gca gca gca cgt gct caa   787
Asp Leu Ala Arg Glu Gln Lys Glu Ala Asp Ala Ala Ala Arg Ala Gln
    215                 220                 225

gct gta gac act tcg acc aca cca aca tca agc aca gaa gat cgt gtc   835
Ala Val Asp Thr Ser Thr Thr Pro Thr Ser Ser Thr Glu Asp Arg Val
230                 235                 240                 245

aac gac att ctt aaa gag tcc cgt acc gat cac agt ggc gac agt tac   883
Asn Asp Ile Leu Lys Glu Ser Arg Thr Asp His Ser Gly Asp Ser Tyr
                250                 255                 260

acg cgc tca acg aca acg agc gca caa agc act gag ccg gat tct gca   931
Thr Arg Ser Thr Thr Thr Ser Ala Gln Ser Thr Glu Pro Asp Ser Ala
            265                 270                 275

acc aac acc tca tat ctg tca cgt cgt ctc gac agc ctg gaa cgc agt   979
Thr Asn Thr Ser Tyr Leu Ser Arg Arg Leu Asp Ser Leu Glu Arg Ser
        280                 285                 290

gcg cag cat att gat ctc aat acc cag tgc gac aac ctc gat gat ctt  1027
Ala Gln His Ile Asp Leu Asn Thr Gln Cys Asp Asn Leu Asp Asp Leu
    295                 300                 305

cgt gaa ctc acc aac aat gac acg cgt gat cac acc ggc tcc gtc att  1075
Arg Glu Leu Thr Asn Asn Asp Thr Arg Asp His Thr Gly Ser Val Ile
310                 315                 320                 325

tcc att gcc gat caa ctc aca gac atc acc aat gaa atc aat gaa tta  1123
Ser Ile Ala Asp Gln Leu Thr Asp Ile Thr Asn Glu Ile Asn Glu Leu
                330                 335                 340

cgc gat agc act ttt gcc acc aga gac agt gcc caa caa gca cag gat  1171
Arg Asp Ser Thr Phe Ala Thr Arg Asp Ser Ala Gln Gln Ala Gln Asp
            345                 350                 355

cag gta att gct caa cgt gaa gaa ctg caa cga gca aag gaa gca cga  1219
Gln Val Ile Ala Gln Arg Glu Glu Leu Gln Arg Ala Lys Glu Ala Arg
        360                 365                 370

cta gaa gaa cag cga ctc gcc aaa gaa gca gaa gag ggc gct cgc aac  1267
Leu Glu Glu Gln Arg Leu Ala Lys Glu Ala Glu Glu Gly Ala Arg Asn
    375                 380                 385

gca gca att cag gaa cgt gac gcg gcc gaa gca gca ctg cgt gaa gca  1315
Ala Ala Ile Gln Glu Arg Asp Ala Ala Glu Ala Ala Leu Arg Glu Ala
390                 395                 400                 405

caa gac ctc ctc agt cgc ctc gat gac aca ggc aac gca acc agt gat  1363
Gln Asp Leu Leu Ser Arg Leu Asp Asp Thr Gly Asn Ala Thr Ser Asp
```

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                410                 415                 420

gac aca gca gcg cta gta gac ggt ctt ctc aat aac taacaatcag        1409
Asp Thr Ala Ala Leu Val Asp Gly Leu Leu Asn Asn
            425                 430

caacaccgct cac                                                   1422


<210> 1554
<211> 433
<212> PRT
<213> Corynebacterium glutamicum

<400> 1554
Met Ser Ala Leu Ser Arg Pro His Lys Ile Ala Thr Gly Val Ala Val
  1               5                  10                  15

Ala Thr Leu Thr Leu Thr Leu Cys Thr Ser Ala Ala Gly Val Val His
             20                  25                  30

Ala Ala Gln Gln Ser Ile Ser Gly Pro Glu Ser Ser Cys Ala Phe Asn
         35                  40                  45

Gln Gln Arg Trp Asp Asp Ser Lys Val Lys Leu Asp Asp Thr Ile Ala
     50                  55                  60

Thr Ala Lys Asn Ser Leu Val Gln Thr Gly Glu Leu His Arg Asn Glu
 65                  70                  75                  80

Gln Asp Leu Leu Thr Gly Tyr Leu Phe Gln Gln Pro His Ser Ser Asn
                 85                  90                  95

Tyr Leu Ala Leu Asn Asn Ala Tyr Ala Asp Ala Val Ala Ile Lys Asp
            100                 105                 110

Ser Phe Val Arg Pro Thr Cys Asp Gly Ser Lys Glu Ser Lys Ile Ala
        115                 120                 125

Ser Glu His Ala Val Ser Glu Val Val Gly Ala Val Asn Val Leu Ala
    130                 135                 140

Arg Ala Gln Lys Ala Leu Gln Ile Asn Ser Asp Thr Tyr Glu Gln Gln
145                 150                 155                 160

Arg Arg Cys Asp Ala Leu Arg Leu Ala Ser Arg Asp Glu Ser Asp Val
                165                 170                 175

Leu Met Arg Ile Asp Arg Thr Met Leu Gln Leu Arg Arg Thr Leu Ala
            180                 185                 190

Asp Ile Asp Gln Ala Ser Thr Asp Ile Arg Asp Ile Arg Ala Gln Thr
        195                 200                 205

Thr Ser Phe Glu Arg Asp Leu Ala Arg Glu Gln Lys Glu Ala Asp Ala
    210                 215                 220

Ala Ala Arg Ala Gln Ala Val Asp Thr Ser Thr Thr Pro Thr Ser Ser
225                 230                 235                 240

Thr Glu Asp Arg Val Asn Asp Ile Leu Lys Glu Ser Arg Thr Asp His
```

```
                245                 250                 255

Ser Gly Asp Ser Tyr Thr Arg Ser Thr Thr Thr Ser Ala Gln Ser Thr
            260                 265                 270

Glu Pro Asp Ser Ala Thr Asn Thr Ser Tyr Leu Ser Arg Arg Leu Asp
        275                 280                 285

Ser Leu Glu Arg Ser Ala Gln His Ile Asp Leu Asn Thr Gln Cys Asp
    290                 295                 300

Asn Leu Asp Asp Leu Arg Glu Leu Thr Asn Asn Asp Thr Arg Asp His
305                 310                 315                 320

Thr Gly Ser Val Ile Ser Ile Ala Asp Gln Leu Thr Asp Ile Thr Asn
                325                 330                 335

Glu Ile Asn Glu Leu Arg Asp Ser Thr Phe Ala Thr Arg Asp Ser Ala
            340                 345                 350

Gln Gln Ala Gln Asp Gln Val Ile Ala Gln Arg Glu Glu Leu Gln Arg
        355                 360                 365

Ala Lys Glu Ala Arg Leu Glu Glu Gln Arg Leu Ala Lys Glu Ala Glu
    370                 375                 380

Glu Gly Ala Arg Asn Ala Ala Ile Gln Glu Arg Asp Ala Ala Glu Ala
385                 390                 395                 400

Ala Leu Arg Glu Ala Gln Asp Leu Leu Ser Arg Leu Asp Asp Thr Gly
                405                 410                 415

Asn Ala Thr Ser Asp Asp Thr Ala Ala Leu Val Asp Gly Leu Leu Asn
            420                 425                 430

Asn
```

<210> 1555
<211> 903
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(880)
<223> RXA00020

<400> 1555
taggagaact acctttcttg ctggtgttac ctagctttaa gtttgttaga gtaattaatg 60

aataactaag taatgtaagt aaagggactt ttaaataact atg act gtg acc acc 115
                                            Met Thr Val Thr Thr
                                              1   5

gca caa cga atc gct gac gaa ttt caa cgt ggc att agt atc ggc ccg 163
Ala Gln Arg Ile Ala Asp Glu Phe Gln Arg Gly Ile Ser Ile Gly Pro
                10   15   20

tgg gat ctg tgc gaa gta cca gca ggc gat gac tat tta gag cac acc 211

```
Trp Asp Leu Cys Glu Val Pro Ala Gly Asp Asp Tyr Leu Glu His Thr
            25                  30                  35

acc aag gtc agg cga cgc cac agc acg gct gta gag att cac act gac   259
Thr Lys Val Arg Arg Arg His Ser Thr Ala Val Glu Ile His Thr Asp
        40                  45                  50

tct ttg atc att tgt gcg cct gaa ggc agt acg tac agc cac aac cgc   307
Ser Leu Ile Ile Cys Ala Pro Glu Gly Ser Thr Tyr Ser His Asn Arg
    55                  60                  65

act aag gct ggt ctt gcg tcc acg ggc aca gtc act gtg cca gtg aag   355
Thr Lys Ala Gly Leu Ala Ser Thr Gly Thr Val Thr Val Pro Val Lys
70                  75                  80                  85

ggg ctt tct gag cct gtg aag ctt agt ctc aat ctt ctt gct gat tat   403
Gly Leu Ser Glu Pro Val Lys Leu Ser Leu Asn Leu Leu Ala Asp Tyr
                90                  95                  100

gga aac tcc ttt gac act gtg cac gac gat ctg tgg caa cga gag ctg   451
Gly Asn Ser Phe Asp Thr Val His Asp Asp Leu Trp Gln Arg Glu Leu
            105                 110                 115

cgt gag cag acg cgg ggg cag tta ctc aca ctt aat gca gtc tcc ggt   499
Arg Glu Gln Thr Arg Gly Gln Leu Leu Thr Leu Asn Ala Val Ser Gly
        120                 125                 130

ctt ggg gat gac agc gtg gcg att atg ggc acg cca tgg ggc gat ggt   547
Leu Gly Asp Asp Ser Val Ala Ile Met Gly Thr Pro Trp Gly Asp Gly
    135                 140                 145

ctc acc ggg gag gcc aac acc att aaa ggt cgt gag cat ttt gtc atg   595
Leu Thr Gly Glu Ala Asn Thr Ile Lys Gly Arg Glu His Phe Val Met
150                 155                 160                 165

tgg gct gca ggg tgc cgc ttt gaa gac ggt tat ggt cgt cac gca ctt   643
Trp Ala Ala Gly Cys Arg Phe Glu Asp Gly Tyr Gly Arg His Ala Leu
                170                 175                 180

cga gag gat cgc cat gtg cga cac cag gca cgt gcg ggt gag gat tcc   691
Arg Glu Asp Arg His Val Arg His Gln Ala Arg Ala Gly Glu Asp Ser
            185                 190                 195

act gca cat cac ggt tgg ttg ctt aaa ggc aca gtg ttc ggg aaa gaa   739
Thr Ala His His Gly Trp Leu Leu Lys Gly Thr Val Phe Gly Lys Glu
        200                 205                 210

ctc acc ggt gat gct gtg acg gca gcc atg aca gtt ttt agt gat gtg   787
Leu Thr Gly Asp Ala Val Thr Ala Ala Met Thr Val Phe Ser Asp Val
    215                 220                 225

gtg gtc act gtc gat gag ggg cgt atc cct ggc atg aaa tca gga caa   835
Val Val Thr Val Asp Glu Gly Arg Ile Pro Gly Met Lys Ser Gly Gln
230                 235                 240                 245

ccg ttt tct atg gca acc cgt tta cgc gca tca tct gcg cct gtg       880
Pro Phe Ser Met Ala Thr Arg Leu Arg Ala Ser Ser Ala Pro Val
                250                 255                 260

tagagacttt ttcagacctt aac                                       903
```

<210> 1556
<211> 260
<212> PRT
<213> Corynebacterium glutamicum

<400> 1556
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Met Thr Val Thr Thr Ala Gln Arg Ile Ala Asp Glu Phe Gln Arg Gly
  1               5                  10                  15

Ile Ser Ile Gly Pro Trp Asp Leu Cys Glu Val Pro Ala Gly Asp Asp
             20                  25                  30

Tyr Leu Glu His Thr Thr Lys Val Arg Arg Arg His Ser Thr Ala Val
         35                  40                  45

Glu Ile His Thr Asp Ser Leu Ile Ile Cys Ala Pro Glu Gly Ser Thr
     50                  55                  60

Tyr Ser His Asn Arg Thr Lys Ala Gly Leu Ala Ser Thr Gly Thr Val
 65                  70                  75                  80

Thr Val Pro Val Lys Gly Leu Ser Glu Pro Val Lys Leu Ser Leu Asn
                 85                  90                  95

Leu Leu Ala Asp Tyr Gly Asn Ser Phe Asp Thr Val His Asp Asp Leu
            100                 105                 110

Trp Gln Arg Glu Leu Arg Glu Gln Thr Arg Gly Gln Leu Leu Thr Leu
        115                 120                 125

Asn Ala Val Ser Gly Leu Gly Asp Asp Ser Val Ala Ile Met Gly Thr
    130                 135                 140

Pro Trp Gly Asp Gly Leu Thr Gly Glu Ala Asn Thr Ile Lys Gly Arg
145                 150                 155                 160

Glu His Phe Val Met Trp Ala Ala Gly Cys Arg Phe Glu Asp Gly Tyr
                165                 170                 175

Gly Arg His Ala Leu Arg Glu Asp Arg His Val Arg His Gln Ala Arg
            180                 185                 190

Ala Gly Glu Asp Ser Thr Ala His His Gly Trp Leu Leu Lys Gly Thr
        195                 200                 205

Val Phe Gly Lys Glu Leu Thr Gly Asp Ala Val Thr Ala Ala Met Thr
    210                 215                 220

Val Phe Ser Asp Val Val Val Thr Val Asp Glu Gly Arg Ile Pro Gly
225                 230                 235                 240

Met Lys Ser Gly Gln Pro Phe Ser Met Ala Thr Arg Leu Arg Ala Ser
                245                 250                 255

Ser Ala Pro Val
            260
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<210> 1557
<211> 1896

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1873)
<223> RXA00021

<400> 1557
aaaagcaact cacttcgtgc ttttttcacc gaccccggct gtgtggatgc cacccactta 60

caccgcacaa tcgaaaataa aagtaaagga tgttcacctt atg tct gac acc aca 115
Met Ser Asp Thr Thr
1 5

gac agc cac gac cca gca acc tcc cct aca gtc gat tca gcc gca tcc 163
Asp Ser His Asp Pro Ala Thr Ser Pro Thr Val Asp Ser Ala Ala Ser
10 15 20

ggt act tct gac ccc aac cag caa ccc aag aag aaa ttc acc atc att 211
Gly Thr Ser Asp Pro Asn Gln Gln Pro Lys Lys Lys Phe Thr Ile Ile
25 30 35

aag cag gtg aac atg att gcg cgt act gcc att gat gac tgc att aat 259
Lys Gln Val Asn Met Ile Ala Arg Thr Ala Ile Asp Asp Cys Ile Asn
40 45 50

cga cta ggc cca gat gtt gtc acc atg tcc agc gaa gac att gct gat 307
Arg Leu Gly Pro Asp Val Val Thr Met Ser Ser Glu Asp Ile Ala Asp
55 60 65

caa gtg gtc aac tcc att aac gtt gct att gcc aga gaa aac aca cgt 355
Gln Val Val Asn Ser Ile Asn Val Ala Ile Ala Arg Glu Asn Thr Arg
70 75 80 85

gcc caa gat gcc aat gct gcg gtg cgt tac aca cct atc ttt aag ctc 403
Ala Gln Asp Ala Asn Ala Ala Val Arg Tyr Thr Pro Ile Phe Lys Leu
90 95 100

gat ttc tcc cat gtc gct gtc ctt atg cgc aga ctg cat gtg att atc 451
Asp Phe Ser His Val Ala Val Leu Met Arg Arg Leu His Val Ile Ile
105 110 115

aac atc gcg cca tcg cat aac tct gat cct gac agc gat atg ttg gct 499
Asn Ile Ala Pro Ser His Asn Ser Asp Pro Asp Ser Asp Met Leu Ala
120 125 130

att tac gac ccc aac cca cgc agc gag cat tac ggg atc tat cgc acc 547
Ile Tyr Asp Pro Asn Pro Arg Ser Glu His Tyr Gly Ile Tyr Arg Thr
135 140 145

tca gag gct gaa ata cgc cgc gta gcc cgt gaa tac tgc cct gac ctc 595
Ser Glu Ala Glu Ile Arg Arg Val Ala Arg Glu Tyr Cys Pro Asp Leu
150 155 160 165

acc tca gcg cag ttt aga gaa ctg cag atg gca ctc tca gat gct gca 643
Thr Ser Ala Gln Phe Arg Glu Leu Gln Met Ala Leu Ser Asp Ala Ala
170 175 180

cct cgt aaa gtc cgc cac aag cag cgt gac ttg att ccc gtg aaa aac 691
Pro Arg Lys Val Arg His Lys Gln Arg Asp Leu Ile Pro Val Lys Asn

```
            185                 190                 195

ggc atc ttt aat tac tcg act aaa caa cta gaa ccg ttt tct caa gag   739
Gly Ile Phe Asn Tyr Ser Thr Lys Gln Leu Glu Pro Phe Ser Gln Glu
        200                 205                 210

ttt gtc ttt ctt gct aaa tct gca gtg aac tac aac cca aat gca caa   787
Phe Val Phe Leu Ala Lys Ser Ala Val Asn Tyr Asn Pro Asn Ala Gln
    215                 220                 225

aac cct gtc atc act cat ccc cag gat ggc tct gtc tgg gat gtt gaa   835
Asn Pro Val Ile Thr His Pro Gln Asp Gly Ser Val Trp Asp Val Glu
230                 235                 240                 245

tca tgg atg aac gat ctc tcc gat gac cct gaa gtc gtt aac ctg ctg   883
Ser Trp Met Asn Asp Leu Ser Asp Asp Pro Glu Val Val Asn Leu Leu
                250                 255                 260

tgg gag att atc ggc gct atc gtg cgc ccc tat gtg tcc tgg aac aag   931
Trp Glu Ile Ile Gly Ala Ile Val Arg Pro Tyr Val Ser Trp Asn Lys
            265                 270                 275

tct gcc tgg ttc tac tca gag gcc ggc aac aac ggt aaa ggc acg ctc   979
Ser Ala Trp Phe Tyr Ser Glu Ala Gly Asn Asn Gly Lys Gly Thr Leu
        280                 285                 290

gtt gag ctc atg cgc aac atc ttg ggc gca gag gcc tat acc agt atc  1027
Val Glu Leu Met Arg Asn Ile Leu Gly Ala Glu Ala Tyr Thr Ser Ile
    295                 300                 305

cag ctc tcg gac ttc tct aaa gag ttc cac ctt gaa tca ctg act cgt  1075
Gln Leu Ser Asp Phe Ser Lys Glu Phe His Leu Glu Ser Leu Thr Arg
310                 315                 320                 325

gca caa gca atc ctt gtt gat gag aac gat gtc ggc gcc ttc tta gaa  1123
Ala Gln Ala Ile Leu Val Asp Glu Asn Asp Val Gly Ala Phe Leu Glu
                330                 335                 340

aag tca gca aac ctt aaa gcg att gtc acc aat gac gtc atc tcc att  1171
Lys Ser Ala Asn Leu Lys Ala Ile Val Thr Asn Asp Val Ile Ser Ile
            345                 350                 355

aac cgc aag cac aaa acc atg ctc agc tat cag ttt tat ggc ttt atg  1219
Asn Arg Lys His Lys Thr Met Leu Ser Tyr Gln Phe Tyr Gly Phe Met
        360                 365                 370

gtg cag tgt att aac ggc ttc ccc aag gtc aaa gac cag tcg gag tca  1267
Val Gln Cys Ile Asn Gly Phe Pro Lys Val Lys Asp Gln Ser Glu Ser
    375                 380                 385

ttt ttc agg cgc caa ctc ttt gtg ccg ttt gag aaa agc ttc acc ggt  1315
Phe Phe Arg Arg Gln Leu Phe Val Pro Phe Glu Lys Ser Phe Thr Gly
390                 395                 400                 405

gcc gag cgc aag tac atc aaa gac gac tac atg tcg cgc act gat gtc  1363
Ala Glu Arg Lys Tyr Ile Lys Asp Asp Tyr Met Ser Arg Thr Asp Val
                410                 415                 420

ctc gaa tat gta ctg cac cgc gta ctg cat atg aac tac gac aat ctc  1411
Leu Glu Tyr Val Leu His Arg Val Leu His Met Asn Tyr Asp Asn Leu
            425                 430                 435
```

```
tcc acc cct gct gca gct ctc gct gtg ctg gat gaa tac aaa gag ttt   1459
Ser Thr Pro Ala Ala Ala Leu Ala Val Leu Asp Glu Tyr Lys Glu Phe
        440                 445                 450

gtc gat cct gtg cgc gca ttc tgg aat gaa ttc agc gat caa ttt gtc   1507
Val Asp Pro Val Arg Ala Phe Trp Asn Glu Phe Ser Asp Gln Phe Val
    455                 460                 465

tgg gat ctt ctt ccc ctg caa ttc ctc tac gag ttt tat cgc aag tgg   1555
Trp Asp Leu Leu Pro Leu Gln Phe Leu Tyr Glu Phe Tyr Arg Lys Trp
470                 475                 480                 485

ttt gac cgt gac agc cca tcc ggg tct gtg ctc ggc aaa cgc agc ttc   1603
Phe Asp Arg Asp Ser Pro Ser Gly Ser Val Leu Gly Lys Arg Ser Phe
                490                 495                 500

att caa aaa atc acc acc atc gcc gtt gat agc ggt cag tgg gag tat   1651
Ile Gln Lys Ile Thr Thr Ile Ala Val Asp Ser Gly Gln Trp Glu Tyr
            505                 510                 515

ccg ctg aca gca cag cgt ccc ggt ggc gat atg gcc gtt cct gag cca   1699
Pro Leu Thr Ala Gln Arg Pro Gly Gly Asp Met Ala Val Pro Glu Pro
        520                 525                 530

tta gtc att gat tat gac ctc acc gag tgg caa aac gcc act gta cct   1747
Leu Val Ile Asp Tyr Asp Leu Thr Glu Trp Gln Asn Ala Thr Val Pro
    535                 540                 545

aaa ggt cac gtc aac aag ggg ctc cct cta cca ctc aag gct aat tat   1795
Lys Gly His Val Asn Lys Gly Leu Pro Leu Pro Leu Lys Ala Asn Tyr
550                 555                 560                 565

cga gga ctg ctc cgc aaa cct cta aca aca cct gct act ccc cct gca   1843
Arg Gly Leu Leu Arg Lys Pro Leu Thr Thr Pro Ala Thr Pro Pro Ala
                570                 575                 580

gcg ccg gtc aac ccc aca cca ccc acc cct taacaaccac aagaaagatt     1893
Ala Pro Val Asn Pro Thr Pro Pro Thr Pro
            585                 590

tat                                                               1896
```

<210> 1558
<211> 591
<212> PRT
<213> Corynebacterium glutamicum

<400> 1558

```
Met Ser Asp Thr Thr Asp Ser His Asp Pro Ala Thr Ser Pro Thr Val
  1               5                  10                  15

Asp Ser Ala Ala Ser Gly Thr Ser Asp Pro Asn Gln Gln Pro Lys Lys
             20                  25                  30

Lys Phe Thr Ile Ile Lys Gln Val Asn Met Ile Ala Arg Thr Ala Ile
         35                  40                  45

Asp Asp Cys Ile Asn Arg Leu Gly Pro Asp Val Val Thr Met Ser Ser
     50                  55                  60
```

```
Glu Asp Ile Ala Asp Gln Val Val Asn Ser Ile Asn Val Ala Ile Ala
 65                  70                  75                  80

Arg Glu Asn Thr Arg Ala Gln Asp Ala Asn Ala Ala Val Arg Tyr Thr
                85                  90                  95

Pro Ile Phe Lys Leu Asp Phe Ser His Val Ala Val Leu Met Arg Arg
            100                 105                 110

Leu His Val Ile Ile Asn Ile Ala Pro Ser His Asn Ser Asp Pro Asp
        115                 120                 125

Ser Asp Met Leu Ala Ile Tyr Asp Pro Asn Pro Arg Ser Glu His Tyr
    130                 135                 140

Gly Ile Tyr Arg Thr Ser Glu Ala Glu Ile Arg Arg Val Ala Arg Glu
145                 150                 155                 160

Tyr Cys Pro Asp Leu Thr Ser Ala Gln Phe Arg Glu Leu Gln Met Ala
                165                 170                 175

Leu Ser Asp Ala Ala Pro Arg Lys Val Arg His Lys Gln Arg Asp Leu
            180                 185                 190

Ile Pro Val Lys Asn Gly Ile Phe Asn Tyr Ser Thr Lys Gln Leu Glu
        195                 200                 205

Pro Phe Ser Gln Glu Phe Val Phe Leu Ala Lys Ser Ala Val Asn Tyr
    210                 215                 220

Asn Pro Asn Ala Gln Asn Pro Val Ile Thr His Pro Gln Asp Gly Ser
225                 230                 235                 240

Val Trp Asp Val Glu Ser Trp Met Asn Asp Leu Ser Asp Asp Pro Glu
                245                 250                 255

Val Val Asn Leu Leu Trp Glu Ile Ile Gly Ala Ile Val Arg Pro Tyr
            260                 265                 270

Val Ser Trp Asn Lys Ser Ala Trp Phe Tyr Ser Glu Ala Gly Asn Asn
        275                 280                 285

Gly Lys Gly Thr Leu Val Glu Leu Met Arg Asn Ile Leu Gly Ala Glu
    290                 295                 300

Ala Tyr Thr Ser Ile Gln Leu Ser Asp Phe Ser Lys Glu Phe His Leu
305                 310                 315                 320

Glu Ser Leu Thr Arg Ala Gln Ala Ile Leu Val Asp Glu Asn Asp Val
                325                 330                 335

Gly Ala Phe Leu Glu Lys Ser Ala Asn Leu Lys Ala Ile Val Thr Asn
            340                 345                 350

Asp Val Ile Ser Ile Asn Arg Lys His Lys Thr Met Leu Ser Tyr Gln
        355                 360                 365

Phe Tyr Gly Phe Met Val Gln Cys Ile Asn Gly Phe Pro Lys Val Lys
    370                 375                 380
```

```
Asp Gln Ser Glu Ser Phe Phe Arg Arg Gln Leu Phe Val Pro Phe Glu
385                 390                 395                 400

Lys Ser Phe Thr Gly Ala Glu Arg Lys Tyr Ile Lys Asp Asp Tyr Met
                405                 410                 415

Ser Arg Thr Asp Val Leu Glu Tyr Val Leu His Arg Val Leu His Met
            420                 425                 430

Asn Tyr Asp Asn Leu Ser Thr Pro Ala Ala Ala Leu Ala Val Leu Asp
        435                 440                 445

Glu Tyr Lys Glu Phe Val Asp Pro Val Arg Ala Phe Trp Asn Glu Phe
    450                 455                 460

Ser Asp Gln Phe Val Trp Asp Leu Leu Pro Leu Gln Phe Leu Tyr Glu
465                 470                 475                 480

Phe Tyr Arg Lys Trp Phe Asp Arg Asp Ser Pro Ser Gly Ser Val Leu
                485                 490                 495

Gly Lys Arg Ser Phe Ile Gln Lys Ile Thr Thr Ile Ala Val Asp Ser
            500                 505                 510

Gly Gln Trp Glu Tyr Pro Leu Thr Ala Gln Arg Pro Gly Gly Asp Met
        515                 520                 525

Ala Val Pro Glu Pro Leu Val Ile Asp Tyr Asp Leu Thr Glu Trp Gln
    530                 535                 540

Asn Ala Thr Val Pro Lys Gly His Val Asn Lys Gly Leu Pro Leu Pro
545                 550                 555                 560

Leu Lys Ala Asn Tyr Arg Gly Leu Leu Arg Lys Pro Leu Thr Thr Pro
                565                 570                 575

Ala Thr Pro Pro Ala Ala Pro Val Asn Pro Thr Pro Pro Thr Pro
            580                 585                 590
```

<210> 1559
<211> 1560
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1537)
<223> RXA00025

<400> 1559

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taaatttctc aatggtgtgg aaacacttgg aaacaagctg cccacaccat ttacgctttt 60

cttgatactt ttcctgatca cggcgctggc ttcatcgatc atg gcg tgg atg aac   115
                                            Met Ala Trp Met Asn
                                              1               5

gta tcc gtg att gtt cca ggc tct gat gag gaa cta ttt gta aaa ggc   163
Val Ser Val Ile Val Pro Gly Ser Asp Glu Glu Leu Phe Val Lys Gly
                10                  15                  20
```

```
ctg ttc acc ggt gaa ggc cta acc tgg ttg act acg aat ctc ggg gca   211
Leu Phe Thr Gly Glu Gly Leu Thr Trp Leu Thr Thr Asn Leu Gly Ala
            25                  30                  35

aac tac atc ggg ttc ccg ccg ttg ctc acc gtg ttg cca att ctg ttg   259
Asn Tyr Ile Gly Phe Pro Pro Leu Leu Thr Val Leu Pro Ile Leu Leu
        40                  45                  50

gca gtg ggt gtt gct gaa cgt tcc ggc atg ttg gct gcg ctg att agg   307
Ala Val Gly Val Ala Glu Arg Ser Gly Met Leu Ala Ala Leu Ile Arg
    55                  60                  65

aaa ctt ttt ggt tcg gcg aaa aag atc gtt ttg cca tat gca gtc ggt   355
Lys Leu Phe Gly Ser Ala Lys Lys Ile Val Leu Pro Tyr Ala Val Gly
70                  75                  80                  85

gtg att ggc gtg acc gcg tcg atc atg gcg gac gct gcc ttc gtg gtg   403
Val Ile Gly Val Thr Ala Ser Ile Met Ala Asp Ala Ala Phe Val Val
                90                  95                  100

gtg cca cct ttg gcc gcg atg gtg ttt aaa gct gct ggt cgg cac cct   451
Val Pro Pro Leu Ala Ala Met Val Phe Lys Ala Ala Gly Arg His Pro
            105                 110                 115

gtg gct ggg cta ttg ggt tcg ttt gca gct gtg ggt gca gga tat tcc   499
Val Ala Gly Leu Leu Gly Ser Phe Ala Ala Val Gly Ala Gly Tyr Ser
        120                 125                 130

aca gcg att gtg ccc acc agc ctt gat gca ctt ttt gcg gga att acc   547
Thr Ala Ile Val Pro Thr Ser Leu Asp Ala Leu Phe Ala Gly Ile Thr
    135                 140                 145

aac gcc gtg atg gag aca ctt cca ggc att gcg aca act gaa gtc aat   595
Asn Ala Val Met Glu Thr Leu Pro Gly Ile Ala Thr Thr Glu Val Asn
150                 155                 160                 165

ccg gtt tct aac tat tac ttc aat att gca tcc tcg att gtg ttg ggt   643
Pro Val Ser Asn Tyr Tyr Phe Asn Ile Ala Ser Ser Ile Val Leu Gly
                170                 175                 180

ctg tta tgt ggt ttc ctc att gat aag gtg ctg gaa cct cgg atg tgg   691
Leu Leu Cys Gly Phe Leu Ile Asp Lys Val Leu Glu Pro Arg Met Trp
            185                 190                 195

cgt cag aaa atc gct acg gag tat gca gaa agc att gaa ccc acc agc   739
Arg Gln Lys Ile Ala Thr Glu Tyr Ala Glu Ser Ile Glu Pro Thr Ser
        200                 205                 210

gca gca gat gat gag gaa atc tct gca acc cta acc gca cag gaa aac   787
Ala Ala Asp Asp Glu Glu Ile Ser Ala Thr Leu Thr Ala Gln Glu Asn
    215                 220                 225

cgc gcg ctg aca att tcc atg tgg acc acc ctg gcg acg gcc atc atc   835
Arg Ala Leu Thr Ile Ser Met Trp Thr Thr Leu Ala Thr Ala Ile Ile
230                 235                 240                 245

gtg ctg gtt gtg gtg ctg att ccg gga tcc cca tgg aga aat gag gat   883
Val Leu Val Val Val Leu Ile Pro Gly Ser Pro Trp Arg Asn Glu Asp
                250                 255                 260

ggt gga ttc ttg cct acc tcg cca ctg ctg agc tct gtg gtg ttt att   931
```

```
Gly Gly Phe Leu Pro Thr Ser Pro Leu Leu Ser Ser Val Val Phe Ile
            265                 270                 275

gta ttt ttg ttt ttc atg gtg atg ggc ctg gcc tac ggc atg gtg gtg   979
Val Phe Leu Phe Phe Met Val Met Gly Leu Ala Tyr Gly Met Val Val
        280                 285                 290

ggc acg atc aag aac atg gat gat gtc gtg aac atg atg ggc gaa gca   1027
Gly Thr Ile Lys Asn Met Asp Asp Val Val Asn Met Met Gly Glu Ala
    295                 300                 305

atc aag gac atg att ggt ttc ttg gtt ttg gcc ttc att ttg gga cag   1075
Ile Lys Asp Met Ile Gly Phe Leu Val Leu Ala Phe Ile Leu Gly Gln
310                 315                 320                 325

ttt gtg gcg ctg ttt aac tgg acg ggc atc ggt acc tgg act gct gtt   1123
Phe Val Ala Leu Phe Asn Trp Thr Gly Ile Gly Thr Trp Thr Ala Val
                330                 335                 340

cag ggt gct gcg gga ttg gaa gcg atc ggg ctt acc gga ttc cct gcg   1171
Gln Gly Ala Ala Gly Leu Glu Ala Ile Gly Leu Thr Gly Phe Pro Ala
            345                 350                 355

atc att gca ttt att att ttg gcg tca tgt ttg aac ctg ctg att att   1219
Ile Ile Ala Phe Ile Ile Leu Ala Ser Cys Leu Asn Leu Leu Ile Ile
        360                 365                 370

tcc ggc tct gcg atg tgg acg ctg atg gct gcg gtg ttc gtc ccg atg   1267
Ser Gly Ser Ala Met Trp Thr Leu Met Ala Ala Val Phe Val Pro Met
    375                 380                 385

ttc gct ctg ctt ggc tat gaa cca tca ttc att cag gca gca ttc cgc   1315
Phe Ala Leu Leu Gly Tyr Glu Pro Ser Phe Ile Gln Ala Ala Phe Arg
390                 395                 400                 405

gtg ggt gac tcg gca act cag gtg atc aca ccg ctg aat ccg tac atg   1363
Val Gly Asp Ser Ala Thr Gln Val Ile Thr Pro Leu Asn Pro Tyr Met
                410                 415                 420

att gtg atc ctc ggt ttg ctc cgt cga tac gaa ccg gat gca ggt tta   1411
Ile Val Ile Leu Gly Leu Leu Arg Arg Tyr Glu Pro Asp Ala Gly Leu
            425                 430                 435

ggc acc ttg atg tca agg ctt atc cca ttt gtg atc cct ttc tgg cta   1459
Gly Thr Leu Met Ser Arg Leu Ile Pro Phe Val Ile Pro Phe Trp Leu
        440                 445                 450

gcc tgg gct aca ttg ttg gca att tgg ttc tac gcc gat ttg ccg ctt   1507
Ala Trp Ala Thr Leu Leu Ala Ile Trp Phe Tyr Ala Asp Leu Pro Leu
    455                 460                 465

gga cct ggc tct gcg atc ttc ctc gaa gga taagttttca tgagtactga     1557
Gly Pro Gly Ser Ala Ile Phe Leu Glu Gly
470                 475

caa                                                               1560
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<210> 1560
<211> 479
<212> PRT

<213> Corynebacterium glutamicum

<400> 1560

```
Met Ala Trp Met Asn Val Ser Val Ile Val Pro Gly Ser Asp Glu Glu
  1               5                  10                  15

Leu Phe Val Lys Gly Leu Phe Thr Gly Glu Gly Leu Thr Trp Leu Thr
             20                  25                  30

Thr Asn Leu Gly Ala Asn Tyr Ile Gly Phe Pro Pro Leu Leu Thr Val
         35                  40                  45

Leu Pro Ile Leu Leu Ala Val Gly Val Ala Glu Arg Ser Gly Met Leu
     50                  55                  60

Ala Ala Leu Ile Arg Lys Leu Phe Gly Ser Ala Lys Lys Ile Val Leu
 65                  70                  75                  80

Pro Tyr Ala Val Gly Val Ile Gly Val Thr Ala Ser Ile Met Ala Asp
                 85                  90                  95

Ala Ala Phe Val Val Val Pro Pro Leu Ala Ala Met Val Phe Lys Ala
            100                 105                 110

Ala Gly Arg His Pro Val Ala Gly Leu Leu Gly Ser Phe Ala Ala Val
        115                 120                 125

Gly Ala Gly Tyr Ser Thr Ala Ile Val Pro Thr Ser Leu Asp Ala Leu
    130                 135                 140

Phe Ala Gly Ile Thr Asn Ala Val Met Glu Thr Leu Pro Gly Ile Ala
145                 150                 155                 160

Thr Thr Glu Val Asn Pro Val Ser Asn Tyr Tyr Phe Asn Ile Ala Ser
                165                 170                 175

Ser Ile Val Leu Gly Leu Leu Cys Gly Phe Leu Ile Asp Lys Val Leu
            180                 185                 190

Glu Pro Arg Met Trp Arg Gln Lys Ile Ala Thr Glu Tyr Ala Glu Ser
        195                 200                 205

Ile Glu Pro Thr Ser Ala Ala Asp Asp Glu Glu Ile Ser Ala Thr Leu
    210                 215                 220

Thr Ala Gln Glu Asn Arg Ala Leu Thr Ile Ser Met Trp Thr Thr Leu
225                 230                 235                 240

Ala Thr Ala Ile Ile Val Leu Val Val Val Leu Ile Pro Gly Ser Pro
                245                 250                 255

Trp Arg Asn Glu Asp Gly Gly Phe Leu Pro Thr Ser Pro Leu Leu Ser
            260                 265                 270

Ser Val Val Phe Ile Val Phe Leu Phe Phe Met Val Met Gly Leu Ala
        275                 280                 285

Tyr Gly Met Val Val Gly Thr Ile Lys Asn Met Asp Asp Val Val Asn
    290                 295                 300

Met Met Gly Glu Ala Ile Lys Asp Met Ile Gly Phe Leu Val Leu Ala
```

```
305                 310                 315                 320

Phe Ile Leu Gly Gln Phe Val Ala Leu Phe Asn Trp Thr Gly Ile Gly
                325                 330                 335

Thr Trp Thr Ala Val Gln Gly Ala Ala Gly Leu Glu Ala Ile Gly Leu
            340                 345                 350

Thr Gly Phe Pro Ala Ile Ile Ala Phe Ile Ile Leu Ala Ser Cys Leu
        355                 360                 365

Asn Leu Leu Ile Ile Ser Gly Ser Ala Met Trp Thr Leu Met Ala Ala
    370                 375                 380

Val Phe Val Pro Met Phe Ala Leu Leu Gly Tyr Glu Pro Ser Phe Ile
385                 390                 395                 400

Gln Ala Ala Phe Arg Val Gly Asp Ser Ala Thr Gln Val Ile Thr Pro
                405                 410                 415

Leu Asn Pro Tyr Met Ile Val Ile Leu Gly Leu Leu Arg Arg Tyr Glu
            420                 425                 430

Pro Asp Ala Gly Leu Gly Thr Leu Met Ser Arg Leu Ile Pro Phe Val
        435                 440                 445

Ile Pro Phe Trp Leu Ala Trp Ala Thr Leu Leu Ala Ile Trp Phe Tyr
    450                 455                 460

Ala Asp Leu Pro Leu Gly Pro Gly Ser Ala Ile Phe Leu Glu Gly
465                 470                 475
```

<210> 1561
<211> 525
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(502)
<223> RXA00031

<400> 1561
cacacatcgc ctcgtcatcc ttagacacgc caaatcttcc tggtccaccg gagtactcga 60

ccataaacgc ccacttaatc aacgtgggct tcgcgatggc gtg gca gct ggc caa 115
                                              Val Ala Ala Gly Gln
                                                1   5

tgg cta gct ggc aac atc ggc gaa att gat cat gtg ctg tgt tca gat 163
Trp Leu Ala Gly Asn Ile Gly Glu Ile Asp His Val Leu Cys Ser Asp
                10   15   20

gcc acc cgc aca caa tta acg tgg gaa cgc gtc cag ctt ggt ggc gca 211
Ala Thr Arg Thr Gln Leu Thr Trp Glu Arg Val Gln Leu Gly Gly Ala
            25   30   35

acc gcc aaa ggc tct agc ttc cac aat gac atc tat gaa aac caa gtg 259
Thr Ala Lys Gly Ser Ser Phe His Asn Asp Ile Tyr Glu Asn Gln Val
        40   45   50
```
```

```
tct gaa ttt aaa cat tta ata aca ggg ctc cca gat gta gtt ggt acc   307
Ser Glu Phe Lys His Leu Ile Thr Gly Leu Pro Asp Val Val Gly Thr
     55                  60                  65

gcc cta ctc atc ggg cac tgg cca ggc gtg gaa gaa cta gcc cat tat   355
Ala Leu Leu Ile Gly His Trp Pro Gly Val Glu Glu Leu Ala His Tyr
 70                  75                  80                  85

ttt ggc atc cgc gat gaa cat ccc ggt tgg gat cag atg gaa gaa aag   403
Phe Gly Ile Arg Asp Glu His Pro Gly Trp Asp Gln Met Glu Glu Lys
                 90                  95                 100

ttt ccc acc agc gcc att gcg gtg ttg gaa ttt aac acc cct tgg tca   451
Phe Pro Thr Ser Ala Ile Ala Val Leu Glu Phe Asn Thr Pro Trp Ser
            105                 110                 115

aaa ctt gag aga aac tct gct cgg ttg aca gat ttt gtc att cca cgg   499
Lys Leu Glu Arg Asn Ser Ala Arg Leu Thr Asp Phe Val Ile Pro Arg
        120                 125                 130

ggt tagttctgct tcaattgaac aat                                    525
Gly
```

<210> 1562
<211> 134
<212> PRT
<213> Corynebacterium glutamicum

<400> 1562

```
Val Ala Ala Gly Gln Trp Leu Ala Gly Asn Ile Gly Glu Ile Asp His
  1               5                  10                  15

Val Leu Cys Ser Asp Ala Thr Arg Thr Gln Leu Thr Trp Glu Arg Val
             20                  25                  30

Gln Leu Gly Gly Ala Thr Ala Lys Gly Ser Ser Phe His Asn Asp Ile
         35                  40                  45

Tyr Glu Asn Gln Val Ser Glu Phe Lys His Leu Ile Thr Gly Leu Pro
     50                  55                  60

Asp Val Val Gly Thr Ala Leu Leu Ile Gly His Trp Pro Gly Val Glu
 65                  70                  75                  80

Glu Leu Ala His Tyr Phe Gly Ile Arg Asp Glu His Pro Gly Trp Asp
                 85                  90                  95

Gln Met Glu Glu Lys Phe Pro Thr Ser Ala Ile Ala Val Leu Glu Phe
            100                 105                 110

Asn Thr Pro Trp Ser Lys Leu Glu Arg Asn Ser Ala Arg Leu Thr Asp
        115                 120                 125

Phe Val Ile Pro Arg Gly
    130
```

<210> 1563

<211> 810
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(787)
<223> RXA00049

<400> 1563
ctgaatcatg attcataaat gaacaagggt tcagatttta caataccccc attccacccc 60

cttatattta agtcaccgca gatcagctaa ggttttccct atg ccc acg cct tcg 115
Met Pro Thr Pro Ser
1 5

cag cac aag gac gct tca aca gca caa acc gac aac cag gta cca act 163
Gln His Lys Asp Ala Ser Thr Ala Gln Thr Asp Asn Gln Val Pro Thr
10 15 20

ggc cgc cgt gca caa aaa cgc gaa caa acc cgc gcg cgc ctg atc act 211
Gly Arg Arg Ala Gln Lys Arg Glu Gln Thr Arg Ala Arg Leu Ile Thr
25 30 35

tcc gct cgc aca ctc atg gca gaa cgg ggt gtc gac aat gta gga ata 259
Ser Ala Arg Thr Leu Met Ala Glu Arg Gly Val Asp Asn Val Gly Ile
40 45 50

gct gaa atc acc gaa ggc gca aac atc gga acg gga acc ttc tac aac 307
Ala Glu Ile Thr Glu Gly Ala Asn Ile Gly Thr Gly Thr Phe Tyr Asn
55 60 65

tac ttc cca gac cgt gaa caa cta ctc caa gct gtc gca gaa gat gcc 355
Tyr Phe Pro Asp Arg Glu Gln Leu Leu Gln Ala Val Ala Glu Asp Ala
70 75 80 85

ttt gaa tcc gtg gga att gcc ctc gac cag gtg cta acc aaa tta gac 403
Phe Glu Ser Val Gly Ile Ala Leu Asp Gln Val Leu Thr Lys Leu Asp
90 95 100

gat ccg gct gaa gta ttt gca ggg tcg ctt cga cat cta gta cgg cac 451
Asp Pro Ala Glu Val Phe Ala Gly Ser Leu Arg His Leu Val Arg His
105 110 115

tcg tta gaa gat cgg att tgg ggc gga ttt ttc ata caa atg ggt gct 499
Ser Leu Glu Asp Arg Ile Trp Gly Gly Phe Phe Ile Gln Met Gly Ala
120 125 130

gct cat ccc gta ctc atg cgc atc cta gga ccc cgc gca cgc cga gat 547
Ala His Pro Val Leu Met Arg Ile Leu Gly Pro Arg Ala Arg Arg Asp
135 140 145

cta ctt cat ggt tta gaa act ggc cga ttc acc atc gaa gat ctg gac 595
Leu Leu His Gly Leu Glu Thr Gly Arg Phe Thr Ile Glu Asp Leu Asp
150 155 160 165

cta gca acc aca tgc act ttt ggt tca ctc atc gca gcg atc caa atg 643
Leu Ala Thr Thr Cys Thr Phe Gly Ser Leu Ile Ala Ala Ile Gln Met
170 175 180

gcg ctt tct gca gat caa gat tcc aac gat gac aaa gat cag att ttc 691

```
Ala Leu Ser Ala Asp Gln Asp Ser Asn Asp Asp Lys Asp Gln Ile Phe
            185                 190                 195

gca gcc gcg atg ctc cgg atg gtg ggt gtt caa gca gca gaa gcc cgg   739
Ala Ala Ala Met Leu Arg Met Val Gly Val Gln Ala Ala Glu Ala Arg
        200                 205                 210

gag atc gct tcg cgt cca ctc ccc gaa ata tcc cca gtc aaa ccg cag   787
Glu Ile Ala Ser Arg Pro Leu Pro Glu Ile Ser Pro Val Lys Pro Gln
    215                 220                 225

tagtgatcgg gcctcaaata aac                                        810


<210> 1564
<211> 229
<212> PRT
<213> Corynebacterium glutamicum

<400> 1564
Met Pro Thr Pro Ser Gln His Lys Asp Ala Ser Thr Ala Gln Thr Asp
  1               5                  10                  15

Asn Gln Val Pro Thr Gly Arg Arg Ala Gln Lys Arg Glu Gln Thr Arg
             20                  25                  30

Ala Arg Leu Ile Thr Ser Ala Arg Thr Leu Met Ala Glu Arg Gly Val
         35                  40                  45

Asp Asn Val Gly Ile Ala Glu Ile Thr Glu Gly Ala Asn Ile Gly Thr
     50                  55                  60

Gly Thr Phe Tyr Asn Tyr Phe Pro Asp Arg Glu Gln Leu Leu Gln Ala
 65                  70                  75                  80

Val Ala Glu Asp Ala Phe Glu Ser Val Gly Ile Ala Leu Asp Gln Val
                 85                  90                  95

Leu Thr Lys Leu Asp Asp Pro Ala Glu Val Phe Ala Gly Ser Leu Arg
            100                 105                 110

His Leu Val Arg His Ser Leu Glu Asp Arg Ile Trp Gly Gly Phe Phe
        115                 120                 125

Ile Gln Met Gly Ala Ala His Pro Val Leu Met Arg Ile Leu Gly Pro
    130                 135                 140

Arg Ala Arg Arg Asp Leu Leu His Gly Leu Glu Thr Gly Arg Phe Thr
145                 150                 155                 160

Ile Glu Asp Leu Asp Leu Ala Thr Thr Cys Thr Phe Gly Ser Leu Ile
                165                 170                 175

Ala Ala Ile Gln Met Ala Leu Ser Ala Asp Gln Asp Ser Asn Asp Asp
            180                 185                 190

Lys Asp Gln Ile Phe Ala Ala Ala Met Leu Arg Met Val Gly Val Gln
        195                 200                 205

Ala Ala Glu Ala Arg Glu Ile Ala Ser Arg Pro Leu Pro Glu Ile Ser
    210                 215                 220
```

Pro Val Lys Pro Gln
225

<210> 1565
<211> 834
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(811)
<223> RXA00052

<400> 1565
agctaaagtt ctaatttcct aaattggtaa agatcggaac tcaaaaatgt cgcttcgaaa 60

gctcacaagc ttaattggca tactggctgt tgttggccta gtg gcg ttt atc ctt 115
Val Ala Phe Ile Leu
1 5

ttc aac ttc gtg aaa aca aac gac gaa aca tcg aat gtc tct cag agc 163
Phe Asn Phe Val Lys Thr Asn Asp Glu Thr Ser Asn Val Ser Gln Ser
10 15 20

gag tca act gca gag aca gtc agc gaa aca aat ggc gtg ctc tcc gac 211
Glu Ser Thr Ala Glu Thr Val Ser Glu Thr Asn Gly Val Leu Ser Asp
25 30 35

ggc gca gaa aac atc gct tct caa tct gat gag agt aaa tcg ggt gta 259
Gly Ala Glu Asn Ile Ala Ser Gln Ser Asp Glu Ser Lys Ser Gly Val
40 45 50

gag att att gat tct gga ttt ggg cag agc tca aat tcg gcg atg gca 307
Glu Ile Ile Asp Ser Gly Phe Gly Gln Ser Ser Asn Ser Ala Met Ala
55 60 65

att gtt att gcc aaa act tct ggt gga agc ctc gca ggg gaa ttt gtt 355
Ile Val Ile Ala Lys Thr Ser Gly Gly Ser Leu Ala Gly Glu Phe Val
70 75 80 85

acg gcg acg gtg aat ttc ctc gat gaa agt ggc gcc gtt gta gcg act 403
Thr Ala Thr Val Asn Phe Leu Asp Glu Ser Gly Ala Val Val Ala Thr
90 95 100

gaa gat caa gta gaa aca ctc agt tgg gaa gac cag gaa ttg gta ttg 451
Glu Asp Gln Val Glu Thr Leu Ser Trp Glu Asp Gln Glu Leu Val Leu
105 110 115

cca gta tct cac tac aag gag gat tca agc cgc cca gaa att aca agc 499
Pro Val Ser His Tyr Lys Glu Asp Ser Ser Arg Pro Glu Ile Thr Ser
120 125 130

att gag gct ttt ctt tca gta acg gat tac ggt tca gga caa cca gat 547
Ile Glu Ala Phe Leu Ser Val Thr Asp Tyr Gly Ser Gly Gln Pro Asp
135 140 145

gaa act gca ttg ccg gtg ttg gaa acc acc gat att tcc aac cca tac 595
Glu Thr Ala Leu Pro Val Leu Glu Thr Thr Asp Ile Ser Asn Pro Tyr
150 155 160 165

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gct ggt agt tac aat gcc tca ttt gcg ttg aaa aat gac tcc tca gat   643
Ala Gly Ser Tyr Asn Ala Ser Phe Ala Leu Lys Asn Asp Ser Ser Asp
                170                 175                 180

gat ttt aag aac ctg aga gtt ggt att gtt tgc tac aac gag caa act   691
Asp Phe Lys Asn Leu Arg Val Gly Ile Val Cys Tyr Asn Glu Gln Thr
            185                 190                 195

gac atc att ggt ggt ggt ttc aaa ttt ccg aac ctg gtt cca gcg ggt   739
Asp Ile Ile Gly Gly Gly Phe Lys Phe Pro Asn Leu Val Pro Ala Gly
        200                 205                 210

ggg agt att cga atg gac gct agt gtg acg gtc tcc gaa atg cca gct   787
Gly Ser Ile Arg Met Asp Ala Ser Val Thr Val Ser Glu Met Pro Ala
    215                 220                 225

tct tgt aag gca tat tta aat cac taatagattc ttaaaaggca gca         834
Ser Cys Lys Ala Tyr Leu Asn His
230                 235
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<210> 1566
<211> 237
<212> PRT
<213> Corynebacterium glutamicum

<400> 1566

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Val Ala Phe Ile Leu Phe Asn Phe Val Lys Thr Asn Asp Glu Thr Ser
  1               5                  10                  15

Asn Val Ser Gln Ser Glu Ser Thr Ala Glu Thr Val Ser Glu Thr Asn
             20                  25                  30

Gly Val Leu Ser Asp Gly Ala Glu Asn Ile Ala Ser Gln Ser Asp Glu
         35                  40                  45

Ser Lys Ser Gly Val Glu Ile Ile Asp Ser Gly Phe Gly Gln Ser Ser
     50                  55                  60

Asn Ser Ala Met Ala Ile Val Ile Ala Lys Thr Ser Gly Gly Ser Leu
 65                  70                  75                  80

Ala Gly Glu Phe Val Thr Ala Thr Val Asn Phe Leu Asp Glu Ser Gly
                 85                  90                  95

Ala Val Val Ala Thr Glu Asp Gln Val Glu Thr Leu Ser Trp Glu Asp
            100                 105                 110

Gln Glu Leu Val Leu Pro Val Ser His Tyr Lys Glu Asp Ser Ser Arg
        115                 120                 125

Pro Glu Ile Thr Ser Ile Glu Ala Phe Leu Ser Val Thr Asp Tyr Gly
    130                 135                 140

Ser Gly Gln Pro Asp Glu Thr Ala Leu Pro Val Leu Glu Thr Thr Asp
145                 150                 155                 160

Ile Ser Asn Pro Tyr Ala Gly Ser Tyr Asn Ala Ser Phe Ala Leu Lys
                165                 170                 175
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Asn Asp Ser Ser Asp Asp Phe Lys Asn Leu Arg Val Gly Ile Val Cys
            180                 185                 190

Tyr Asn Glu Gln Thr Asp Ile Ile Gly Gly Gly Phe Lys Phe Pro Asn
        195                 200                 205

Leu Val Pro Ala Gly Gly Ser Ile Arg Met Asp Ala Ser Val Thr Val
    210                 215                 220

Ser Glu Met Pro Ala Ser Cys Lys Ala Tyr Leu Asn His
225                 230                 235


<210> 1567
<211> 3036
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(3013)
<223> RXA00054

<400> 1567
atgctgagat ccgctgggtg gcaccacacg aattggaatc tttggagtgg gcacctgctg 60

atattcctgc ggtgaaactt ctcgtcgagc agcttgctta atg agc cca ttc gat   115
                                        Met Ser Pro Phe Asp
                                          1               5

tca aag ctt ggt cgc gat acc cat ttt gga ttc ctc gat aag acc act   163
Ser Lys Leu Gly Arg Asp Thr His Phe Gly Phe Leu Asp Lys Thr Thr
                10                  15                  20

gct tcg caa caa ctg ctg aat cct tca ttg att tct aat gag gat ccg   211
Ala Ser Gln Gln Leu Leu Asn Pro Ser Leu Ile Ser Asn Glu Asp Pro
            25                  30                  35

cac acc atg ttg cag gcg atc aag tta gag ctt cgt acc gca cag tct   259
His Thr Met Leu Gln Ala Ile Lys Leu Glu Leu Arg Thr Ala Gln Ser
        40                  45                  50

ttt aca ttt tca gtc gct ttt att tcc agt cgc ggt atc gcg ttg ttg   307
Phe Thr Phe Ser Val Ala Phe Ile Ser Ser Arg Gly Ile Ala Leu Leu
    55                  60                  65

aaa cag gca ttg ttg gac ttc aag ggt aaa gga cga att atc acg tcc   355
Lys Gln Ala Leu Leu Asp Phe Lys Gly Lys Gly Arg Ile Ile Thr Ser
70                  75                  80                  85

cgc tac ctg gat ttc aat gat cca acg atg ttt cgt gag ctt ctt act   403
Arg Tyr Leu Asp Phe Asn Asp Pro Thr Met Phe Arg Glu Leu Leu Thr
                90                  95                  100

ttg gag aac gtg gaa gtc ctc ata cat caa ggc gat ggt ttc cac tcc   451
Leu Glu Asn Val Glu Val Leu Ile His Gln Gly Asp Gly Phe His Ser
            105                 110                 115

aag ggc tac gtt ttc cat cac gac gtg gga atc acc gca gta gtg ggt   499
Lys Gly Tyr Val Phe His His Asp Val Gly Ile Thr Ala Val Val Gly
        120                 125                 130
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agt tcc aac ctc aca gat aat gct ctg ttg gta aac cgg gaa tgg aat   547
Ser Ser Asn Leu Thr Asp Asn Ala Leu Leu Val Asn Arg Glu Trp Asn
    135                 140                 145

ctg aag ttc tct gcc agc aag aat ggc gac att gct ttt caa ctt gat   595
Leu Lys Phe Ser Ala Ser Lys Asn Gly Asp Ile Ala Phe Gln Leu Asp
150                 155                 160                 165

gat gcg att aat cgc caa att gaa cga tcc acg cca ctg acg cct gaa   643
Asp Ala Ile Asn Arg Gln Ile Glu Arg Ser Thr Pro Leu Thr Pro Glu
                170                 175                 180

tgg atc tca gag tat gag gca acc aga cgt gta cct gag cgt ttg gtg   691
Trp Ile Ser Glu Tyr Glu Ala Thr Arg Arg Val Pro Glu Arg Leu Val
            185                 190                 195

tct cag aat att cct ctc gag gat caa agt aac gcc gga aca att gtt   739
Ser Gln Asn Ile Pro Leu Glu Asp Gln Ser Asn Ala Gly Thr Ile Val
        200                 205                 210

cca aac gtc atg cag gaa gag gcc ctc gac gct cta ctt tct ttg acg   787
Pro Asn Val Met Gln Glu Glu Ala Leu Asp Ala Leu Leu Ser Leu Thr
    215                 220                 225

gag aag gga gag aaa cgt ggt gtc att att tct gcg aca gga act ggc   835
Glu Lys Gly Glu Lys Arg Gly Val Ile Ile Ser Ala Thr Gly Thr Gly
230                 235                 240                 245

aag act atc ctg gct gct cta gct aca aga atg ctc aag cct gaa cga   883
Lys Thr Ile Leu Ala Ala Leu Ala Thr Arg Met Leu Lys Pro Glu Arg
                250                 255                 260

gtt ttg ttt gtc gtg cac cgc gaa caa att ctg gat aag gcg cga tcc   931
Val Leu Phe Val Val His Arg Glu Gln Ile Leu Asp Lys Ala Arg Ser
            265                 270                 275

gag ttc atc aaa gtt ctt gaa cgt ccc gct gtt gat ttc gga aaa atg   979
Glu Phe Ile Lys Val Leu Glu Arg Pro Ala Val Asp Phe Gly Lys Met
        280                 285                 290

tct ggc tcg acc aag gag cta gat aag ccg ttt gtg ttt ggc acc atc  1027
Ser Gly Ser Thr Lys Glu Leu Asp Lys Pro Phe Val Phe Gly Thr Ile
    295                 300                 305

caa acg ctg aca aag gaa gct aca ctt tcc cag atc tcc cct act gac  1075
Gln Thr Leu Thr Lys Glu Ala Thr Leu Ser Gln Ile Ser Pro Thr Asp
310                 315                 320                 325

ttt gat tta gtc atc gtc gat gaa gtc cat cgc gcc ggt gcc gaa tcc  1123
Phe Asp Leu Val Ile Val Asp Glu Val His Arg Ala Gly Ala Glu Ser
                330                 335                 340

tat ttg gca ttg ctc aat cat ctg cag cca cag ttt tta ttg ggc ctg  1171
Tyr Leu Ala Leu Leu Asn His Leu Gln Pro Gln Phe Leu Leu Gly Leu
            345                 350                 355

act gct acc cca gag cga act gat gga ttc aat att tat gag ttg ttc  1219
Thr Ala Thr Pro Glu Arg Thr Asp Gly Phe Asn Ile Tyr Glu Leu Phe
        360                 365                 370
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gat ttc aac gtg cca tat gag atc cga ctt caa gct gct tta gaa tcc   1267
Asp Phe Asn Val Pro Tyr Glu Ile Arg Leu Gln Ala Ala Leu Glu Ser
    375                 380                 385

aac atg ctc gta ccg ttt cac tat tac ggt gtc aca gac ttc acg ctt   1315
Asn Met Leu Val Pro Phe His Tyr Tyr Gly Val Thr Asp Phe Thr Leu
390                 395                 400                 405

gat tct gaa aca acg gtg act gat acc tcc aaa cta agt gcc ttg gtg   1363
Asp Ser Glu Thr Thr Val Thr Asp Thr Ser Lys Leu Ser Ala Leu Val
                410                 415                 420

agc gaa gag aga gtc cat cac att ctg gag gcc ctc aaa act tat ggt   1411
Ser Glu Glu Arg Val His His Ile Leu Glu Ala Leu Lys Thr Tyr Gly
            425                 430                 435

cat cca gaa aat gtt cgt gga ctg atc ttc tgt tcc aag act gaa gag   1459
His Pro Glu Asn Val Arg Gly Leu Ile Phe Cys Ser Lys Thr Glu Glu
        440                 445                 450

gct gag gag ctg tca aaa ctt ctc gac cag tcg ttg ttt aat ggc agc   1507
Ala Glu Glu Leu Ser Lys Leu Leu Asp Gln Ser Leu Phe Asn Gly Ser
    455                 460                 465

ttg ctt aaa acc aag gcg ctc tct gcg aag gac tca att ccc tac cgc   1555
Leu Leu Lys Thr Lys Ala Leu Ser Ala Lys Asp Ser Ile Pro Tyr Arg
470                 475                 480                 485

gaa gag gtt gta gct gag ctg gag tcc ggc gac ctg gac tac atc ttg   1603
Glu Glu Val Val Ala Glu Leu Glu Ser Gly Asp Leu Asp Tyr Ile Leu
                490                 495                 500

acg gtt gac atc ttc aat gaa ggc att gat att cct tcg gtg aat caa   1651
Thr Val Asp Ile Phe Asn Glu Gly Ile Asp Ile Pro Ser Val Asn Gln
            505                 510                 515

atc gta atg att cgt agt act caa tca agc att gtg ttt acg cag cag   1699
Ile Val Met Ile Arg Ser Thr Gln Ser Ser Ile Val Phe Thr Gln Gln
        520                 525                 530

ctc ggg cgt gga ctc cga aaa gct gct ggc aaa gac cat ctg cgc gtt   1747
Leu Gly Arg Gly Leu Arg Lys Ala Ala Gly Lys Asp His Leu Arg Val
    535                 540                 545

att gat ttc att ggc aac tac gcg aac aac tat ctc att ccc atc gca   1795
Ile Asp Phe Ile Gly Asn Tyr Ala Asn Asn Tyr Leu Ile Pro Ile Ala
550                 555                 560                 565

ttg ttt ggc gat aat tct cgc aat aag aac agc atc aga cgc cgc ctg   1843
Leu Phe Gly Asp Asn Ser Arg Asn Lys Asn Ser Ile Arg Arg Arg Leu
                570                 575                 580

att gag agc gat att gat gga aca atc tca ggt gtt tca agt gtt aac   1891
Ile Glu Ser Asp Ile Asp Gly Thr Ile Ser Gly Val Ser Ser Val Asn
            585                 590                 595

ttt gat ccc atc gcg cag gag aga att ttt gct gcg ttg aag gct gcg   1939
Phe Asp Pro Ile Ala Gln Glu Arg Ile Phe Ala Ala Leu Lys Ala Ala
        600                 605                 610

aag ttg gac tca aaa gca caa ttc aag cag gat att gtt cag ctt caa   1987
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Lys Leu Asp Ser Lys Ala Gln Phe Lys Gln Asp Ile Val Gln Leu Gln
    615                 620                 625

gat cga ctc aat cat gtg cca gca ctg tta gac ttc gct cgc ttc aat   2035
Asp Arg Leu Asn His Val Pro Ala Leu Leu Asp Phe Ala Arg Phe Asn
630                 635                 640                 645

act gtt gat ccg ttt atc ctt gcc acg cat tct ggc aac tac tgg tcg   2083
Thr Val Asp Pro Phe Ile Leu Ala Thr His Ser Gly Asn Tyr Trp Ser
                650                 655                 660

ctg ctc agt tca gtg aag ttt gtc gat cac gct ccc agc gaa tcg gag   2131
Leu Leu Ser Ser Val Lys Phe Val Asp His Ala Pro Ser Glu Ser Glu
            665                 670                 675

aag tac ttt ctg gat ttc ctt acc gga gag ctt ctt aac ggc aag cga   2179
Lys Tyr Phe Leu Asp Phe Leu Thr Gly Glu Leu Leu Asn Gly Lys Arg
        680                 685                 690

cct cat gag ctg ttg ctg atc cag gaa cta atg aaa cag cct gaa act   2227
Pro His Glu Leu Leu Leu Ile Gln Glu Leu Met Lys Gln Pro Glu Thr
    695                 700                 705

tct act gaa gaa ttc cgt aag ctc ttg cag gcc caa tcg act agt tca   2275
Ser Thr Glu Glu Phe Arg Lys Leu Leu Gln Ala Gln Ser Thr Ser Ser
710                 715                 720                 725

gat gag caa aca atc aac tcg gtt gaa agg att ttg agc caa gaa ttc   2323
Asp Glu Gln Thr Ile Asn Ser Val Glu Arg Ile Leu Ser Gln Glu Phe
                730                 735                 740

tat acg gga cca aac cgc aag aag ttt ggc gaa cat ccg atc ctc tct   2371
Tyr Thr Gly Pro Asn Arg Lys Lys Phe Gly Glu His Pro Ile Leu Ser
            745                 750                 755

gtt caa aac cgc acc tac tct ttt act ccc gag ttc cga cgt gcc ctc   2419
Val Gln Asn Arg Thr Tyr Ser Phe Thr Pro Glu Phe Arg Arg Ala Leu
        760                 765                 770

gac gaa agc cta gaa gtg acg gac cga gat gag gct gct cag aat ttt   2467
Asp Glu Ser Leu Glu Val Thr Asp Arg Asp Glu Ala Ala Gln Asn Phe
    775                 780                 785

aag ttt cac gtc caa gac atc atc gac act ggt ttg ttt atc gcc aga   2515
Lys Phe His Val Gln Asp Ile Ile Asp Thr Gly Leu Phe Ile Ala Arg
790                 795                 800                 805

aac aat gga ttt tgg caa gga aac ctc gtt gtt ggc gag aga tac tcc   2563
Asn Asn Gly Phe Trp Gln Gly Asn Leu Val Val Gly Glu Arg Tyr Ser
                810                 815                 820

cga cga gat gtc tgc cga att ctc aat tgg gaa cga aac aac gag agc   2611
Arg Arg Asp Val Cys Arg Ile Leu Asn Trp Glu Arg Asn Asn Glu Ser
            825                 830                 835

acg att tat gga tac aaa gtg gac agt tac aca tct act tgc cca atc   2659
Thr Ile Tyr Gly Tyr Lys Val Asp Ser Tyr Thr Ser Thr Cys Pro Ile
        840                 845                 850

ttt gtg acc tat cac aag gct gat gat gta tcc gaa agt act cgt tac   2707
Phe Val Thr Tyr His Lys Ala Asp Asp Val Ser Glu Ser Thr Arg Tyr
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    855                 860                 865

cag gat gaa ctc gtc gat ccg aat acc ctt cat tgg tat tcc cgc ggc   2755
Gln Asp Glu Leu Val Asp Pro Asn Thr Leu His Trp Tyr Ser Arg Gly
870                 875                 880                 885

aac cga aag atc acg tct aat gag atc aag ccc atc gct gcg aat gct   2803
Asn Arg Lys Ile Thr Ser Asn Glu Ile Lys Pro Ile Ala Ala Asn Ala
                890                 895                 900

gtg gat ctt cat gtt ttt gtg aag aag gac gat gcc gaa ggc ctt gat   2851
Val Asp Leu His Val Phe Val Lys Lys Asp Asp Ala Glu Gly Leu Asp
            905                 910                 915

ttc ttc tac ctt ggt caa gcg cat tca gaa aac agc aaa cag tca tcg   2899
Phe Phe Tyr Leu Gly Gln Ala His Ser Glu Asn Ser Lys Gln Ser Ser
        920                 925                 930

atg ccc gga aac aaa gga gtt gtg caa ccg gtg gtc aca atg gat cta   2947
Met Pro Gly Asn Lys Gly Val Val Gln Pro Val Val Thr Met Asp Leu
    935                 940                 945

cag ttc gac aca ccc gtc gaa caa agc ctg ttt gag tac ctg agc aca   2995
Gln Phe Asp Thr Pro Val Glu Gln Ser Leu Phe Glu Tyr Leu Ser Thr
950                 955                 960                 965

aat ctc gcc gta acg gag taaccaccgc aaccaagcgt cga                3036
Asn Leu Ala Val Thr Glu
                970
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<210> 1568
<211> 971
<212> PRT
<213> Corynebacterium glutamicum

<400> 1568

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Met Ser Pro Phe Asp Ser Lys Leu Gly Arg Asp Thr His Phe Gly Phe
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Leu Asp Lys Thr Thr Ala Ser Gln Gln Leu Leu Asn Pro Ser Leu Ile
             20                  25                  30

Ser Asn Glu Asp Pro His Thr Met Leu Gln Ala Ile Lys Leu Glu Leu
         35                  40                  45

Arg Thr Ala Gln Ser Phe Thr Phe Ser Val Ala Phe Ile Ser Ser Arg
     50                  55                  60

Gly Ile Ala Leu Leu Lys Gln Ala Leu Leu Asp Phe Lys Gly Lys Gly
 65                  70                  75                  80

Arg Ile Ile Thr Ser Arg Tyr Leu Asp Phe Asn Asp Pro Thr Met Phe
                 85                  90                  95

Arg Glu Leu Leu Thr Leu Glu Asn Val Glu Val Leu Ile His Gln Gly
            100                 105                 110

Asp Gly Phe His Ser Lys Gly Tyr Val Phe His His Asp Val Gly Ile
        115                 120                 125
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Thr Ala Val Val Gly Ser Ser Asn Leu Thr Asp Asn Ala Leu Leu Val
    130                 135                 140

Asn Arg Glu Trp Asn Leu Lys Phe Ser Ala Ser Lys Asn Gly Asp Ile
145                 150                 155                 160

Ala Phe Gln Leu Asp Asp Ala Ile Asn Arg Gln Ile Glu Arg Ser Thr
                165                 170                 175

Pro Leu Thr Pro Glu Trp Ile Ser Glu Tyr Glu Ala Thr Arg Arg Val
            180                 185                 190

Pro Glu Arg Leu Val Ser Gln Asn Ile Pro Leu Glu Asp Gln Ser Asn
        195                 200                 205

Ala Gly Thr Ile Val Pro Asn Val Met Gln Glu Glu Ala Leu Asp Ala
    210                 215                 220

Leu Leu Ser Leu Thr Glu Lys Gly Glu Lys Arg Gly Val Ile Ile Ser
225                 230                 235                 240

Ala Thr Gly Thr Gly Lys Thr Ile Leu Ala Ala Leu Ala Thr Arg Met
                245                 250                 255

Leu Lys Pro Glu Arg Val Leu Phe Val Val His Arg Glu Gln Ile Leu
            260                 265                 270

Asp Lys Ala Arg Ser Glu Phe Ile Lys Val Leu Glu Arg Pro Ala Val
        275                 280                 285

Asp Phe Gly Lys Met Ser Gly Ser Thr Lys Glu Leu Asp Lys Pro Phe
    290                 295                 300

Val Phe Gly Thr Ile Gln Thr Leu Thr Lys Glu Ala Thr Leu Ser Gln
305                 310                 315                 320

Ile Ser Pro Thr Asp Phe Asp Leu Val Ile Val Asp Glu Val His Arg
                325                 330                 335

Ala Gly Ala Glu Ser Tyr Leu Ala Leu Leu Asn His Leu Gln Pro Gln
            340                 345                 350

Phe Leu Leu Gly Leu Thr Ala Thr Pro Glu Arg Thr Asp Gly Phe Asn
        355                 360                 365

Ile Tyr Glu Leu Phe Asp Phe Asn Val Pro Tyr Glu Ile Arg Leu Gln
    370                 375                 380

Ala Ala Leu Glu Ser Asn Met Leu Val Pro Phe His Tyr Tyr Gly Val
385                 390                 395                 400

Thr Asp Phe Thr Leu Asp Ser Glu Thr Thr Val Thr Asp Thr Ser Lys
                405                 410                 415

Leu Ser Ala Leu Val Ser Glu Glu Arg Val His His Ile Leu Glu Ala
            420                 425                 430

Leu Lys Thr Tyr Gly His Pro Glu Asn Val Arg Gly Leu Ile Phe Cys
        435                 440                 445

Ser Lys Thr Glu Glu Ala Glu Glu Leu Ser Lys Leu Leu Asp Gln Ser
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    450                 455                 460

Leu Phe Asn Gly Ser Leu Leu Lys Thr Lys Ala Leu Ser Ala Lys Asp
465                 470                 475                 480

Ser Ile Pro Tyr Arg Glu Glu Val Val Ala Glu Leu Glu Ser Gly Asp
                485                 490                 495

Leu Asp Tyr Ile Leu Thr Val Asp Ile Phe Asn Glu Gly Ile Asp Ile
            500                 505                 510

Pro Ser Val Asn Gln Ile Val Met Ile Arg Ser Thr Gln Ser Ser Ile
        515                 520                 525

Val Phe Thr Gln Gln Leu Gly Arg Gly Leu Arg Lys Ala Ala Gly Lys
    530                 535                 540

Asp His Leu Arg Val Ile Asp Phe Ile Gly Asn Tyr Ala Asn Asn Tyr
545                 550                 555                 560

Leu Ile Pro Ile Ala Leu Phe Gly Asp Asn Ser Arg Asn Lys Asn Ser
                565                 570                 575

Ile Arg Arg Arg Leu Ile Glu Ser Asp Ile Asp Gly Thr Ile Ser Gly
            580                 585                 590

Val Ser Ser Val Asn Phe Asp Pro Ile Ala Gln Glu Arg Ile Phe Ala
        595                 600                 605

Ala Leu Lys Ala Ala Lys Leu Asp Ser Lys Ala Gln Phe Lys Gln Asp
    610                 615                 620

Ile Val Gln Leu Gln Asp Arg Leu Asn His Val Pro Ala Leu Leu Asp
625                 630                 635                 640

Phe Ala Arg Phe Asn Thr Val Asp Pro Phe Ile Leu Ala Thr His Ser
                645                 650                 655

Gly Asn Tyr Trp Ser Leu Leu Ser Ser Val Lys Phe Val Asp His Ala
            660                 665                 670

Pro Ser Glu Ser Glu Lys Tyr Phe Leu Asp Phe Leu Thr Gly Glu Leu
        675                 680                 685

Leu Asn Gly Lys Arg Pro His Glu Leu Leu Leu Ile Gln Glu Leu Met
    690                 695                 700

Lys Gln Pro Glu Thr Ser Thr Glu Glu Phe Arg Lys Leu Leu Gln Ala
705                 710                 715                 720

Gln Ser Thr Ser Ser Asp Glu Gln Thr Ile Asn Ser Val Glu Arg Ile
                725                 730                 735

Leu Ser Gln Glu Phe Tyr Thr Gly Pro Asn Arg Lys Lys Phe Gly Glu
            740                 745                 750

His Pro Ile Leu Ser Val Gln Asn Arg Thr Tyr Ser Phe Thr Pro Glu
        755                 760                 765

Phe Arg Arg Ala Leu Asp Glu Ser Leu Glu Val Thr Asp Arg Asp Glu
    770                 775                 780
```

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Ala Ala Gln Asn Phe Lys Phe His Val Gln Asp Ile Ile Asp Thr Gly
785                 790                 795                 800

Leu Phe Ile Ala Arg Asn Asn Gly Phe Trp Gln Gly Asn Leu Val Val
                805                 810                 815

Gly Glu Arg Tyr Ser Arg Arg Asp Val Cys Arg Ile Leu Asn Trp Glu
            820                 825                 830

Arg Asn Asn Glu Ser Thr Ile Tyr Gly Tyr Lys Val Asp Ser Tyr Thr
        835                 840                 845

Ser Thr Cys Pro Ile Phe Val Thr Tyr His Lys Ala Asp Asp Val Ser
    850                 855                 860

Glu Ser Thr Arg Tyr Gln Asp Glu Leu Val Asp Pro Asn Thr Leu His
865                 870                 875                 880

Trp Tyr Ser Arg Gly Asn Arg Lys Ile Thr Ser Asn Glu Ile Lys Pro
                885                 890                 895

Ile Ala Ala Asn Ala Val Asp Leu His Val Phe Val Lys Lys Asp Asp
            900                 905                 910

Ala Glu Gly Leu Asp Phe Phe Tyr Leu Gly Gln Ala His Ser Glu Asn
        915                 920                 925

Ser Lys Gln Ser Ser Met Pro Gly Asn Lys Gly Val Val Gln Pro Val
    930                 935                 940

Val Thr Met Asp Leu Gln Phe Asp Thr Pro Val Glu Gln Ser Leu Phe
945                 950                 955                 960

Glu Tyr Leu Ser Thr Asn Leu Ala Val Thr Glu
                965                 970
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<210> 1569
<211> 687
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(664)
<223> RXA00058

<400> 1569

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atcactaggc tatcttccgg ttcacctgaa gttagtaaca caccggtcac agaagttccg 60

gctcgtgtaa tctccgctta tctagctcaa aggaatactt atg aag ttc ttc ggg   115
                                            Met Lys Phe Phe Gly
                                              1               5

ttt tat cgt cct att gct tta att gct ggc att acc gtt tca gca tct   163
Phe Tyr Arg Pro Ile Ala Leu Ile Ala Gly Ile Thr Val Ser Ala Ser
                 10                  15                  20

att ctc aca tcc gta gct act gca gct gaa tct cca act agc ttt caa   211
Ile Leu Thr Ser Val Ala Thr Ala Ala Glu Ser Pro Thr Ser Phe Gln
```

```
            25                  30                  35

gcg att aca cct gca ttc tct tca tca tcg gct cca gaa gca gac gca   259
Ala Ile Thr Pro Ala Phe Ser Ser Ser Ser Ala Pro Glu Ala Asp Ala
         40                  45                  50

gaa gca aac acc agt gaa gct acc gca gac ctg ctt tac gtg gca gaa   307
Glu Ala Asn Thr Ser Glu Ala Thr Ala Asp Leu Leu Tyr Val Ala Glu
     55                  60                  65

aac caa cta ctt att aag ctt tct aac gcc gtc gtc gaa gat gtt aac   355
Asn Gln Leu Leu Ile Lys Leu Ser Asn Ala Val Val Glu Asp Val Asn
 70                  75                  80                  85

ggc gaa atc tta atg aaa gat aat aag ggc act ctt ctg gag aat ttg   403
Gly Glu Ile Leu Met Lys Asp Asn Lys Gly Thr Leu Leu Glu Asn Leu
                 90                  95                 100

aca gct gaa ctt caa gcc caa cca ggc ttc tca atc gag aaa gtc gat   451
Thr Ala Glu Leu Gln Ala Gln Pro Gly Phe Ser Ile Glu Lys Val Asp
            105                 110                 115

tcc cat act gct ttg ttg acc atg aat cca gat gag gtg cca gat tta   499
Ser His Thr Ala Leu Leu Thr Met Asn Pro Asp Glu Val Pro Asp Leu
        120                 125                 130

cag gac tgg cga tgc gga gtc ggc gct ttg tca ggc ggg gta gca ggt   547
Gln Asp Trp Arg Cys Gly Val Gly Ala Leu Ser Gly Gly Val Ala Gly
    135                 140                 145

gtg gtg gca act ggt cta gct ctc gcc gct ttg gga gtt gcc aca ggt   595
Val Val Ala Thr Gly Leu Ala Leu Ala Ala Leu Gly Val Ala Thr Gly
150                 155                 160                 165

ggc acg ggg ttt gct gtg ctt gca gca ggg gga ctt gct gga tat ggc   643
Gly Thr Gly Phe Ala Val Leu Ala Ala Gly Gly Leu Ala Gly Tyr Gly
                170                 175                 180

act ggc gct gtc gcc aac tgc taaggagaaa taatgggaat tgt             687
Thr Gly Ala Val Ala Asn Cys
            185
```

<210> 1570
<211> 188
<212> PRT
<213> Corynebacterium glutamicum

<400> 1570

```
Met Lys Phe Phe Gly Phe Tyr Arg Pro Ile Ala Leu Ile Ala Gly Ile
  1               5                  10                  15

Thr Val Ser Ala Ser Ile Leu Thr Ser Val Ala Thr Ala Ala Glu Ser
             20                  25                  30

Pro Thr Ser Phe Gln Ala Ile Thr Pro Ala Phe Ser Ser Ser Ser Ala
         35                  40                  45

Pro Glu Ala Asp Ala Glu Ala Asn Thr Ser Glu Ala Thr Ala Asp Leu
     50                  55                  60
```

```
Leu Tyr Val Ala Glu Asn Gln Leu Leu Ile Lys Leu Ser Asn Ala Val
 65                  70                  75                  80

Val Glu Asp Val Asn Gly Glu Ile Leu Met Lys Asp Asn Lys Gly Thr
                85                  90                  95

Leu Leu Glu Asn Leu Thr Ala Glu Leu Gln Ala Gln Pro Gly Phe Ser
            100                 105                 110

Ile Glu Lys Val Asp Ser His Thr Ala Leu Leu Thr Met Asn Pro Asp
        115                 120                 125

Glu Val Pro Asp Leu Gln Asp Trp Arg Cys Gly Val Gly Ala Leu Ser
    130                 135                 140

Gly Gly Val Ala Gly Val Val Ala Thr Gly Leu Ala Leu Ala Ala Leu
145                 150                 155                 160

Gly Val Ala Thr Gly Gly Thr Gly Phe Ala Val Leu Ala Ala Gly Gly
                165                 170                 175

Leu Ala Gly Tyr Gly Thr Gly Ala Val Ala Asn Cys
            180                 185
```

Application Filed on 2004-12-29 by BGI-SHENZHEN

<210> 1571
<211> 405
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(382)
<223> RXA00059

<400> 1571

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ctggcaggcg attgttctct tactacttgc gctaggtaca ggtggtgcct atctgctggc 60

cggtggtgat gtcactcaaa ctgcccgact ggtgttgtgg gtg ttg acc gga atc   115
                                              Val Leu Thr Gly Ile
                                                1               5

tta ctg gct atg gtc tct acc gcc cta cga atc cgc ttc gga tca ggg   163
Leu Leu Ala Met Val Ser Thr Ala Leu Arg Ile Arg Phe Gly Ser Gly
                10                  15                  20

gta gct atc gct gca acc gtg ctg tgg aca gtt atc tca ata acc ttg   211
Val Ala Ile Ala Ala Thr Val Leu Trp Thr Val Ile Ser Ile Thr Leu
            25                  30                  35

ggc gga gat gtg cta gcc gag acc atg ctc tgg ctt gta gca gta cca   259
Gly Gly Asp Val Leu Ala Glu Thr Met Leu Trp Leu Val Ala Val Pro
        40                  45                  50

tcc tgg cca gaa aca gcg gat act act acc cgc ttc ctt att gcg atg   307
Ser Trp Pro Glu Thr Ala Asp Thr Thr Thr Arg Phe Leu Ile Ala Met
    55                  60                  65

cta ctg cag gca gtt ctt atc acc ggc agc act atc tgg gct atc cga   355
Leu Leu Gln Ala Val Leu Ile Thr Gly Ser Thr Ile Trp Ala Ile Arg
70                  75                  80                  85
```

```
gag atc cgg gat tca gag cgc cgt ggc taagttcagc acctccgaca          402
Glu Ile Arg Asp Ser Glu Arg Arg Gly
                 90

acg                                                                405


<210> 1572
<211> 94
<212> PRT
<213> Corynebacterium glutamicum

<400> 1572
Val Leu Thr Gly Ile Leu Leu Ala Met Val Ser Thr Ala Leu Arg Ile
  1               5                  10                  15

Arg Phe Gly Ser Gly Val Ala Ile Ala Ala Thr Val Leu Trp Thr Val
             20                  25                  30

Ile Ser Ile Thr Leu Gly Gly Asp Val Leu Ala Glu Thr Met Leu Trp
         35                  40                  45

Leu Val Ala Val Pro Ser Trp Pro Glu Thr Ala Asp Thr Thr Thr Arg
     50                  55                  60

Phe Leu Ile Ala Met Leu Leu Gln Ala Val Leu Ile Thr Gly Ser Thr
 65                  70                  75                  80

Ile Trp Ala Ile Arg Glu Ile Arg Asp Ser Glu Arg Arg Gly
                 85                  90


<210> 1573
<211> 396
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(373)
<223> RXA00065

<400> 1573
atgcttctca gacgcctccc tctccttcaa atccgccacc gattccagcg tcactcccat 60

gcatgcccaa ccgggacaga tcttgccgtg cgtaggaatt atg gcg aat ctt ccc   115
                                        Met Ala Asn Leu Pro
                                          1               5

caa gag ggt ttt tct gtg gtg cac gga att ttg gcg gat ccc cgc att   163
Gln Glu Gly Phe Ser Val Val His Gly Ile Leu Ala Asp Pro Arg Ile
                 10                  15                  20

tgg ggc ccg gag att ccg tat gtt cgt gaa gaa gca ggt caa gta aat   211
Trp Gly Pro Glu Ile Pro Tyr Val Arg Glu Glu Ala Gly Gln Val Asn
             25                  30                  35

gtg gaa gca ccc gac gag gct ggc gat cta gcc cga ttg acg ttg cct   259
Val Glu Ala Pro Asp Glu Ala Gly Asp Leu Ala Arg Leu Thr Leu Pro
         40                  45                  50
```

```
ctg cag ttg atc ctg ctc acg gag gaa gag ttt gcc atc gct ctc aac   307
Leu Gln Leu Ile Leu Leu Thr Glu Glu Glu Phe Ala Ile Ala Leu Asn
     55                  60                  65

gag ggc agc gac gtc atg ttc gaa cga atg gcg gag caa gaa gtc gat   355
Glu Gly Ser Asp Val Met Phe Glu Arg Met Ala Glu Gln Glu Val Asp
 70                  75                  80                  85

ctt ctg gat ctg aaa cgt taagacggta ggctcaattc cgt                 396
Leu Leu Asp Leu Lys Arg
                 90
```

<210> 1574
<211> 91
<212> PRT
<213> Corynebacterium glutamicum

<400> 1574

```
Met Ala Asn Leu Pro Gln Glu Gly Phe Ser Val Val His Gly Ile Leu
  1               5                  10                  15

Ala Asp Pro Arg Ile Trp Gly Pro Glu Ile Pro Tyr Val Arg Glu Glu
             20                  25                  30

Ala Gly Gln Val Asn Val Glu Ala Pro Asp Glu Ala Gly Asp Leu Ala
         35                  40                  45

Arg Leu Thr Leu Pro Leu Gln Leu Ile Leu Leu Thr Glu Glu Glu Phe
     50                  55                  60

Ala Ile Ala Leu Asn Glu Gly Ser Asp Val Met Phe Glu Arg Met Ala
 65                  70                  75                  80

Glu Gln Glu Val Asp Leu Leu Asp Leu Lys Arg
                 85                  90
```

<210> 1575
<211> 705
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(682)
<223> RXA00068

<400> 1575

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ggctgctaaa cggcaaccaa tagagcgata attcgctaag gcgaatgtaa tcgcagcaac 60

atatagcacc ggcttaacag gccggtgcta ttctgttcgc atg act tcg aag gat   115
                                            Met Thr Ser Lys Asp
                                              1               5

ctg att gtg acc tcc tat acg tct tgg ggc aag cgt ttc aag aat gac   163
Leu Ile Val Thr Ser Tyr Thr Ser Trp Gly Lys Arg Phe Lys Asn Asp
                 10                  15                  20

ggg aag ctt ttt att aac cta ctt cgc agc acc act gat agt gct gat   211
```

```
Gly Lys Leu Phe Ile Asn Leu Leu Arg Ser Thr Thr Asp Ser Ala Asp
            25                  30                  35

gaa aag gtt tta gcc act ttc ggt gaa gtt ccc agc aaa tca ttt gaa   259
Glu Lys Val Leu Ala Thr Phe Gly Glu Val Pro Ser Lys Ser Phe Glu
         40                  45                  50

acc acc gca acg gtt gat gag cag cag tgg gaa ctg tcc ttc agt att   307
Thr Thr Ala Thr Val Asp Glu Gln Gln Trp Glu Leu Ser Phe Ser Ile
     55                  60                  65

gat gga acg gca act gcc aag ctt cct gat ggt cgt gtg ttc agc gcg   355
Asp Gly Thr Ala Thr Ala Lys Leu Pro Asp Gly Arg Val Phe Ser Ala
 70                  75                  80                  85

aat gca ggt gag aag acc ttt acc aag tcc aag cgg att gaa atc gac   403
Asn Ala Gly Glu Lys Thr Phe Thr Lys Ser Lys Arg Ile Glu Ile Asp
                 90                  95                 100

atg gac ggc acc gcg atg gct gct gtt aat gaa gat aaa aac aat tgg   451
Met Asp Gly Thr Ala Met Ala Ala Val Asn Glu Asp Lys Asn Asn Trp
            105                 110                 115

att atc gac gat tct gaa gag aat aaa gtc gct cag ttt acc ggt atg   499
Ile Ile Asp Asp Ser Glu Glu Asn Lys Val Ala Gln Phe Thr Gly Met
        120                 125                 130

aac aac ggt gtg cgt cgc gcg att gtg gag ttt gag cct gac gta gaa   547
Asn Asn Gly Val Arg Arg Ala Ile Val Glu Phe Glu Pro Asp Val Glu
    135                 140                 145

gtc acc cag gag cag gaa att ttc ttg tcg tgg gtt gct cgg aaa act   595
Val Thr Gln Glu Gln Glu Ile Phe Leu Ser Trp Val Ala Arg Lys Thr
150                 155                 160                 165

ctg gaa tcc cgc atg ttg ggc tcc agt tgg gga ctg act ctg ttt ttg   643
Leu Glu Ser Arg Met Leu Gly Ser Ser Trp Gly Leu Thr Leu Phe Leu
                170                 175                 180

atc att ttg acg cca atc att att ttc ctc act ttc agc taaaaggacc    692
Ile Ile Leu Thr Pro Ile Ile Ile Phe Leu Thr Phe Ser
            185                 190

atgcaatggt aga                                                   705


<210> 1576
<211> 194
<212> PRT
<213> Corynebacterium glutamicum

<400> 1576
Met Thr Ser Lys Asp Leu Ile Val Thr Ser Tyr Thr Ser Trp Gly Lys
  1               5                  10                  15

Arg Phe Lys Asn Asp Gly Lys Leu Phe Ile Asn Leu Leu Arg Ser Thr
            20                  25                  30

Thr Asp Ser Ala Asp Glu Lys Val Leu Ala Thr Phe Gly Glu Val Pro
        35                  40                  45
```

```
Ser Lys Ser Phe Glu Thr Thr Ala Thr Val Asp Glu Gln Gln Trp Glu
     50                  55                  60

Leu Ser Phe Ser Ile Asp Gly Thr Ala Thr Ala Lys Leu Pro Asp Gly
 65                  70                  75                  80

Arg Val Phe Ser Ala Asn Ala Gly Glu Lys Thr Phe Thr Lys Ser Lys
                85                  90                  95

Arg Ile Glu Ile Asp Met Asp Gly Thr Ala Met Ala Ala Val Asn Glu
            100                 105                 110

Asp Lys Asn Asn Trp Ile Ile Asp Asp Ser Glu Glu Asn Lys Val Ala
        115                 120                 125

Gln Phe Thr Gly Met Asn Asn Gly Val Arg Arg Ala Ile Val Glu Phe
    130                 135                 140

Glu Pro Asp Val Glu Val Thr Gln Glu Gln Glu Ile Phe Leu Ser Trp
145                 150                 155                 160

Val Ala Arg Lys Thr Leu Glu Ser Arg Met Leu Gly Ser Ser Trp Gly
                165                 170                 175

Leu Thr Leu Phe Leu Ile Ile Leu Thr Pro Ile Ile Ile Phe Leu Thr
            180                 185                 190

Phe Ser
```

Sequence Listing - 2004-12-22 - 13:37:40

<210> 1577
<211> 345
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(322)
<223> RXA00079

<400> 1577

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gatagcgcgc gatcttccta ggctgcccgc ttgggcttca ggtttagcaa gcgggacgct 60

ttcgcttatc gacgccaact ccctccattt ggaatccccc atg ggc cta gtt cac   115
                                              Met Gly Leu Val His
                                                1               5

acc gaa ttc acc cca ata aac acc tac gga atc ctc gac cac gta gtc   163
Thr Glu Phe Thr Pro Ile Asn Thr Tyr Gly Ile Leu Asp His Val Val
                10                  15                  20

acc ctc ccc gac gga act aaa gtg ctc aac cct ttc cga gtc atc ccc   211
Thr Leu Pro Asp Gly Thr Lys Val Leu Asn Pro Phe Arg Val Ile Pro
            25                  30                  35

cac gac acc ggc tcc gaa ctc att ttc acc gtc cgc ccc aac gaa aac   259
His Asp Thr Gly Ser Glu Leu Ile Phe Thr Val Arg Pro Asn Glu Asn
        40                  45                  50

ttc gaa gaa gat tgc caa gca gtc gca gca gac ctc gaa agg ctg gtc   307
```

```
Phe Glu Glu Asp Cys Gln Ala Val Ala Ala Asp Leu Glu Arg Leu Val
     55                  60                  65

gca ctg gcc gaa aaa tgaccccaca gaatggtctc taa                    345
Ala Leu Ala Glu Lys
 70


<210> 1578
<211> 74
<212> PRT
<213> Corynebacterium glutamicum

<400> 1578
Met Gly Leu Val His Thr Glu Phe Thr Pro Ile Asn Thr Tyr Gly Ile
  1               5                  10                  15

Leu Asp His Val Val Thr Leu Pro Asp Gly Thr Lys Val Leu Asn Pro
             20                  25                  30

Phe Arg Val Ile Pro His Asp Thr Gly Ser Glu Leu Ile Phe Thr Val
         35                  40                  45

Arg Pro Asn Glu Asn Phe Glu Glu Asp Cys Gln Ala Val Ala Ala Asp
     50                  55                  60

Leu Glu Arg Leu Val Ala Leu Ala Glu Lys
 65                  70


<210> 1579
<211> 666
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (80)..(643)
<223> RXA00082

<400> 1579
cacttgaagg cgaagaactc gaccagtttg ttgaagatga aattgaccga attgatcagc 60

tattcaagaa gatgggctagtg aac gtc act gaa caa tcc ggc gag tcc cat   112
                    Val Asn Val Thr Glu Gln Ser Gly Glu Ser His
                      1               5                  10

atc gac atc ccg gaa tca cac cag ctg ccc gga cct cgt cca gtt ggc   160
Ile Asp Ile Pro Glu Ser His Gln Leu Pro Gly Pro Arg Pro Val Gly
             15                  20                  25

gag ggc act ttc tgg gaa ggc cgc tcc ggg ctc atc atg ccc gca att   208
Glu Gly Thr Phe Trp Glu Gly Arg Ser Gly Leu Ile Met Pro Ala Ile
         30                  35                  40

ctt acg gca ttt agt ttg tat ttg ctc atc ggt gtt tta aac atg gat   256
Leu Thr Ala Phe Ser Leu Tyr Leu Leu Ile Gly Val Leu Asn Met Asp
     45                  50                  55

gtg ggc aat gca gca ttc cca gga cct cga ttc ttc cca aca atc ctc   304
Val Gly Asn Ala Ala Phe Pro Gly Pro Arg Phe Phe Pro Thr Ile Leu
```

```
 60                  65                  70                  75

ggc atc gcg ggt ttg ttg gtg gca gtg gca ttg acc att caa acc atc   352
Gly Ile Ala Gly Leu Leu Val Ala Val Ala Leu Thr Ile Gln Thr Ile
                80                  85                  90

aag tac ccc atg cat cca gaa aat gaa tct ggc cga agc tgg aaa ttc   400
Lys Tyr Pro Met His Pro Glu Asn Glu Ser Gly Arg Ser Trp Lys Phe
            95                  100                 105

cac tct gat tac gtc tca ctc gcg tgg gcg atc ggt ggc ttc ttc gcc   448
His Ser Asp Tyr Val Ser Leu Ala Trp Ala Ile Gly Gly Phe Phe Ala
        110                 115                 120

ttt gca gtc ttg ctt cca tat ctt ggc tgg gtc ctt gct ggc tcc ttg   496
Phe Ala Val Leu Leu Pro Tyr Leu Gly Trp Val Leu Ala Gly Ser Leu
    125                 130                 135

ttg ttc tgg aca atg acc agg gct ttc ggt tcc aaa cgc cca ggt ttc   544
Leu Phe Trp Thr Met Thr Arg Ala Phe Gly Ser Lys Arg Pro Gly Phe
140                 145                 150                 155

gat gtt ctt gtt tcc ctc atg atg agc tcc gtg gtc tac ctc gca ttc   592
Asp Val Leu Val Ser Leu Met Met Ser Ser Val Val Tyr Leu Ala Phe
                160                 165                 170

gat gtg ggc ttg gga ctt aat ctt cct tcc gga ctt ttg ggt ggt ggc   640
Asp Val Gly Leu Gly Leu Asn Leu Pro Ser Gly Leu Leu Gly Gly Gly
            175                 180                 185

ttt taatggatat tttgtccctc ttg                                    666
Phe
```

Sequence Listing

<210> 1580
<211> 188
<212> PRT
<213> Corynebacterium glutamicum

<400> 1580

```
Val Asn Val Thr Glu Gln Ser Gly Glu Ser His Ile Asp Ile Pro Glu
  1               5                  10                  15

Ser His Gln Leu Pro Gly Pro Arg Pro Val Gly Glu Gly Thr Phe Trp
             20                  25                  30

Glu Gly Arg Ser Gly Leu Ile Met Pro Ala Ile Leu Thr Ala Phe Ser
         35                  40                  45

Leu Tyr Leu Leu Ile Gly Val Leu Asn Met Asp Val Gly Asn Ala Ala
     50                  55                  60

Phe Pro Gly Pro Arg Phe Phe Pro Thr Ile Leu Gly Ile Ala Gly Leu
 65                  70                  75                  80

Leu Val Ala Val Ala Leu Thr Ile Gln Thr Ile Lys Tyr Pro Met His
                 85                  90                  95

Pro Glu Asn Glu Ser Gly Arg Ser Trp Lys Phe His Ser Asp Tyr Val
            100                 105                 110
```

```
Ser Leu Ala Trp Ala Ile Gly Gly Phe Phe Ala Phe Ala Val Leu Leu
        115                 120                 125

Pro Tyr Leu Gly Trp Val Leu Ala Gly Ser Leu Leu Phe Trp Thr Met
    130                 135                 140

Thr Arg Ala Phe Gly Ser Lys Arg Pro Gly Phe Asp Val Leu Val Ser
145                 150                 155                 160

Leu Met Met Ser Ser Val Val Tyr Leu Ala Phe Asp Val Gly Leu Gly
                165                 170                 175

Leu Asn Leu Pro Ser Gly Leu Leu Gly Gly Gly Phe
            180                 185


<210> 1581
<211> 423
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(400)
<223> RXA00083

<400> 1581
gaagatacag ggggccacgg tggggtggtg aacaagagca ggcacgaggc ctggtagata 60

cggattcgac caagaaaacg tacaccactc aggagcactc gtg ctt gcc ctt cca   115
                                        Val Leu Ala Leu Pro
                                          1               5

tcc tct atc atc gac ccc ctc tgg tgc cag ttc gcc gcg ctg atc cca   163
Ser Ser Ile Ile Asp Pro Leu Trp Cys Gln Phe Ala Ala Leu Ile Pro
                 10                  15                  20

ccc gtg acc gac acc cac cca ctt cgg tgc cac cgc cca cgc atc ccg   211
Pro Val Thr Asp Thr His Pro Leu Arg Cys His Arg Pro Arg Ile Pro
             25                  30                  35

gac cgg atc atc ttc gac aag ctc atc cag gtc ctc gtc ctc ggc gcc   259
Asp Arg Ile Ile Phe Asp Lys Leu Ile Gln Val Leu Val Leu Gly Ala
         40                  45                  50

tcc tat gcc aag atc gcc gac acg aca tgc tcg gcc acc acc ttg cgc   307
Ser Tyr Ala Lys Ile Ala Asp Thr Thr Cys Ser Ala Thr Thr Leu Arg
     55                  60                  65

acc cgc cgg gac gag tgg atc acc gct ggc atc ttc gag cag ctg gaa   355
Thr Arg Arg Asp Glu Trp Ile Thr Ala Gly Ile Phe Glu Gln Leu Glu
 70                  75                  80                  85

cag atc tgt ttg gaa ttc tac gac cgt atc gtc gga ctc gat ctc       400
Gln Ile Cys Leu Glu Phe Tyr Asp Arg Ile Val Gly Leu Asp Leu
                 90                  95                 100

taagttcgga ttggctcgaa ttg                                        423
```

<210> 1582
<211> 100
<212> PRT
<213> Corynebacterium glutamicum

<400> 1582

```
Val Leu Ala Leu Pro Ser Ser Ile Ile Asp Pro Leu Trp Cys Gln Phe
  1               5                  10                  15

Ala Ala Leu Ile Pro Pro Val Thr Asp Thr His Pro Leu Arg Cys His
             20                  25                  30

Arg Pro Arg Ile Pro Asp Arg Ile Ile Phe Asp Lys Leu Ile Gln Val
         35                  40                  45

Leu Val Leu Gly Ala Ser Tyr Ala Lys Ile Ala Asp Thr Thr Cys Ser
     50                  55                  60

Ala Thr Thr Leu Arg Thr Arg Arg Asp Glu Trp Ile Thr Ala Gly Ile
 65                  70                  75                  80

Phe Glu Gln Leu Glu Gln Ile Cys Leu Glu Phe Tyr Asp Arg Ile Val
                 85                  90                  95

Gly Leu Asp Leu
            100
```

<210> 1583
<211> 2346
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2323)
<223> RXA00093

<400> 1583

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aaagaatcga ttccggtgcc gcaggcctcc ttgtcaccca cgaaccccgc ttcgccgcgt 60

gggcagaccg aacaatcatg cttagggatg gtgaaatcca gtg acc aca ctt cta   115
                                              Val Thr Thr Leu Leu
                                                1               5

gca gca acc cgc ccc acc ctg cgc gat gcc ttt aaa cac cca tgg cga   163
Ala Ala Thr Arg Pro Thr Leu Arg Asp Ala Phe Lys His Pro Trp Arg
                10                  15                  20

tcg ctg gca gcc atc ttg ttg gtg gcc gta ccg atg ttc ctg gtg agt   211
Ser Leu Ala Ala Ile Leu Leu Val Ala Val Pro Met Phe Leu Val Ser
             25                  30                  35

ttc ttt ctt acc tat gat caa tca atc aac aat gca gct agc tat cct   259
Phe Phe Leu Thr Tyr Asp Gln Ser Ile Asn Asn Ala Ala Ser Tyr Pro
         40                  45                  50

ggt tcc cag gta caa gct cac tat gac gga gaa gga gcc tac caa ctc   307
Gly Ser Gln Val Gln Ala His Tyr Asp Gly Glu Gly Ala Tyr Gln Leu
     55                  60                  65
```

```
ctc caa gaa aac ctt cca gaa gac ttc cac ctg gaa ctc ttt gcc aat   355
Leu Gln Glu Asn Leu Pro Glu Asp Phe His Leu Glu Leu Phe Ala Asn
 70                  75                  80                  85

ggt tat cca gaa gtc tcc ttc ggt gat gaa gaa gtc aat ttc ttt gtt   403
Gly Tyr Pro Glu Val Ser Phe Gly Asp Glu Glu Val Asn Phe Phe Val
                90                  95                 100

gtg caa tca aca aac gta caa caa gcc tca ttt ccc gcc gat gca ctc   451
Val Gln Ser Thr Asn Val Gln Gln Ala Ser Phe Pro Ala Asp Ala Leu
            105                 110                 115

gat gtt tta ggt gcc aca atc ggt gat acc gtg acc att cac ggc acc   499
Asp Val Leu Gly Ala Thr Ile Gly Asp Thr Val Thr Ile His Gly Thr
        120                 125                 130

ccg gtg gaa gtt cag tcg att tct ccc aca aat atc tta ttg ccc gaa   547
Pro Val Glu Val Gln Ser Ile Ser Pro Thr Asn Ile Leu Leu Pro Glu
    135                 140                 145

ggt act ctg ttt tct ctt gag aat ttc tcc gaa tca gaa act ttt tcc   595
Gly Thr Leu Phe Ser Leu Glu Asn Phe Ser Glu Ser Glu Thr Phe Ser
150                 155                 160                 165

ggc acc tgg tac ttc ccc gga tcg aat ttc acc gaa gaa aac cga caa   643
Gly Thr Trp Tyr Phe Pro Gly Ser Asn Phe Thr Glu Glu Asn Arg Gln
                170                 175                 180

gca cta gaa gca gtt ggc ttt gaa gtt aat gaa tat cgg cgc ggc ccc   691
Ala Leu Glu Ala Val Gly Phe Glu Val Asn Glu Tyr Arg Arg Gly Pro
            185                 190                 195

ata tcc gtc gac cca aat ttg atc cca agc tac atc atg gga ttt tta   739
Ile Ser Val Asp Pro Asn Leu Ile Pro Ser Tyr Ile Met Gly Phe Leu
        200                 205                 210

tcg acg aca att ctc gcc gtc gtt gca ctc atg ctg atc tca cca gta   787
Ser Thr Thr Ile Leu Ala Val Val Ala Leu Met Leu Ile Ser Pro Val
    215                 220                 225

ttt aca att tcc gcc tca agg caa acc aga act ttc gca ctg ctc gcc   835
Phe Thr Ile Ser Ala Ser Arg Gln Thr Arg Thr Phe Ala Leu Leu Ala
230                 235                 240                 245

tca cag ggt gcc aca cct aga cac att cgg tgg gca gtg ctt aca tat   883
Ser Gln Gly Ala Thr Pro Arg His Ile Arg Trp Ala Val Leu Thr Tyr
                250                 255                 260

ggg ctc ttc gca ggt ctt gtt ggg gca tcc att ggt tta gtt ctg ggg   931
Gly Leu Phe Ala Gly Leu Val Gly Ala Ser Ile Gly Leu Val Leu Gly
            265                 270                 275

caa ata ggc atc tac ggc tgg tgg aaa tac acc tat cct gaa ttc tcc   979
Gln Ile Gly Ile Tyr Gly Trp Trp Lys Tyr Thr Tyr Pro Glu Phe Ser
        280                 285                 290

ctc acc acc ccc tgg cta gtt ctt gta ggt ttt tgg gcg ctg gca atc   1027
Leu Thr Thr Pro Trp Leu Val Leu Val Gly Phe Trp Ala Leu Ala Ile
    295                 300                 305

atc gct tca acg att gct gca ttc tta ccg gca gtt ttt gtc agt aga   1075
```

```
Ile Ala Ser Thr Ile Ala Ala Phe Leu Pro Ala Val Phe Val Ser Arg
310                 315                 320                 325

tca agc atc atc aac gga atc tac gga gga atc tcc gac aaa atc atc   1123
Ser Ser Ile Ile Asn Gly Ile Tyr Gly Gly Ile Ser Asp Lys Ile Ile
                330                 335                 340

cgg tgg agc cct cga atg ctc atc ggg cca atc gtc tta att gca gct   1171
Arg Trp Ser Pro Arg Met Leu Ile Gly Pro Ile Val Leu Ile Ala Ala
            345                 350                 355

gcg gta atc gcc ttg ttt atc ggt gac gga gag tgg gga ggc gtc gtc   1219
Ala Val Ile Ala Leu Phe Ile Gly Asp Gly Glu Trp Gly Gly Val Val
        360                 365                 370

aag caa tta tgc ttc ctg gca gcc gtc atc gcc ctg ccg gcc tca gtg   1267
Lys Gln Leu Cys Phe Leu Ala Ala Val Ile Ala Leu Pro Ala Ser Val
    375                 380                 385

cct gcg gtg ttg tgg gcg ctt ggg cgc ctg cct ggt ttg aca ttc aaa   1315
Pro Ala Val Leu Trp Ala Leu Gly Arg Leu Pro Gly Leu Thr Phe Lys
390                 395                 400                 405

cta gct acg cgc gat atg ctg cgc cga tca atg cac tcc att cct gcg   1363
Leu Ala Thr Arg Asp Met Leu Arg Arg Ser Met His Ser Ile Pro Ala
                410                 415                 420

att ggt gcg ctg gcg gca gtg att atg ctt ggt aca ttt atg caa aca   1411
Ile Gly Ala Leu Ala Ala Val Ile Met Leu Gly Thr Phe Met Gln Thr
            425                 430                 435

act gga ctt gca acc caa gcc agc gat aga gaa gct acc gcc tcg gtg   1459
Thr Gly Leu Ala Thr Gln Ala Ser Asp Arg Glu Ala Thr Ala Ser Val
        440                 445                 450

tat cct gag gcc gta ttc tta cgc ggt gac aca caa atc cct gga ctc   1507
Tyr Pro Glu Ala Val Phe Leu Arg Gly Asp Thr Gln Ile Pro Gly Leu
    455                 460                 465

atg ggg caa aaa atc gat gta tac ggt gat aac cat ggc ttt ggt atc   1555
Met Gly Gln Lys Ile Asp Val Tyr Gly Asp Asn His Gly Phe Gly Ile
470                 475                 480                 485

tat gaa cta gat gta gat ttt tac tcg gcc aac tat gtg ccc gca ctg   1603
Tyr Glu Leu Asp Val Asp Phe Tyr Ser Ala Asn Tyr Val Pro Ala Leu
                490                 495                 500

acc tca ttt ttt ggc gga cca gtt att gcc acg ccc aag att tta gac   1651
Thr Ser Phe Phe Gly Gly Pro Val Ile Ala Thr Pro Lys Ile Leu Asp
            505                 510                 515

atg ttc ggt gtc cac gaa caa gcc gac atc tac gcg cca tca acc tat   1699
Met Phe Gly Val His Glu Gln Ala Asp Ile Tyr Ala Pro Ser Thr Tyr
        520                 525                 530

aat tcc ggg ctg caa gaa tac gca ata tac ccc ggc gat gaa acc tac   1747
Asn Ser Gly Leu Gln Glu Tyr Ala Ile Tyr Pro Gly Asp Glu Thr Tyr
    535                 540                 545

atg cta gac acc gct gct gtt tta ccg ccg ctg tac tca cat gtt tta   1795
Met Leu Asp Thr Ala Ala Val Leu Pro Pro Leu Tyr Ser His Val Leu
```

```
550                 555                 560                 565

tta agc cca gaa act ttt gaa gaa atc gga gga caa aca gaa ttc ttg   1843
Leu Ser Pro Glu Thr Phe Glu Glu Ile Gly Gly Gln Thr Glu Phe Leu
                570                 575                 580

gga aca atc gtg ctt ccc caa gaa cta gat gac caa act gta caa gca   1891
Gly Thr Ile Val Leu Pro Gln Glu Leu Asp Asp Gln Thr Val Gln Ala
            585                 590                 595

atc aat cgg tca aga gat gcg cat ttc agc cac gac ggc cat aat tct   1939
Ile Asn Arg Ser Arg Asp Ala His Phe Ser His Asp Gly His Asn Ser
        600                 605                 610

tca ctt gct tcc agt gct gca cta act gcg gtg gca att gtg gtc gtt   1987
Ser Leu Ala Ser Ser Ala Ala Leu Thr Ala Val Ala Ile Val Val Val
    615                 620                 625

tcc ctt gtg atc gtg ctg gct aat cgc aaa ctc caa cag cac gca ttg   2035
Ser Leu Val Ile Val Leu Ala Asn Arg Lys Leu Gln Gln His Ala Leu
630                 635                 640                 645

att gcc atc gga gca aca cct gga aca atc tac aaa gtc aat gcc tta   2083
Ile Ala Ile Gly Ala Thr Pro Gly Thr Ile Tyr Lys Val Asn Ala Leu
                650                 655                 660

aat gca gcg ttg ctt gcc ctt gtc gga ggc atc atg ggc ctt gtc tcc   2131
Asn Ala Ala Leu Leu Ala Leu Val Gly Gly Ile Met Gly Leu Val Ser
            665                 670                 675

gga tgg att gca gcg ctg ctg aca ggc acc act gat gaa att gtt gat   2179
Gly Trp Ile Ala Ala Leu Leu Thr Gly Thr Thr Asp Glu Ile Val Asp
        680                 685                 690

gga gca att ttg aac tac ggc acg ctt gaa cac atg atg ctg ccg tgg   2227
Gly Ala Ile Leu Asn Tyr Gly Thr Leu Glu His Met Met Leu Pro Trp
    695                 700                 705

cct ctg ttg gta agc ctc ctc gtt gtg gcg ccg ctg gtg tgc gcc gtg   2275
Pro Leu Leu Val Ser Leu Leu Val Val Ala Pro Leu Val Cys Ala Val
710                 715                 720                 725

att ggg gct ata gct tct cca tcg gga cgc cac caa gaa gca tca atc   2323
Ile Gly Ala Ile Ala Ser Pro Ser Gly Arg His Gln Glu Ala Ser Ile
                730                 735                 740

taaccttgcc ggaggaaccg aaa                                        2346
```

<210> 1584
<211> 741
<212> PRT
<213> Corynebacterium glutamicum

<400> 1584

```
Val Thr Thr Leu Leu Ala Ala Thr Arg Pro Thr Leu Arg Asp Ala Phe
  1               5                  10                  15

Lys His Pro Trp Arg Ser Leu Ala Ala Ile Leu Leu Val Ala Val Pro
             20                  25                  30
```

```
Met Phe Leu Val Ser Phe Phe Leu Thr Tyr Asp Gln Ser Ile Asn Asn
         35                  40                  45

Ala Ala Ser Tyr Pro Gly Ser Gln Val Gln Ala His Tyr Asp Gly Glu
     50                  55                  60

Gly Ala Tyr Gln Leu Leu Gln Glu Asn Leu Pro Glu Asp Phe His Leu
 65                  70                  75                  80

Glu Leu Phe Ala Asn Gly Tyr Pro Glu Val Ser Phe Gly Asp Glu Glu
                85                  90                  95

Val Asn Phe Phe Val Val Gln Ser Thr Asn Val Gln Gln Ala Ser Phe
            100                 105                 110

Pro Ala Asp Ala Leu Asp Val Leu Gly Ala Thr Ile Gly Asp Thr Val
        115                 120                 125

Thr Ile His Gly Thr Pro Val Glu Val Gln Ser Ile Ser Pro Thr Asn
    130                 135                 140

Ile Leu Leu Pro Glu Gly Thr Leu Phe Ser Leu Glu Asn Phe Ser Glu
145                 150                 155                 160

Ser Glu Thr Phe Ser Gly Thr Trp Tyr Phe Pro Gly Ser Asn Phe Thr
                165                 170                 175

Glu Glu Asn Arg Gln Ala Leu Glu Ala Val Gly Phe Glu Val Asn Glu
            180                 185                 190

Tyr Arg Arg Gly Pro Ile Ser Val Asp Pro Asn Leu Ile Pro Ser Tyr
        195                 200                 205

Ile Met Gly Phe Leu Ser Thr Thr Ile Leu Ala Val Val Ala Leu Met
    210                 215                 220

Leu Ile Ser Pro Val Phe Thr Ile Ser Ala Ser Arg Gln Thr Arg Thr
225                 230                 235                 240

Phe Ala Leu Leu Ala Ser Gln Gly Ala Thr Pro Arg His Ile Arg Trp
                245                 250                 255

Ala Val Leu Thr Tyr Gly Leu Phe Ala Gly Leu Val Gly Ala Ser Ile
            260                 265                 270

Gly Leu Val Leu Gly Gln Ile Gly Ile Tyr Gly Trp Trp Lys Tyr Thr
        275                 280                 285

Tyr Pro Glu Phe Ser Leu Thr Thr Pro Trp Leu Val Leu Val Gly Phe
    290                 295                 300

Trp Ala Leu Ala Ile Ile Ala Ser Thr Ile Ala Ala Phe Leu Pro Ala
305                 310                 315                 320

Val Phe Val Ser Arg Ser Ser Ile Ile Asn Gly Ile Tyr Gly Gly Ile
                325                 330                 335

Ser Asp Lys Ile Ile Arg Trp Ser Pro Arg Met Leu Ile Gly Pro Ile
            340                 345                 350

Val Leu Ile Ala Ala Ala Val Ile Ala Leu Phe Ile Gly Asp Gly Glu
```

```
        355                 360                 365

Trp Gly Gly Val Val Lys Gln Leu Cys Phe Leu Ala Ala Val Ile Ala
    370                 375                 380

Leu Pro Ala Ser Val Pro Ala Val Leu Trp Ala Leu Gly Arg Leu Pro
385                 390                 395                 400

Gly Leu Thr Phe Lys Leu Ala Thr Arg Asp Met Leu Arg Arg Ser Met
                405                 410                 415

His Ser Ile Pro Ala Ile Gly Ala Leu Ala Ala Val Ile Met Leu Gly
            420                 425                 430

Thr Phe Met Gln Thr Thr Gly Leu Ala Thr Gln Ala Ser Asp Arg Glu
        435                 440                 445

Ala Thr Ala Ser Val Tyr Pro Glu Ala Val Phe Leu Arg Gly Asp Thr
    450                 455                 460

Gln Ile Pro Gly Leu Met Gly Gln Lys Ile Asp Val Tyr Gly Asp Asn
465                 470                 475                 480

His Gly Phe Gly Ile Tyr Glu Leu Asp Val Asp Phe Tyr Ser Ala Asn
                485                 490                 495

Tyr Val Pro Ala Leu Thr Ser Phe Phe Gly Gly Pro Val Ile Ala Thr
            500                 505                 510

Pro Lys Ile Leu Asp Met Phe Gly Val His Glu Gln Ala Asp Ile Tyr
        515                 520                 525

Ala Pro Ser Thr Tyr Asn Ser Gly Leu Gln Glu Tyr Ala Ile Tyr Pro
    530                 535                 540

Gly Asp Glu Thr Tyr Met Leu Asp Thr Ala Ala Val Leu Pro Pro Leu
545                 550                 555                 560

Tyr Ser His Val Leu Leu Ser Pro Glu Thr Phe Glu Glu Ile Gly Gly
                565                 570                 575

Gln Thr Glu Phe Leu Gly Thr Ile Val Leu Pro Gln Glu Leu Asp Asp
            580                 585                 590

Gln Thr Val Gln Ala Ile Asn Arg Ser Arg Asp Ala His Phe Ser His
        595                 600                 605

Asp Gly His Asn Ser Ser Leu Ala Ser Ser Ala Ala Leu Thr Ala Val
    610                 615                 620

Ala Ile Val Val Val Ser Leu Val Ile Val Leu Ala Asn Arg Lys Leu
625                 630                 635                 640

Gln Gln His Ala Leu Ile Ala Ile Gly Ala Thr Pro Gly Thr Ile Tyr
                645                 650                 655

Lys Val Asn Ala Leu Asn Ala Ala Leu Leu Ala Leu Val Gly Gly Ile
            660                 665                 670

Met Gly Leu Val Ser Gly Trp Ile Ala Ala Leu Leu Thr Gly Thr Thr
        675                 680                 685
```

```
Asp Glu Ile Val Asp Gly Ala Ile Leu Asn Tyr Gly Thr Leu Glu His
    690                 695                 700

Met Met Leu Pro Trp Pro Leu Leu Val Ser Leu Leu Val Val Ala Pro
705                 710                 715                 720

Leu Val Cys Ala Val Ile Gly Ala Ile Ala Ser Pro Ser Gly Arg His
                725                 730                 735

Gln Glu Ala Ser Ile
            740
```

<210> 1585
<211> 531
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(508)
<223> RXA00101

<400> 1585

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taaaccgtgc aggagatgcc gaaccccaat cgtgaaagcc gagttggggg agcgaataat 60

ctggtggtgt ccgcgctgcc aaccgctaaa ctcgtgaagc atg aga cta ata ctc   115
                                            Met Arg Leu Ile Leu
                                              1               5

aac ctg att tgg tta ttc ttc ggt ggc att tgg ctc gcg ttg gga tac   163
Asn Leu Ile Trp Leu Phe Phe Gly Gly Ile Trp Leu Ala Leu Gly Tyr
                10                  15                  20

gta ttc ttc gga atc atc gca tgt atc ttc atc gtg acg att ccc gcc   211
Val Phe Phe Gly Ile Ile Ala Cys Ile Phe Ile Val Thr Ile Pro Ala
            25                  30                  35

ggt atc gca agc ttc cgc atg gct aac tac gcg ctg tgg ccg ttt ggt   259
Gly Ile Ala Ser Phe Arg Met Ala Asn Tyr Ala Leu Trp Pro Phe Gly
        40                  45                  50

agg acg gtt gtt cgt aat cct aaa gcc gga ggg ttt tct gcc ctg agc   307
Arg Thr Val Val Arg Asn Pro Lys Ala Gly Gly Phe Ser Ala Leu Ser
    55                  60                  65

aac gga ctg tgg ttt atc att gct gga ctg tgg ctg gcg atc ggg cac   355
Asn Gly Leu Trp Phe Ile Ile Ala Gly Leu Trp Leu Ala Ile Gly His
70                  75                  80                  85

ctc acc acc gcg gct gcc cag gcg atc acc atc atc gga att cca ctg   403
Leu Thr Thr Ala Ala Ala Gln Ala Ile Thr Ile Ile Gly Ile Pro Leu
                90                  95                  100

gcg atc gca aac atc cga atg atc ccc gtg acg tgt ttc ccg ttc ggc   451
Ala Ile Ala Asn Ile Arg Met Ile Pro Val Thr Cys Phe Pro Phe Gly
            105                 110                 115

aaa gaa atc tat gac agc aac cgc att ccc ttc ggc tac gaa ccg atg   499
Lys Glu Ile Tyr Asp Ser Asn Arg Ile Pro Phe Gly Tyr Glu Pro Met
```

```
        120                 125                 130

gtt aag ttt taattcggcg acggactaaa cca                              531
Val Lys Phe
    135


<210> 1586
<211> 136
<212> PRT
<213> Corynebacterium glutamicum

<400> 1586
Met Arg Leu Ile Leu Asn Leu Ile Trp Leu Phe Phe Gly Gly Ile Trp
  1               5                  10                  15

Leu Ala Leu Gly Tyr Val Phe Phe Gly Ile Ile Ala Cys Ile Phe Ile
             20                  25                  30

Val Thr Ile Pro Ala Gly Ile Ala Ser Phe Arg Met Ala Asn Tyr Ala
         35                  40                  45

Leu Trp Pro Phe Gly Arg Thr Val Val Arg Asn Pro Lys Ala Gly Gly
     50                  55                  60

Phe Ser Ala Leu Ser Asn Gly Leu Trp Phe Ile Ile Ala Gly Leu Trp
 65                  70                  75                  80

Leu Ala Ile Gly His Leu Thr Thr Ala Ala Ala Gln Ala Ile Thr Ile
                 85                  90                  95

Ile Gly Ile Pro Leu Ala Ile Ala Asn Ile Arg Met Ile Pro Val Thr
            100                 105                 110

Cys Phe Pro Phe Gly Lys Glu Ile Tyr Asp Ser Asn Arg Ile Pro Phe
        115                 120                 125

Gly Tyr Glu Pro Met Val Lys Phe
    130                 135


<210> 1587
<211> 643
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(643)
<223> RXA00108

<400> 1587
gaattgggtt ttgagcatcg tggcggtgct tgttgttgca agtgccatcg tcatgatgat 60

tgcaaagaat cgtaaccaga aataagaggg tttattcacc atg aag aag ttt ttt   115
                                            Met Lys Lys Phe Phe
                                              1               5

gtc gca ggt gct gta ctg agc agt gcg ttg gtt atg gcg gcg tgt tcg   163
Val Ala Gly Ala Val Leu Ser Ser Ala Leu Val Met Ala Ala Cys Ser
                10                  15                  20
```

```
cct gct aat caa agt gat tcc acc tcc acg agc gtg gag act act tcc   211
Pro Ala Asn Gln Ser Asp Ser Thr Ser Thr Ser Val Glu Thr Thr Ser
            25                  30                  35

tcc agc agc acg cag gta agc gat gct gtg atc acc acg gaa aac gct   259
Ser Ser Ser Thr Gln Val Ser Asp Ala Val Ile Thr Thr Glu Asn Ala
        40                  45                  50

gtt gtt cgt gcg tct gtg gag gac agc gac atg acg gca gtg ttc gct   307
Val Val Arg Ala Ser Val Glu Asp Ser Asp Met Thr Ala Val Phe Ala
    55                  60                  65

acg ttg gtg aac aat tct gat gat gag atc aac gtt tct ggc ttt act   355
Thr Leu Val Asn Asn Ser Asp Asp Glu Ile Asn Val Ser Gly Phe Thr
70                  75                  80                  85

gct gat gtt gat gct gcc agc ttt gag gtc cat gag gtt gtt gat ggc   403
Ala Asp Val Asp Ala Ala Ser Phe Glu Val His Glu Val Val Asp Gly
                90                  95                  100

gtc atg cag gaa aag cca ggt ggt ttt gtg atc cct gca ggg gag agc   451
Val Met Gln Glu Lys Pro Gly Gly Phe Val Ile Pro Ala Gly Glu Ser
            105                 110                 115

atc gag ctg gca cca ggt ggc gat cat ttg atg atc atg ggg ctt gcg   499
Ile Glu Leu Ala Pro Gly Gly Asp His Leu Met Ile Met Gly Leu Ala
        120                 125                 130

aac cca atc gag gct ggc gat gaa gtg acg gtc act ctt gaa ttg gct   547
Asn Pro Ile Glu Ala Gly Asp Glu Val Thr Val Thr Leu Glu Leu Ala
    135                 140                 145

gat ggt tct gaa gtt aag ctt gat ccg atc ccg gcg cgc acc att gct   595
Asp Gly Ser Glu Val Lys Leu Asp Pro Ile Pro Ala Arg Thr Ile Ala
150                 155                 160                 165

gct ggt gat gag gat tat ggc gat ctg gga act gaa ggc cac gag ggc   643
Ala Gly Asp Glu Asp Tyr Gly Asp Leu Gly Thr Glu Gly His Glu Gly
                170                 175                 180
```

<210> 1588
<211> 181
<212> PRT
<213> Corynebacterium glutamicum

<400> 1588

```
Met Lys Lys Phe Phe Val Ala Gly Ala Val Leu Ser Ser Ala Leu Val
  1               5                  10                  15

Met Ala Ala Cys Ser Pro Ala Asn Gln Ser Asp Ser Thr Ser Thr Ser
            20                  25                  30

Val Glu Thr Thr Ser Ser Ser Ser Thr Gln Val Ser Asp Ala Val Ile
        35                  40                  45

Thr Thr Glu Asn Ala Val Val Arg Ala Ser Val Glu Asp Ser Asp Met
    50                  55                  60

Thr Ala Val Phe Ala Thr Leu Val Asn Asn Ser Asp Asp Glu Ile Asn
```

```
 65                  70                  75                  80

Val Ser Gly Phe Thr Ala Asp Val Asp Ala Ala Ser Phe Glu Val His
                 85                  90                  95

Glu Val Val Asp Gly Val Met Gln Glu Lys Pro Gly Gly Phe Val Ile
            100                 105                 110

Pro Ala Gly Glu Ser Ile Glu Leu Ala Pro Gly Gly Asp His Leu Met
        115                 120                 125

Ile Met Gly Leu Ala Asn Pro Ile Glu Ala Gly Asp Glu Val Thr Val
    130                 135                 140

Thr Leu Glu Leu Ala Asp Gly Ser Glu Val Lys Leu Asp Pro Ile Pro
145                 150                 155                 160

Ala Arg Thr Ile Ala Ala Gly Asp Glu Asp Tyr Gly Asp Leu Gly Thr
                165                 170                 175

Glu Gly His Glu Gly
            180
```

<210> 1589
<211> 672
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(649)
<223> RXA00110

<400> 1589

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atatcgaatg tccagtcacg ctaaacttca cccaagatga gatttcgtgg cacgattggg 60

aataacgaac gctaatttta aacactggag gagcttccac gtg agc aac aaa gac   115
                                              Val Ser Asn Lys Asp
                                                1               5

ggc ctt ttt act gac ggt aac agc acg ttt gca cct aag gtg gat tca   163
Gly Leu Phe Thr Asp Gly Asn Ser Thr Phe Ala Pro Lys Val Asp Ser
                10                  15                  20

att ccc ctc agc gat gtg gat acc agc gtt agc ggt gaa gcc tcc atc   211
Ile Pro Leu Ser Asp Val Asp Thr Ser Val Ser Gly Glu Ala Ser Ile
            25                  30                  35

ggc acg ctg atc tcc aac gca acc tcc caa atg tcc agc ctt ttc cgc   259
Gly Thr Leu Ile Ser Asn Ala Thr Ser Gln Met Ser Ser Leu Phe Arg
        40                  45                  50

gca gaa gtt gag ctg gcg aag act gaa ctc gca ggc gaa gcc aag aaa   307
Ala Glu Val Glu Leu Ala Lys Thr Glu Leu Ala Gly Glu Ala Lys Lys
    55                  60                  65

gct gcc atc ggc ggc ggc gca ttc agc gtt gct ggc gta atc gca ctg   355
Ala Ala Ile Gly Gly Gly Ala Phe Ser Val Ala Gly Val Ile Ala Leu
70                  75                  80                  85
```

```
tac agc tcc ttc ttc ttt ttc ttc ttc gtc gca gca ctg ctg agc gag   403
Tyr Ser Ser Phe Phe Phe Phe Phe Phe Val Ala Ala Leu Leu Ser Glu
                 90                  95                 100

tgg att aag cct tgg gca gca ttc ctc atc gtg ttc ctc ttc atg ctg   451
Trp Ile Lys Pro Trp Ala Ala Phe Leu Ile Val Phe Leu Phe Met Leu
            105                 110                 115

gtc atc gcc gca gct ctc gca ctg ttc ggc tgg cgc aag gtg aag aag   499
Val Ile Ala Ala Ala Leu Ala Leu Phe Gly Trp Arg Lys Val Lys Lys
        120                 125                 130

atg ggc gct ccg aag aac acc atc caa tcg gtc aac caa ctg aag aac   547
Met Gly Ala Pro Lys Asn Thr Ile Gln Ser Val Asn Gln Leu Lys Asn
    135                 140                 145

ctg gtc cca ggt cag gca tcc gag aag ctg gag aag gcc aac aag cgt   595
Leu Val Pro Gly Gln Ala Ser Glu Lys Leu Glu Lys Ala Asn Lys Arg
150                 155                 160                 165

ggc ctc tac acc tcc gcg tcc ttc cac agc ccc ggc gcc atc act ggc   643
Gly Leu Tyr Thr Ser Ala Ser Phe His Ser Pro Gly Ala Ile Thr Gly
                170                 175                 180

gac cac taaaaaagga gacttcgatg gcc                                672
Asp His
```

<210> 1590
<211> 183
<212> PRT
<213> Corynebacterium glutamicum

<400> 1590

```
Val Ser Asn Lys Asp Gly Leu Phe Thr Asp Gly Asn Ser Thr Phe Ala
  1               5                  10                  15

Pro Lys Val Asp Ser Ile Pro Leu Ser Asp Val Asp Thr Ser Val Ser
             20                  25                  30

Gly Glu Ala Ser Ile Gly Thr Leu Ile Ser Asn Ala Thr Ser Gln Met
         35                  40                  45

Ser Ser Leu Phe Arg Ala Glu Val Glu Leu Ala Lys Thr Glu Leu Ala
     50                  55                  60

Gly Glu Ala Lys Lys Ala Ala Ile Gly Gly Gly Ala Phe Ser Val Ala
 65                  70                  75                  80

Gly Val Ile Ala Leu Tyr Ser Ser Phe Phe Phe Phe Phe Phe Val Ala
                 85                  90                  95

Ala Leu Leu Ser Glu Trp Ile Lys Pro Trp Ala Ala Phe Leu Ile Val
            100                 105                 110

Phe Leu Phe Met Leu Val Ile Ala Ala Ala Leu Ala Leu Phe Gly Trp
        115                 120                 125

Arg Lys Val Lys Lys Met Gly Ala Pro Lys Asn Thr Ile Gln Ser Val
    130                 135                 140
```

```
Asn Gln Leu Lys Asn Leu Val Pro Gly Gln Ala Ser Glu Lys Leu Glu
145                 150                 155                 160

Lys Ala Asn Lys Arg Gly Leu Tyr Thr Ser Ala Ser Phe His Ser Pro
                165                 170                 175

Gly Ala Ile Thr Gly Asp His
            180


<210> 1591
<211> 714
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(691)
<223> RXA00117

<400> 1591
gttgatccca cagtataccc ccacccctat cttgaatacc ccccagggta tatggcacac 60

ttggaatcgc ccatcacttt gagattgaaa aggacaaggt atg act tcc gct caa   115
                                            Met Thr Ser Ala Gln
                                              1               5

ccg att act tcc gta gat gca cag act cta aaa tcg tgg atc gat aag   163
Pro Ile Thr Ser Val Asp Ala Gln Thr Leu Lys Ser Trp Ile Asp Lys
                10                  15                  20

cat gaa gga ctc acc gtc att gac gtc cgc act gca cat gag ttt tca   211
His Glu Gly Leu Thr Val Ile Asp Val Arg Thr Ala His Glu Phe Ser
            25                  30                  35

aat ttg cac att aaa ggc tct tac aac gtg cct cta act aca ctt gct   259
Asn Leu His Ile Lys Gly Ser Tyr Asn Val Pro Leu Thr Thr Leu Ala
        40                  45                  50

gag cat tcc gaa gag att tcc tct cgt gtt gga gaa cat gtt gtt ttg   307
Glu His Ser Glu Glu Ile Ser Ser Arg Val Gly Glu His Val Val Leu
    55                  60                  65

gtg tgt caa tcc ggc att cga gca ggt cag gca caa caa aag ctg gca   355
Val Cys Gln Ser Gly Ile Arg Ala Gly Gln Ala Gln Gln Lys Leu Ala
70                  75                  80                  85

cct ttg gga att tcc acc gtg gct gtt ttg gag ggt ggc atc aat agt   403
Pro Leu Gly Ile Ser Thr Val Ala Val Leu Glu Gly Gly Ile Asn Ser
                90                  95                  100

ttt gct aag gct gac ggt gat gtg gtc cgc gga acc cag gtg tgg gat   451
Phe Ala Lys Ala Asp Gly Asp Val Val Arg Gly Thr Gln Val Trp Asp
            105                 110                 115

atc gaa cgt cag gtg cgt ttt gcc gct gga tca ttg gtg ctc gca ggg   499
Ile Glu Arg Gln Val Arg Phe Ala Ala Gly Ser Leu Val Leu Ala Gly
        120                 125                 130

ctt gcg gga ggt aaa ttc ctt tca cca aaa gtt cgc acc ctg tcg gga   547
```

```
Leu Ala Gly Gly Lys Phe Leu Ser Pro Lys Val Arg Thr Leu Ser Gly
    135                 140                 145

att att ggt gcg ggt ctg aca ttt tct ggc gtt tcc aac acc tgt gcc   595
Ile Ile Gly Ala Gly Leu Thr Phe Ser Gly Val Ser Asn Thr Cys Ala
150                 155                 160                 165

atg ggc aaa gct ctg tcc gcc ttg ccg tgg aat aaa act aag cca gtt   643
Met Gly Lys Ala Leu Ser Ala Leu Pro Trp Asn Lys Thr Lys Pro Val
                170                 175                 180

cct acc gaa acc gag aca ttg agc aag ctt cca agc cct aag gag aac   691
Pro Thr Glu Thr Glu Thr Leu Ser Lys Leu Pro Ser Pro Lys Glu Asn
            185                 190                 195

taaatgtcta tcaccattac tga                                        714


<210> 1592
<211> 197
<212> PRT
<213> Corynebacterium glutamicum

<400> 1592
Met Thr Ser Ala Gln Pro Ile Thr Ser Val Asp Ala Gln Thr Leu Lys
  1               5                  10                  15

Ser Trp Ile Asp Lys His Glu Gly Leu Thr Val Ile Asp Val Arg Thr
             20                  25                  30

Ala His Glu Phe Ser Asn Leu His Ile Lys Gly Ser Tyr Asn Val Pro
         35                  40                  45

Leu Thr Thr Leu Ala Glu His Ser Glu Glu Ile Ser Ser Arg Val Gly
     50                  55                  60

Glu His Val Val Leu Val Cys Gln Ser Gly Ile Arg Ala Gly Gln Ala
 65                  70                  75                  80

Gln Gln Lys Leu Ala Pro Leu Gly Ile Ser Thr Val Ala Val Leu Glu
                 85                  90                  95

Gly Gly Ile Asn Ser Phe Ala Lys Ala Asp Gly Asp Val Val Arg Gly
            100                 105                 110

Thr Gln Val Trp Asp Ile Glu Arg Gln Val Arg Phe Ala Ala Gly Ser
        115                 120                 125

Leu Val Leu Ala Gly Leu Ala Gly Gly Lys Phe Leu Ser Pro Lys Val
    130                 135                 140

Arg Thr Leu Ser Gly Ile Ile Gly Ala Gly Leu Thr Phe Ser Gly Val
145                 150                 155                 160

Ser Asn Thr Cys Ala Met Gly Lys Ala Leu Ser Ala Leu Pro Trp Asn
                165                 170                 175

Lys Thr Lys Pro Val Pro Thr Glu Thr Glu Thr Leu Ser Lys Leu Pro
            180                 185                 190

Ser Pro Lys Glu Asn
```

195

<210> 1593
<211> 378
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(355)
<223> RXA00118

<400> 1593
atgggcgatt ccaagtgtgc catataccct ggggggtatt caagataggg gtgggggtat 60

actgtgggat caacgttcca gggcaacaaa aggagaaaaa atg caa ctc aat cct 115
Met Gln Leu Asn Pro
1 5

gat gag atc acc cca gtg ctc aac cga ctc aag cgc gcc caa ggt caa 163
Asp Glu Ile Thr Pro Val Leu Asn Arg Leu Lys Arg Ala Gln Gly Gln
10 15 20

ctc acc gga gta atc cga atg ctt gat gaa ggc gaa gac tgt aaa gcc 211
Leu Thr Gly Val Ile Arg Met Leu Asp Glu Gly Glu Asp Cys Lys Ala
25 30 35

gta gtc acc caa ctt gcc gca gtc aca aaa gcg ctg gac agg gca ggc 259
Val Val Thr Gln Leu Ala Ala Val Thr Lys Ala Leu Asp Arg Ala Gly
40 45 50

ttc gcc atc att gcc aca ggt ttg gaa cag tgc ctc acc aac cct gat 307
Phe Ala Ile Ile Ala Thr Gly Leu Glu Gln Cys Leu Thr Asn Pro Asp
55 60 65

ggc gac atg gac aaa aag gaa cta gaa aaa ctg ttc ctg tcg ctg gct 355
Gly Asp Met Asp Lys Lys Glu Leu Glu Lys Leu Phe Leu Ser Leu Ala
70 75 80 85

taactatggc ctagttcagg gcg 378

<210> 1594
<211> 85
<212> PRT
<213> Corynebacterium glutamicum

<400> 1594
Met Gln Leu Asn Pro Asp Glu Ile Thr Pro Val Leu Asn Arg Leu Lys
1 5 10 15

Arg Ala Gln Gly Gln Leu Thr Gly Val Ile Arg Met Leu Asp Glu Gly
20 25 30

Glu Asp Cys Lys Ala Val Val Thr Gln Leu Ala Ala Val Thr Lys Ala
35 40 45

Leu Asp Arg Ala Gly Phe Ala Ile Ile Ala Thr Gly Leu Glu Gln Cys
50 55 60

```
Leu Thr Asn Pro Asp Gly Asp Met Asp Lys Lys Glu Leu Glu Lys Leu
 65                  70                  75                  80

Phe Leu Ser Leu Ala
                85
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<210> 1595
<211> 882
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(859)
<223> RXA00119

<400> 1595

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actaatgaga actgtttttc aattggtgca ggatttccac aaggaagcta ggggagaggg 60

gcttccaatc aagtggggtc catcgcgtgg agaatttggc atg ctg gag ttt cct   115
                                            Met Leu Glu Phe Pro
                                              1               5

gca gat gtc att ccc gag aac atc aaa cac att gcg cag aca aag ttc   163
Ala Asp Val Ile Pro Glu Asn Ile Lys His Ile Ala Gln Thr Lys Phe
                10                  15                  20

cag act gaa gca act tcg gtg gag gat att cgt cgt gcg att aac ctg   211
Gln Thr Glu Ala Thr Ser Val Glu Asp Ile Arg Arg Ala Ile Asn Leu
            25                  30                  35

ctg agt gat cag gcg gag cgt gcg ggt gcg tcc ttt aat cct ggt ttc   259
Leu Ser Asp Gln Ala Glu Arg Ala Gly Ala Ser Phe Asn Pro Gly Phe
        40                  45                  50

att ctt gcg cag gtg ggc tcc acc atc gtg gag gtt tat ggc ggt gct   307
Ile Leu Ala Gln Val Gly Ser Thr Ile Val Glu Val Tyr Gly Gly Ala
    55                  60                  65

ccg gtt gct tgg ctg gat gcg gtt gag ctg ttg att agt cct gat gtg   355
Pro Val Ala Trp Leu Asp Ala Val Glu Leu Leu Ile Ser Pro Asp Val
70                  75                  80                  85

gag tgg gtt ggg gtt cat ggc tca agg aag ctc gat att aat gtc agc   403
Glu Trp Val Gly Val His Gly Ser Arg Lys Leu Asp Ile Asn Val Ser
                90                  95                  100

gga gaa ttg tcc ggg gtg att tct gct ggt gac aag ttg ggt gaa ctg   451
Gly Glu Leu Ser Gly Val Ile Ser Ala Gly Asp Lys Leu Gly Glu Leu
            105                 110                 115

ctt ggc gat gat tgg aca atc aac att gtt cac ggc gag tac aaa atc   499
Leu Gly Asp Asp Trp Thr Ile Asn Ile Val His Gly Glu Tyr Lys Ile
        120                 125                 130

cag atc gaa gat gct cga cca agt act gca ttc ctt gcg gac gcg act   547
Gln Ile Glu Asp Ala Arg Pro Ser Thr Ala Phe Leu Ala Asp Ala Thr
    135                 140                 145

gaa ctg att aat cag gca aac tct gag att gtt ccg ttc cat gtt cgg   595
```

```
Glu Leu Ile Asn Gln Ala Asn Ser Glu Ile Val Pro Phe His Val Arg
150                 155                 160                 165

atg ctc agc aac tcg aaa att gtg atg tct ggc ttt agt gat tat tca   643
Met Leu Ser Asn Ser Lys Ile Val Met Ser Gly Phe Ser Asp Tyr Ser
                170                 175                 180

cta gcg ggt gat gcg att aca tct gcg gga aaa ctg gct gaa ttg gcg   691
Leu Ala Gly Asp Ala Ile Thr Ser Ala Gly Lys Leu Ala Glu Leu Ala
            185                 190                 195

agg cct ttt gcc cac tgg aaa gaa aac gtc att cct acg ata gaa ata   739
Arg Pro Phe Ala His Trp Lys Glu Asn Val Ile Pro Thr Ile Glu Ile
        200                 205                 210

gcc atg gac tat gaa cca tca ccg gtg gca gat ctt tgg cag gga gat   787
Ala Met Asp Tyr Glu Pro Ser Pro Val Ala Asp Leu Trp Gln Gly Asp
    215                 220                 225

tct tcg gag aca cct gag cct ttc gac gat ttt gag cgc tta ttg cgg   835
Ser Ser Glu Thr Pro Glu Pro Phe Asp Asp Phe Glu Arg Leu Leu Arg
230                 235                 240                 245

gaa gaa atg ctt att cct gag att tagctggtca tagacctgct gtt         882
Glu Glu Met Leu Ile Pro Glu Ile
                250
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Applicant: BASF Aktiengesellschaft
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<210> 1596
<211> 253
<212> PRT
<213> Corynebacterium glutamicum

<400> 1596

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Met Leu Glu Phe Pro Ala Asp Val Ile Pro Glu Asn Ile Lys His Ile
  1               5                  10                  15

Ala Gln Thr Lys Phe Gln Thr Glu Ala Thr Ser Val Glu Asp Ile Arg
             20                  25                  30

Arg Ala Ile Asn Leu Leu Ser Asp Gln Ala Glu Arg Ala Gly Ala Ser
         35                  40                  45

Phe Asn Pro Gly Phe Ile Leu Ala Gln Val Gly Ser Thr Ile Val Glu
     50                  55                  60

Val Tyr Gly Gly Ala Pro Val Ala Trp Leu Asp Ala Val Glu Leu Leu
 65                  70                  75                  80

Ile Ser Pro Asp Val Glu Trp Val Gly Val His Gly Ser Arg Lys Leu
                 85                  90                  95

Asp Ile Asn Val Ser Gly Glu Leu Ser Gly Val Ile Ser Ala Gly Asp
            100                 105                 110

Lys Leu Gly Glu Leu Leu Gly Asp Asp Trp Thr Ile Asn Ile Val His
        115                 120                 125

Gly Glu Tyr Lys Ile Gln Ile Glu Asp Ala Arg Pro Ser Thr Ala Phe
    130                 135                 140
```

```
Leu Ala Asp Ala Thr Glu Leu Ile Asn Gln Ala Asn Ser Glu Ile Val
145                 150                 155                 160

Pro Phe His Val Arg Met Leu Ser Asn Ser Lys Ile Val Met Ser Gly
                165                 170                 175

Phe Ser Asp Tyr Ser Leu Ala Gly Asp Ala Ile Thr Ser Ala Gly Lys
            180                 185                 190

Leu Ala Glu Leu Ala Arg Pro Phe Ala His Trp Lys Glu Asn Val Ile
        195                 200                 205

Pro Thr Ile Glu Ile Ala Met Asp Tyr Glu Pro Ser Pro Val Ala Asp
    210                 215                 220

Leu Trp Gln Gly Asp Ser Ser Glu Thr Pro Glu Pro Phe Asp Asp Phe
225                 230                 235                 240

Glu Arg Leu Leu Arg Glu Glu Met Leu Ile Pro Glu Ile
                245                 250
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Sequence Listing

<210> 1597
<211> 834
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(811)
<223> RXA00121

<400> 1597

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cgctgtcgac cccatcttct aaacaagaaa ggcccctcca atg ttg agc gat ctg   115
                                            Met Leu Ser Asp Leu
                                              1               5

agc tcc att ttt gac ttc caa gac ctc tcc ggc acc ttc tct gtc gtc   163
Ser Ser Ile Phe Asp Phe Gln Asp Leu Ser Gly Thr Phe Ser Val Val
                 10                  15                  20

gac gtt ctc atc act ttg gtc ttg tcc ttc gtc ctg acc tcc atc gtg   211
Asp Val Leu Ile Thr Leu Val Leu Ser Phe Val Leu Thr Ser Ile Val
             25                  30                  35

ggt gtg gtg tac caa aag acc cac cgc cac atc tcc tac agc cag tca   259
Gly Val Val Tyr Gln Lys Thr His Arg His Ile Ser Tyr Ser Gln Ser
         40                  45                  50

ttc gta caa acg ttg gtg ctg gtg gga atg gtc att gca atc atc atg   307
Phe Val Gln Thr Leu Val Leu Val Gly Met Val Ile Ala Ile Ile Met
     55                  60                  65

ctg gtg gtc ggc tcc aac att gca cgt gca ttc gcc ctg gtt ggc gcg   355
Leu Val Val Gly Ser Asn Ile Ala Arg Ala Phe Ala Leu Val Gly Ala
 70                  75                  80                  85

ctt tcg gtg att cga ttc cgc aac gca gtg aaa gaa acc cga gat gtg   403
Leu Ser Val Ile Arg Phe Arg Asn Ala Val Lys Glu Thr Arg Asp Val
```

```
                90                  95                 100

ggc ttc ctt ttc ctt gcc atg gca atc ggc atg act tgc ggt acc cgc   451
Gly Phe Leu Phe Leu Ala Met Ala Ile Gly Met Thr Cys Gly Thr Arg
            105                 110                 115

ttc tac gtt ctg gcg atc gct gca acc atc gtt gtc tgt ggc gtt ctg   499
Phe Tyr Val Leu Ala Ile Ala Ala Thr Ile Val Val Cys Gly Val Leu
        120                 125                 130

ttc atc atg tac cgc ttc gac tgg ttc aag gct gat atc cag cgc cag   547
Phe Ile Met Tyr Arg Phe Asp Trp Phe Lys Ala Asp Ile Gln Arg Gln
    135                 140                 145

gtc atc aag gtg cag gtc cca gcc gat gga caa gct gat tcc ggc agg   595
Val Ile Lys Val Gln Val Pro Ala Asp Gly Gln Ala Asp Ser Gly Arg
150                 155                 160                 165

tcc tac gca gaa gaa gtt gaa ctg atc ctc gca cag tac tgc act tcc   643
Ser Tyr Ala Glu Glu Val Glu Leu Ile Leu Ala Gln Tyr Cys Thr Ser
                170                 175                 180

ttt gag atg atg tcc gct gaa tct gtc cgc ggc gga gcc ctg acc gag   691
Phe Glu Met Met Ser Ala Glu Ser Val Arg Gly Gly Ala Leu Thr Glu
            185                 190                 195

ttc tcc tac acc gct caa atg cgc aag aac gtg aag cca cat gag ctg   739
Phe Ser Tyr Thr Ala Gln Met Arg Lys Asn Val Lys Pro His Glu Leu
        200                 205                 210

gtc gcc aag atg cgc gat gtg aac tac ggc caa aaa gcg act gtc ctg   787
Val Ala Lys Met Arg Asp Val Asn Tyr Gly Gln Lys Ala Thr Val Leu
    215                 220                 225

acc ggt cac gat caa acg gat gta tagaaaatgc ctagctttaa atc         834
Thr Gly His Asp Gln Thr Asp Val
230                 235
```

Do not delete, alter, or write over this page

<210> 1598
<211> 237
<212> PRT
<213> Corynebacterium glutamicum

<400> 1598

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Met Leu Ser Asp Leu Ser Ser Ile Phe Asp Phe Gln Asp Leu Ser Gly
  1               5                  10                  15

Thr Phe Ser Val Val Asp Val Leu Ile Thr Leu Val Leu Ser Phe Val
             20                  25                  30

Leu Thr Ser Ile Val Gly Val Val Tyr Gln Lys Thr His Arg His Ile
         35                  40                  45

Ser Tyr Ser Gln Ser Phe Val Gln Thr Leu Val Leu Val Gly Met Val
     50                  55                  60

Ile Ala Ile Ile Met Leu Val Val Gly Ser Asn Ile Ala Arg Ala Phe
 65                  70                  75                  80

Ala Leu Val Gly Ala Leu Ser Val Ile Arg Phe Arg Asn Ala Val Lys
```

```
                85                  90                  95

Glu Thr Arg Asp Val Gly Phe Leu Phe Leu Ala Met Ala Ile Gly Met
            100                 105                 110

Thr Cys Gly Thr Arg Phe Tyr Val Leu Ala Ile Ala Ala Thr Ile Val
        115                 120                 125

Val Cys Gly Val Leu Phe Ile Met Tyr Arg Phe Asp Trp Phe Lys Ala
    130                 135                 140

Asp Ile Gln Arg Gln Val Ile Lys Val Gln Val Pro Ala Asp Gly Gln
145                 150                 155                 160

Ala Asp Ser Gly Arg Ser Tyr Ala Glu Glu Val Glu Leu Ile Leu Ala
                165                 170                 175

Gln Tyr Cys Thr Ser Phe Glu Met Met Ser Ala Glu Ser Val Arg Gly
            180                 185                 190

Gly Ala Leu Thr Glu Phe Ser Tyr Thr Ala Gln Met Arg Lys Asn Val
        195                 200                 205

Lys Pro His Glu Leu Val Ala Lys Met Arg Asp Val Asn Tyr Gly Gln
    210                 215                 220

Lys Ala Thr Val Leu Thr Gly His Asp Gln Thr Asp Val
225                 230                 235
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<210> 1599
<211> 1746
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1723)
<223> RXA00122

<400> 1599

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gatgcgcgat gtgaactacg gccaaaaagc gactgtcctg accggtcacg atcaaacgga 60

tgtatagaaa atgcctagct ttaaatctgc tcgatggagg atg aac aga cgc ctc   115
                                              Met Asn Arg Arg Leu
                                                1               5

ttc cta gga act tcc gca gct atc atc gct gtc ggt ggc gtg ctc ggt   163
Phe Leu Gly Thr Ser Ala Ala Ile Ile Ala Val Gly Gly Val Leu Gly
                10                  15                  20

gga gtg cag gtt gta cct tat att tcc tct ggt gaa atc caa acg tca   211
Gly Val Gln Val Val Pro Tyr Ile Ser Ser Gly Glu Ile Gln Thr Ser
            25                  30                  35

gca tca tcg act gcc acg atc gat gtc ggt gca ggc aat gtc gat att   259
Ala Ser Ser Thr Ala Thr Ile Asp Val Gly Ala Gly Asn Val Asp Ile
        40                  45                  50

ttt gat acc tcc gtt tcc cat gaa atc agc ctg cag gtt tcg cag gaa   307
Phe Asp Thr Ser Val Ser His Glu Ile Ser Leu Gln Val Ser Gln Glu
```

```
     55                  60                  65

agc ctc gat gag atg ctc gcg gac tat caa gaa gac ggt tcc aaa acc   355
Ser Leu Asp Glu Met Leu Ala Asp Tyr Gln Glu Asp Gly Ser Lys Thr
 70                  75                  80                  85

tgg gtg aaa gca acc atc acg att gat ggc gtg acc att gaa aac gtc   403
Trp Val Lys Ala Thr Ile Thr Ile Asp Gly Val Thr Ile Glu Asn Val
                 90                  95                 100

ggc atc cgc ctc aag ggc aac tcc acg ctg tcc ggg ttg ggt cga aca   451
Gly Ile Arg Leu Lys Gly Asn Ser Thr Leu Ser Gly Leu Gly Arg Thr
            105                 110                 115

tct gaa gaa ggc gga cct cag gca cca gaa ggc gtc gaa gag ttt aca   499
Ser Glu Glu Gly Gly Pro Gln Ala Pro Glu Gly Val Glu Glu Phe Thr
        120                 125                 130

gat ctc agt gaa gag gaa atc gcc cag ttt gag gaa cag ttc gcg gcg   547
Asp Leu Ser Glu Glu Glu Ile Ala Gln Phe Glu Glu Gln Phe Ala Ala
    135                 140                 145

cag caa gag act act gac gct tca gag acc ggt gaa act gcg gaa aat   595
Gln Gln Glu Thr Thr Asp Ala Ser Glu Thr Gly Glu Thr Ala Glu Asn
150                 155                 160                 165

gaa gag act cgc ggc ccc ggc ggt ggc atg ggt ggt ggc ggc atg ggt   643
Glu Glu Thr Arg Gly Pro Gly Gly Gly Met Gly Gly Gly Gly Met Gly
                170                 175                 180

ggc atg act tcg gtc gat gcc gac gat gtc agc acc tgg cca ctt ctg   691
Gly Met Thr Ser Val Asp Ala Asp Asp Val Ser Thr Trp Pro Leu Leu
            185                 190                 195

atc agc ttc gac aaa tac gaa gac ggc cgc gtc tac caa ggc atg acc   739
Ile Ser Phe Asp Lys Tyr Glu Asp Gly Arg Val Tyr Gln Gly Met Thr
        200                 205                 210

caa ctg gca cta cgc ccc ggc acc acc gtg gtc aac gaa gca atg gcg   787
Gln Leu Ala Leu Arg Pro Gly Thr Thr Val Val Asn Glu Ala Met Ala
    215                 220                 225

ctg gcc ctg acc gca gaa acc ggc cag gtc tcg cag caa tcc agc ttc   835
Leu Ala Leu Thr Ala Glu Thr Gly Gln Val Ser Gln Gln Ser Ser Phe
230                 235                 240                 245

aca acg ttt tcg ctt aac gac gag ccc tcc acc act cga ctc ctt ttg   883
Thr Thr Phe Ser Leu Asn Asp Glu Pro Ser Thr Thr Arg Leu Leu Leu
                250                 255                 260

aag cac ccc gat gaa aat tat gcc gac gcg ctc ggc aac gga gtc ctc   931
Lys His Pro Asp Glu Asn Tyr Ala Asp Ala Leu Gly Asn Gly Val Leu
            265                 270                 275

ttc aaa gca gat tcc aac agt tcc ttc acc tac caa ggc gaa gac caa   979
Phe Lys Ala Asp Ser Asn Ser Ser Phe Thr Tyr Gln Gly Glu Asp Gln
        280                 285                 290

act gaa tac gac gga cag ttc aag cag atc aac ggt gac ggc aac gga   1027
Thr Glu Tyr Asp Gly Gln Phe Lys Gln Ile Asn Gly Asp Gly Asn Gly
    295                 300                 305
```

```
gac atc caa ccg atc atc aac ctg ctg aaa tgg ctc gac acc gca agc   1075
Asp Ile Gln Pro Ile Ile Asn Leu Leu Lys Trp Leu Asp Thr Ala Ser
310                 315                 320                 325

gat gaa gag ttt gct gaa cac ctc tct gac tac gtc gat gtg gaa agc   1123
Asp Glu Glu Phe Ala Glu His Leu Ser Asp Tyr Val Asp Val Glu Ser
                330                 335                 340

ttt gct cgc tac gtt gcc act caa aac ctg ttg gta aat tcc gac gac   1171
Phe Ala Arg Tyr Val Ala Thr Gln Asn Leu Leu Val Asn Ser Asp Asp
            345                 350                 355

atg gct ggt ccc ggt agt aat tac tac ctg tgg tac gac tac gac acc   1219
Met Ala Gly Pro Gly Ser Asn Tyr Tyr Leu Trp Tyr Asp Tyr Asp Thr
        360                 365                 370

ggc ctg atc agc gtg atc tct tgg gat ttg aac ctc gca atg tcc ggc   1267
Gly Leu Ile Ser Val Ile Ser Trp Asp Leu Asn Leu Ala Met Ser Gly
    375                 380                 385

tca act gat gct ggc cca gat gat gaa atc tcc atg ggc gga ggt ggc   1315
Ser Thr Asp Ala Gly Pro Asp Asp Glu Ile Ser Met Gly Gly Gly Gly
390                 395                 400                 405

ggt ggc gga atg cgt cct ggt gga acg acc gac act gaa att gaa ggt   1363
Gly Gly Gly Met Arg Pro Gly Gly Thr Thr Asp Thr Glu Ile Glu Gly
                410                 415                 420

act gcg acc gag gat atg cct gac atg ggc aat atg cag caa cgt gaa   1411
Thr Ala Thr Glu Asp Met Pro Asp Met Gly Asn Met Gln Gln Arg Glu
            425                 430                 435

cgc cct gaa gga atg cca gac atg ggt gag atg cct gat atg ggt gac   1459
Arg Pro Glu Gly Met Pro Asp Met Gly Glu Met Pro Asp Met Gly Asp
        440                 445                 450

cgg gaa ggc ggt gga tcg atg gga gga aac cag ctc aag gaa cgt ttc   1507
Arg Glu Gly Gly Gly Ser Met Gly Gly Asn Gln Leu Lys Glu Arg Phe
    455                 460                 465

ctc gct tcc gat gca ttc acg gaa atc tat gag cag gtg tac tgg gag   1555
Leu Ala Ser Asp Ala Phe Thr Glu Ile Tyr Glu Gln Val Tyr Trp Glu
470                 475                 480                 485

ctg tat gaa gaa atg tat ggt tcc gga act gcc atc gag ttg ttg gat   1603
Leu Tyr Glu Glu Met Tyr Gly Ser Gly Thr Ala Ile Glu Leu Leu Asp
                490                 495                 500

gag att gca gcg tca att cca gaa act gat gcg gtg act gca gat gag   1651
Glu Ile Ala Ala Ser Ile Pro Glu Thr Asp Ala Val Thr Ala Asp Glu
            505                 510                 515

atc gct acg gaa gtg gcg tca atg cgg gaa tgg atc act gcc cgc aca   1699
Ile Ala Thr Glu Val Ala Ser Met Arg Glu Trp Ile Thr Ala Arg Thr
        520                 525                 530

gaa gcg ttg gct gct ttg caa gag tgatcaaact agaaaaccaa caa         1746
Glu Ala Leu Ala Ala Leu Gln Glu
    535                 540
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<210> 1600
<211> 541
<212> PRT
<213> Corynebacterium glutamicum

<400> 1600
Met Asn Arg Arg Leu Phe Leu Gly Thr Ser Ala Ala Ile Ile Ala Val
1 5 10 15

Gly Gly Val Leu Gly Gly Val Gln Val Val Pro Tyr Ile Ser Ser Gly
20 25 30

Glu Ile Gln Thr Ser Ala Ser Ser Thr Ala Thr Ile Asp Val Gly Ala
35 40 45

Gly Asn Val Asp Ile Phe Asp Thr Ser Val Ser His Glu Ile Ser Leu
50 55 60

Gln Val Ser Gln Glu Ser Leu Asp Glu Met Leu Ala Asp Tyr Gln Glu
65 70 75 80

Asp Gly Ser Lys Thr Trp Val Lys Ala Thr Ile Thr Ile Asp Gly Val
85 90 95

Thr Ile Glu Asn Val Gly Ile Arg Leu Lys Gly Asn Ser Thr Leu Ser
100 105 110

Gly Leu Gly Arg Thr Ser Glu Glu Gly Gly Pro Gln Ala Pro Glu Gly
115 120 125

Val Glu Glu Phe Thr Asp Leu Ser Glu Glu Glu Ile Ala Gln Phe Glu
130 135 140

Glu Gln Phe Ala Ala Gln Gln Glu Thr Thr Asp Ala Ser Glu Thr Gly
145 150 155 160

Glu Thr Ala Glu Asn Glu Glu Thr Arg Gly Pro Gly Gly Gly Met Gly
165 170 175

Gly Gly Gly Met Gly Gly Met Thr Ser Val Asp Ala Asp Asp Val Ser
180 185 190

Thr Trp Pro Leu Leu Ile Ser Phe Asp Lys Tyr Glu Asp Gly Arg Val
195 200 205

Tyr Gln Gly Met Thr Gln Leu Ala Leu Arg Pro Gly Thr Thr Val Val
210 215 220

Asn Glu Ala Met Ala Leu Ala Leu Thr Ala Glu Thr Gly Gln Val Ser
225 230 235 240

Gln Gln Ser Ser Phe Thr Thr Phe Ser Leu Asn Asp Glu Pro Ser Thr
245 250 255

Thr Arg Leu Leu Leu Lys His Pro Asp Glu Asn Tyr Ala Asp Ala Leu
260 265 270

Gly Asn Gly Val Leu Phe Lys Ala Asp Ser Asn Ser Ser Phe Thr Tyr
275 280 285

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Gln Gly Glu Asp Gln Thr Glu Tyr Asp Gly Gln Phe Lys Gln Ile Asn
    290                 295                 300

Gly Asp Gly Asn Gly Asp Ile Gln Pro Ile Ile Asn Leu Leu Lys Trp
305                 310                 315                 320

Leu Asp Thr Ala Ser Asp Glu Glu Phe Ala Glu His Leu Ser Asp Tyr
                325                 330                 335

Val Asp Val Glu Ser Phe Ala Arg Tyr Val Ala Thr Gln Asn Leu Leu
            340                 345                 350

Val Asn Ser Asp Asp Met Ala Gly Pro Gly Ser Asn Tyr Tyr Leu Trp
        355                 360                 365

Tyr Asp Tyr Asp Thr Gly Leu Ile Ser Val Ile Ser Trp Asp Leu Asn
    370                 375                 380

Leu Ala Met Ser Gly Ser Thr Asp Ala Gly Pro Asp Asp Glu Ile Ser
385                 390                 395                 400

Met Gly Gly Gly Gly Gly Gly Gly Met Arg Pro Gly Gly Thr Thr Asp
                405                 410                 415

Thr Glu Ile Glu Gly Thr Ala Thr Glu Asp Met Pro Asp Met Gly Asn
            420                 425                 430

Met Gln Gln Arg Glu Arg Pro Glu Gly Met Pro Asp Met Gly Glu Met
        435                 440                 445

Pro Asp Met Gly Asp Arg Glu Gly Gly Gly Ser Met Gly Gly Asn Gln
    450                 455                 460

Leu Lys Glu Arg Phe Leu Ala Ser Asp Ala Phe Thr Glu Ile Tyr Glu
465                 470                 475                 480

Gln Val Tyr Trp Glu Leu Tyr Glu Glu Met Tyr Gly Ser Gly Thr Ala
                485                 490                 495

Ile Glu Leu Leu Asp Glu Ile Ala Ala Ser Ile Pro Glu Thr Asp Ala
            500                 505                 510

Val Thr Ala Asp Glu Ile Ala Thr Glu Val Ala Ser Met Arg Glu Trp
        515                 520                 525

Ile Thr Ala Arg Thr Glu Ala Leu Ala Ala Leu Gln Glu
    530                 535                 540
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<210> 1601
<211> 579
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> RXA00127

<400> 1601
ttgtggggcg ccgggggcgt cgttatgcag tgactgccag cgtgtgtgga ggaagccgcc 60

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aacattggcg cggcttgatt tagatttacc ggtgtggacg ttg tcg ccg tat gac   115
                                             Leu Ser Pro Tyr Asp
                                               1               5

ggc ccg cat cgc aac gtg ctc att gcg ctg aag gag cac ggc cgt gca   163
Gly Pro His Arg Asn Val Leu Ile Ala Leu Lys Glu His Gly Arg Ala
                10                  15                  20

gac ctt gtg gcg ttt gtg ggc gcg gtg gtg ggg gcg tcg ata agc tat   211
Asp Leu Val Ala Phe Val Gly Ala Val Val Gly Ala Ser Ile Ser Tyr
            25                  30                  35

ctg gcg gct cag ggg gaa att gag cac gac atc acg ctg gtt ccg gcg   259
Leu Ala Ala Gln Gly Glu Ile Glu His Asp Ile Thr Leu Val Pro Ala
        40                  45                  50

ccc acc cgc gcc acc tcg cga cgc cgg cgg ggc ggc gat ccg gtt gag   307
Pro Thr Arg Ala Thr Ser Arg Arg Arg Arg Gly Gly Asp Pro Val Glu
    55                  60                  65

cgg gtg tgc aat gca tca cgc tta tcg acg ttt ccc tgc ctt caa atc   355
Arg Val Cys Asn Ala Ser Arg Leu Ser Thr Phe Pro Cys Leu Gln Ile
70                  75                  80                  85

tca tcc cgc aca cca gac tcc gtc ggt caa act gcg caa cag cga aga   403
Ser Ser Arg Thr Pro Asp Ser Val Gly Gln Thr Ala Gln Gln Arg Arg
                90                  95                  100

ctc aat atg cga gtg gag tta gtc cga caa cct cgg ggt tct gtc ttg   451
Leu Asn Met Arg Val Glu Leu Val Arg Gln Pro Arg Gly Ser Val Leu
            105                 110                 115

atc atc gac gat gtg gta aca acg ggg gca act att tcc gca tct gca   499
Ile Ile Asp Asp Val Val Thr Thr Gly Ala Thr Ile Ser Ala Ser Ala
        120                 125                 130

aac gtt ctt cgc gca gcg ggt gtg cag gtc aga gga gct tta act tat   547
Asn Val Leu Arg Ala Ala Gly Val Gln Val Arg Gly Ala Leu Thr Tyr
    135                 140                 145

tgc caa gcg tgatcttgga tataaaaggg gcc                            579
Cys Gln Ala
150


<210> 1602
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 1602
Leu Ser Pro Tyr Asp Gly Pro His Arg Asn Val Leu Ile Ala Leu Lys
  1               5                  10                  15

Glu His Gly Arg Ala Asp Leu Val Ala Phe Val Gly Ala Val Val Gly
            20                  25                  30

Ala Ser Ile Ser Tyr Leu Ala Ala Gln Gly Glu Ile Glu His Asp Ile
        35                  40                  45
```

```
Thr Leu Val Pro Ala Pro Thr Arg Ala Thr Ser Arg Arg Arg Arg Gly
     50                  55                  60

Gly Asp Pro Val Glu Arg Val Cys Asn Ala Ser Arg Leu Ser Thr Phe
 65                  70                  75                  80

Pro Cys Leu Gln Ile Ser Ser Arg Thr Pro Asp Ser Val Gly Gln Thr
                85                  90                  95

Ala Gln Gln Arg Arg Leu Asn Met Arg Val Glu Leu Val Arg Gln Pro
            100                 105                 110

Arg Gly Ser Val Leu Ile Ile Asp Asp Val Val Thr Thr Gly Ala Thr
        115                 120                 125

Ile Ser Ala Ser Ala Asn Val Leu Arg Ala Ala Gly Val Gln Val Arg
    130                 135                 140

Gly Ala Leu Thr Tyr Cys Gln Ala
145                 150
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<210> 1603
<211> 693
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(670)
<223> RXA00134

<400> 1603

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gcagctgtgc tccaccagtg actaaaaact tgtctttcac gtgccccacc ttatccgtgt 60

tccccacccc tgtgcgtaac gacagctaga atctcaagtt atg gcc gtt cat tta   115
                                              Met Ala Val His Leu
                                                1               5

acc aag atc tat acg cga acc ggg gac gat gga acc acg ggg ctc tca   163
Thr Lys Ile Tyr Thr Arg Thr Gly Asp Asp Gly Thr Thr Gly Leu Ser
                10                  15                  20

aat ttt gag cga gtt ccc aag gac gat ccc cgc ctt att gca tac gcc   211
Asn Phe Glu Arg Val Pro Lys Asp Asp Pro Arg Leu Ile Ala Tyr Ala
            25                  30                  35

gac tcc gat gaa gca aac tgt gcg att ggc caa gtg ctt gca ctc agc   259
Asp Ser Asp Glu Ala Asn Cys Ala Ile Gly Gln Val Leu Ala Leu Ser
        40                  45                  50

agc cct acg gaa gat atg gca acc tta ttg cgg act att caa aat gaa   307
Ser Pro Thr Glu Asp Met Ala Thr Leu Leu Arg Thr Ile Gln Asn Glu
    55                  60                  65

ctt ttt gat gtg ggc gca gac tta gca acc ccg att gag gag aat ccg   355
Leu Phe Asp Val Gly Ala Asp Leu Ala Thr Pro Ile Glu Glu Asn Pro
70                  75                  80                  85

aag tat ccc cca ctt cga gtt ctt ccg gaa tat atc gaa cga ctt gag   403
Lys Tyr Pro Pro Leu Arg Val Leu Pro Glu Tyr Ile Glu Arg Leu Glu
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```
                    90                  95                  100

aag gag tgc gat aaa tgg aac gag gat gtg ccg gcg ttg gat tcc ttc   451
Lys Glu Cys Asp Lys Trp Asn Glu Asp Val Pro Ala Leu Asp Ser Phe
            105                 110                 115

att ttg ccg ggt ggc acg cca gca gcg gca ctc ttg cac acc gca agg   499
Ile Leu Pro Gly Gly Thr Pro Ala Ala Ala Leu Leu His Thr Ala Arg
        120                 125                 130

gta att acg agg cgc gcg gag aga gca gct tgg ata gcg gtg cgg gaa   547
Val Ile Thr Arg Arg Ala Glu Arg Ala Ala Trp Ile Ala Val Arg Glu
    135                 140                 145

ttt ccg agc acc acc tct acc ttg cca gcc caa tac ctg aat cgt ctt   595
Phe Pro Ser Thr Thr Ser Thr Leu Pro Ala Gln Tyr Leu Asn Arg Leu
150                 155                 160                 165

agc gat ctg ctg ttt att ctt tcc cgt gtt gcc aac aat ggc aat gat   643
Ser Asp Leu Leu Phe Ile Leu Ser Arg Val Ala Asn Asn Gly Asn Asp
                170                 175                 180

gtg aag tgg gtt ccg ggc gga aaa aga tgaaaaccac cctgcgaccg         690
Val Lys Trp Val Pro Gly Gly Lys Arg
            185                 190

tga                                                              693


<210> 1604
<211> 190
<212> PRT
<213> Corynebacterium glutamicum

<400> 1604
Met Ala Val His Leu Thr Lys Ile Tyr Thr Arg Thr Gly Asp Asp Gly
  1               5                  10                  15

Thr Thr Gly Leu Ser Asn Phe Glu Arg Val Pro Lys Asp Asp Pro Arg
             20                  25                  30

Leu Ile Ala Tyr Ala Asp Ser Asp Glu Ala Asn Cys Ala Ile Gly Gln
         35                  40                  45

Val Leu Ala Leu Ser Ser Pro Thr Glu Asp Met Ala Thr Leu Leu Arg
     50                  55                  60

Thr Ile Gln Asn Glu Leu Phe Asp Val Gly Ala Asp Leu Ala Thr Pro
 65                  70                  75                  80

Ile Glu Glu Asn Pro Lys Tyr Pro Pro Leu Arg Val Leu Pro Glu Tyr
                 85                  90                  95

Ile Glu Arg Leu Glu Lys Glu Cys Asp Lys Trp Asn Glu Asp Val Pro
            100                 105                 110

Ala Leu Asp Ser Phe Ile Leu Pro Gly Gly Thr Pro Ala Ala Ala Leu
        115                 120                 125

Leu His Thr Ala Arg Val Ile Thr Arg Arg Ala Glu Arg Ala Ala Trp
    130                 135                 140
```

```
Ile Ala Val Arg Glu Phe Pro Ser Thr Thr Ser Thr Leu Pro Ala Gln
145                 150                 155                 160

Tyr Leu Asn Arg Leu Ser Asp Leu Leu Phe Ile Leu Ser Arg Val Ala
                165                 170                 175

Asn Asn Gly Asn Asp Val Lys Trp Val Pro Gly Gly Lys Arg
            180                 185                 190


<210> 1605
<211> 309
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(286)
<223> RXA00140

<400> 1605
ctcaacgata ttcagctttc cgcaatgctg aaaaacgcca tcgatcacgt cctcgcgatt 60

caagatgccg tagccaatgc aggcaaggaa atcggctaac atg tcg gac gag tcc   115
                                            Met Ser Asp Glu Ser
                                              1               5

atc gaa gag cag gaa aaa gaa ctc gcg gcg ctg aag gct caa atc gat   163
Ile Glu Glu Gln Glu Lys Glu Leu Ala Ala Leu Lys Ala Gln Ile Asp
                10                  15                  20

gaa ctg gaa aag aaa gac aag cag aac aag cta atc atc gag att ttg   211
Glu Leu Glu Lys Lys Asp Lys Gln Asn Lys Leu Ile Ile Glu Ile Leu
            25                  30                  35

tcc aag gcc gtc gaa aag aat gtg gca gag gca gaa gcg aaa aga gcc   259
Ser Lys Ala Val Glu Lys Asn Val Ala Glu Ala Glu Ala Lys Arg Ala
        40                  45                  50

cgc aaa tat ccg ccc aat ccc ctg tgg tgaattctaa ggcgtcgaac        306
Arg Lys Tyr Pro Pro Asn Pro Leu Trp
    55                  60

ttt                                                              309


<210> 1606
<211> 62
<212> PRT
<213> Corynebacterium glutamicum

<400> 1606
Met Ser Asp Glu Ser Ile Glu Glu Gln Glu Lys Glu Leu Ala Ala Leu
  1               5                  10                  15

Lys Ala Gln Ile Asp Glu Leu Glu Lys Lys Asp Lys Gln Asn Lys Leu
            20                  25                  30

Ile Ile Glu Ile Leu Ser Lys Ala Val Glu Lys Asn Val Ala Glu Ala
        35                  40                  45
```

```
Glu Ala Lys Arg Ala Arg Lys Tyr Pro Pro Asn Pro Leu Trp
     50                  55                  60


<210> 1607
<211> 585
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(562)
<223> RXA00141

<400> 1607
gtcggctcct acgttatgag ctccatcgaa tccgctgttc agtgcttcga atggcttgag 60

cagcaattcc cagatctagt cacctggaag gacgaacacc atg acc act gat tcc   115
                                            Met Thr Thr Asp Ser
                                              1               5

aat tct gcg aca atc cca acc cca aag ccg att cca gtg acc atc gac   163
Asn Ser Ala Thr Ile Pro Thr Pro Lys Pro Ile Pro Val Thr Ile Asp
                 10                  15                  20

cga atc tcc ctc atc atg aaa gaa ttc ggc att gac cta tcc atc gcc   211
Arg Ile Ser Leu Ile Met Lys Glu Phe Gly Ile Asp Leu Ser Ile Ala
             25                  30                  35

gat gaa caa ggc acc gga tcc caa gta gcc agc gcc aac ctc aac ggc   259
Asp Glu Gln Gly Thr Gly Ser Gln Val Ala Ser Ala Asn Leu Asn Gly
         40                  45                  50

cat cac gtc atg ttc gct gtc atc ggt tca gtc ctg atc gtt cgt gcc   307
His His Val Met Phe Ala Val Ile Gly Ser Val Leu Ile Val Arg Ala
     55                  60                  65

gat cgc gcc acc gaa atg cca gtc tcc gac ggc aac ccc gca tgg cat   355
Asp Arg Ala Thr Glu Met Pro Val Ser Asp Gly Asn Pro Ala Trp His
 70                  75                  80                  85

ctc gcc tgc aac caa gtc aac tgt ttc aac ttc gct gcc aag gct gtc   403
Leu Ala Cys Asn Gln Val Asn Cys Phe Asn Phe Ala Ala Lys Ala Val
                 90                  95                 100

gta gtt gat cgc acc gac aac atc gtg atc cgc gcc gag aag gat gtc   451
Val Val Asp Arg Thr Asp Asn Ile Val Ile Arg Ala Glu Lys Asp Val
            105                 110                 115

ccc atc gcc gct ggg ctc aac gat att cag ctt tcc gca atg ctg aaa   499
Pro Ile Ala Ala Gly Leu Asn Asp Ile Gln Leu Ser Ala Met Leu Lys
        120                 125                 130

aac gcc atc gat cac gtc ctc gcg att caa gat gcc gta gcc aat gca   547
Asn Ala Ile Asp His Val Leu Ala Ile Gln Asp Ala Val Ala Asn Ala
    135                 140                 145

ggc aag gaa atc ggc taacatgtcg gacgagtcca tcg                    585
Gly Lys Glu Ile Gly
150
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<210> 1608
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 1608
Met Thr Thr Asp Ser Asn Ser Ala Thr Ile Pro Thr Pro Lys Pro Ile
1 5 10 15

Pro Val Thr Ile Asp Arg Ile Ser Leu Ile Met Lys Glu Phe Gly Ile
20 25 30

Asp Leu Ser Ile Ala Asp Glu Gln Gly Thr Gly Ser Gln Val Ala Ser
35 40 45

Ala Asn Leu Asn Gly His His Val Met Phe Ala Val Ile Gly Ser Val
50 55 60

Leu Ile Val Arg Ala Asp Arg Ala Thr Glu Met Pro Val Ser Asp Gly
65 70 75 80

Asn Pro Ala Trp His Leu Ala Cys Asn Gln Val Asn Cys Phe Asn Phe
85 90 95

Ala Ala Lys Ala Val Val Val Asp Arg Thr Asp Asn Ile Val Ile Arg
100 105 110

Ala Glu Lys Asp Val Pro Ile Ala Ala Gly Leu Asn Asp Ile Gln Leu
115 120 125

Ser Ala Met Leu Lys Asn Ala Ile Asp His Val Leu Ala Ile Gln Asp
130 135 140

Ala Val Ala Asn Ala Gly Lys Glu Ile Gly
145 150

<210> 1609
<211> 600
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(577)
<223> RXA00142

<400> 1609
atcctcaatt tccgccgtaa gcgcaacgac taaaaccacc atctgtagtg tggtggaaaa 60

gttacttta aaaggatttt ggaaggactg aaactcccca gtg cct caa tca ccc 115
Val Pro Gln Ser Pro
1 5

aca gca cac gac ccc aac gac atc cag gaa ttt aac ctc gat gcc gtt 163
Thr Ala His Asp Pro Asn Asp Ile Gln Glu Phe Asn Leu Asp Ala Val
10 15 20

gca ggg att ctc cag gac gaa aaa ctg gac tac cgc atc gat gaa cac 211

```
Ala Gly Ile Leu Gln Asp Glu Lys Leu Asp Tyr Arg Ile Asp Glu His
            25                  30                  35

gac ggc gaa aaa gta atc cgc acc gga ttc atc aac gcc gcc atc agc   259
Asp Gly Glu Lys Val Ile Arg Thr Gly Phe Ile Asn Ala Ala Ile Ser
        40                  45                  50

ttc atc ctc tta gac ggc agc tta acc atg gaa gcc atg tgg cga gga   307
Phe Ile Leu Leu Asp Gly Ser Leu Thr Met Glu Ala Met Trp Arg Gly
    55                  60                  65

gcc ccc tcc acc gat gct gcc gca caa gtt ctc gcg gcc acc aac gaa   355
Ala Pro Ser Thr Asp Ala Ala Ala Gln Val Leu Ala Ala Thr Asn Glu
70                  75                  80                  85

tgg aac ctc acc cag ttc gca ccc acc att cga ttc ttc gaa ctc aac   403
Trp Asn Leu Thr Gln Phe Ala Pro Thr Ile Arg Phe Phe Glu Leu Asn
                90                  95                  100

gaa ggc acc ctc gcc atc aat gca ctg cga cac gtc gtt gtt tcc gca   451
Glu Gly Thr Leu Ala Ile Asn Ala Leu Arg His Val Val Val Ser Ala
            105                 110                 115

ggc atg agc cac aac caa gtc ggc tcc tac gtt atg agc tcc atc gaa   499
Gly Met Ser His Asn Gln Val Gly Ser Tyr Val Met Ser Ser Ile Glu
        120                 125                 130

tcc gct gtt cag tgc ttc gaa tgg ctt gag cag caa ttc cca gat cta   547
Ser Ala Val Gln Cys Phe Glu Trp Leu Glu Gln Gln Phe Pro Asp Leu
    135                 140                 145

gtc acc tgg aag gac gaa cac cat gac cac tgattccaat tctgcgacaa     597
Val Thr Trp Lys Asp Glu His His Asp His
150                 155

tcc                                                               600


<210> 1610
<211> 159
<212> PRT
<213> Corynebacterium glutamicum

<400> 1610
Val Pro Gln Ser Pro Thr Ala His Asp Pro Asn Asp Ile Gln Glu Phe
  1               5                  10                  15

Asn Leu Asp Ala Val Ala Gly Ile Leu Gln Asp Glu Lys Leu Asp Tyr
            20                  25                  30

Arg Ile Asp Glu His Asp Gly Glu Lys Val Ile Arg Thr Gly Phe Ile
        35                  40                  45

Asn Ala Ala Ile Ser Phe Ile Leu Leu Asp Gly Ser Leu Thr Met Glu
    50                  55                  60

Ala Met Trp Arg Gly Ala Pro Ser Thr Asp Ala Ala Ala Gln Val Leu
65                  70                  75                  80

Ala Ala Thr Asn Glu Trp Asn Leu Thr Gln Phe Ala Pro Thr Ile Arg
                85                  90                  95
```

```
Phe Phe Glu Leu Asn Glu Gly Thr Leu Ala Ile Asn Ala Leu Arg His
            100                 105                 110

Val Val Val Ser Ala Gly Met Ser His Asn Gln Val Gly Ser Tyr Val
        115                 120                 125

Met Ser Ser Ile Glu Ser Ala Val Gln Cys Phe Glu Trp Leu Glu Gln
    130                 135                 140

Gln Phe Pro Asp Leu Val Thr Trp Lys Asp Glu His His Asp His
145                 150                 155


<210> 1611
<211> 897
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(874)
<223> RXA00150

<400> 1611
agctgagcag ggatcggcac tagcttctac tacgataacg agaactttgt ttcaatacat 60

tcaaaatggc ggaatatttt gatcacgggg gtgcaactgt atg gtg ttt tct atg   115
                                            Met Val Phe Ser Met
                                              1               5

cat gac aaa ggt gag acc cag gag aat cct gcg gac atg tca gga cgc   163
His Asp Lys Gly Glu Thr Gln Glu Asn Pro Ala Asp Met Ser Gly Arg
                10                  15                  20

cta aac aca cca att tcc acg gtc ttt cac ttc ttt agc tca ctt ttc   211
Leu Asn Thr Pro Ile Ser Thr Val Phe His Phe Phe Ser Ser Leu Phe
            25                  30                  35

cat gac gct ctg cgc agt gtt gcc cag tgg agt gcg tgg aag aaa atc   259
His Asp Ala Leu Arg Ser Val Ala Gln Trp Ser Ala Trp Lys Lys Ile
        40                  45                  50

gct gta tcg gtt gtc atc gtc gca att att tcc gta act ttt ctt gtc   307
Ala Val Ser Val Val Ile Val Ala Ile Ile Ser Val Thr Phe Leu Val
    55                  60                  65

gat gtc ccc ccg att tcg gtt tat cgt gac tgg gca aac aac gcc ggc   355
Asp Val Pro Pro Ile Ser Val Tyr Arg Asp Trp Ala Asn Asn Ala Gly
70                  75                  80                  85

gac gct ttt gtc tta gtt ttt tgc gcc ttt tat atc ctc att act cag   403
Asp Ala Phe Val Leu Val Phe Cys Ala Phe Tyr Ile Leu Ile Thr Gln
                90                  95                  100

ttc cct atc ccc cgc aca gtt ctc aca ctg gcc tcc ggc gtg ctg ttc   451
Phe Pro Ile Pro Arg Thr Val Leu Thr Leu Ala Ser Gly Val Leu Phe
            105                 110                 115

ggg ccg gtt ctt gga tca gtc gtg gcg ctg ggt tcc acc aca gtg tca   499
Gly Pro Val Leu Gly Ser Val Val Ala Leu Gly Ser Thr Thr Val Ser
```

```
        120                 125                 130

gcg gta atc tcg ctc ctc att gtt cgg ggt ctg ctt ggc gat tgg atg   547
Ala Val Ile Ser Leu Leu Ile Val Arg Gly Leu Leu Gly Asp Trp Met
    135                 140                 145

gcg cca cgt tta acg cac ccc gca gtc tca cgc atc aat acc cga ctt   595
Ala Pro Arg Leu Thr His Pro Ala Val Ser Arg Ile Asn Thr Arg Leu
150                 155                 160                 165

gag caa cgt gga tgg ctg gcg att acc tct tta aga atg atc gcc gct   643
Glu Gln Arg Gly Trp Leu Ala Ile Thr Ser Leu Arg Met Ile Ala Ala
                170                 175                 180

atc ccc ttt tcc atc ctc aac tat gtt gca gcc ttg act agc gtt cct   691
Ile Pro Phe Ser Ile Leu Asn Tyr Val Ala Ala Leu Thr Ser Val Pro
            185                 190                 195

gtt ttt tct ttt gcc atc gct acc ttg atc gga tct gca cca gga acc   739
Val Phe Ser Phe Ala Ile Ala Thr Leu Ile Gly Ser Ala Pro Gly Thr
        200                 205                 210

atc gtc acc gtc gtt ttg gga gat gca gtc aca ggt tct gga aac tgg   787
Ile Val Thr Val Val Leu Gly Asp Ala Val Thr Gly Ser Gly Asn Trp
    215                 220                 225

act gcc gtt gca ttc acg gta ttt tta gcg att ttg ggt gtt tta ggt   835
Thr Ala Val Ala Phe Thr Val Phe Leu Ala Ile Leu Gly Val Leu Gly
230                 235                 240                 245

atc ttt tta gat caa aag atg cca gtc aag cct gga aag tagacaatat    884
Ile Phe Leu Asp Gln Lys Met Pro Val Lys Pro Gly Lys
                250                 255

aaggtagggt tgg                                                   897


<210> 1612
<211> 258
<212> PRT
<213> Corynebacterium glutamicum

<400> 1612
Met Val Phe Ser Met His Asp Lys Gly Glu Thr Gln Glu Asn Pro Ala
  1               5                  10                  15

Asp Met Ser Gly Arg Leu Asn Thr Pro Ile Ser Thr Val Phe His Phe
             20                  25                  30

Phe Ser Ser Leu Phe His Asp Ala Leu Arg Ser Val Ala Gln Trp Ser
         35                  40                  45

Ala Trp Lys Lys Ile Ala Val Ser Val Val Ile Val Ala Ile Ile Ser
     50                  55                  60

Val Thr Phe Leu Val Asp Val Pro Pro Ile Ser Val Tyr Arg Asp Trp
 65                  70                  75                  80

Ala Asn Asn Ala Gly Asp Ala Phe Val Leu Val Phe Cys Ala Phe Tyr
                 85                  90                  95
```

```
Ile Leu Ile Thr Gln Phe Pro Ile Pro Arg Thr Val Leu Thr Leu Ala
            100                 105                 110

Ser Gly Val Leu Phe Gly Pro Val Leu Gly Ser Val Val Ala Leu Gly
        115                 120                 125

Ser Thr Thr Val Ser Ala Val Ile Ser Leu Leu Ile Val Arg Gly Leu
    130                 135                 140

Leu Gly Asp Trp Met Ala Pro Arg Leu Thr His Pro Ala Val Ser Arg
145                 150                 155                 160

Ile Asn Thr Arg Leu Glu Gln Arg Gly Trp Leu Ala Ile Thr Ser Leu
                165                 170                 175

Arg Met Ile Ala Ala Ile Pro Phe Ser Ile Leu Asn Tyr Val Ala Ala
            180                 185                 190

Leu Thr Ser Val Pro Val Phe Ser Phe Ala Ile Ala Thr Leu Ile Gly
        195                 200                 205

Ser Ala Pro Gly Thr Ile Val Thr Val Val Leu Gly Asp Ala Val Thr
    210                 215                 220

Gly Ser Gly Asn Trp Thr Ala Val Ala Phe Thr Val Phe Leu Ala Ile
225                 230                 235                 240

Leu Gly Val Leu Gly Ile Phe Leu Asp Gln Lys Met Pro Val Lys Pro
                245                 250                 255

Gly Lys
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<210> 1613
<211> 720
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(697)
<223> RXA00151

<400> 1613

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aagtagacaa tataaggtag ggttggagaa gattctttac ttcttcactc attcgccctg 60

acagcgaatc cactacaata aacaaagggg gcagccaccc atg tgg gca ctg cat   115
                                              Met Trp Ala Leu His
                                                1               5

gcc aga tac cgc ggc cga gac aca cga cga gcc gaa ttg gtt aaa aga   163
Ala Arg Tyr Arg Gly Arg Asp Thr Arg Arg Ala Glu Leu Val Lys Arg
                10                  15                  20

ttt gca gaa gct ttg tcc acc ctc gaa ggt gct ggc cag ttt gaa gtc   211
Phe Ala Glu Ala Leu Ser Thr Leu Glu Gly Ala Gly Gln Phe Glu Val
            25                  30                  35

att ggt gtc gaa gac atc cga gca cac atc acc tca ccg tta acc aca   259
Ile Gly Val Glu Asp Ile Arg Ala His Ile Thr Ser Pro Leu Thr Thr
```

```
         40                  45                  50

tgt gat gtt gtc atg gcg cta ctc gca gct ggc gat tgg gca atc gga   307
Cys Asp Val Val Met Ala Leu Leu Ala Ala Gly Asp Trp Ala Ile Gly
     55                  60                  65

att ggt gtt atc ccc acc gtt gac gga aca gtc gat gaa tcg gat gag   355
Ile Gly Val Ile Pro Thr Val Asp Gly Thr Val Asp Glu Ser Asp Glu
 70                  75                  80                  85

gcc atc atc gaa cag gta aag aaa att tcc tct gat gct ctg cgc ccc   403
Ala Ile Ile Glu Gln Val Lys Lys Ile Ser Ser Asp Ala Leu Arg Pro
                90                  95                 100

acc gcc aag gcg gga acg gtc aaa gtt agg atc gcc gga acc aaa cgg   451
Thr Ala Lys Ala Gly Thr Val Lys Val Arg Ile Ala Gly Thr Lys Arg
            105                 110                 115

gac aat act caa gcc ttc aac atc tcc gct gca ttc acg ttg att ggg   499
Asp Asn Thr Gln Ala Phe Asn Ile Ser Ala Ala Phe Thr Leu Ile Gly
        120                 125                 130

caa gtt ctg tca aag cgc acc atc gaa gga cgc gaa gcc acc gca ctc   547
Gln Val Leu Ser Lys Arg Thr Ile Glu Gly Arg Glu Ala Thr Ala Leu
    135                 140                 145

gtc cgt tct gga ctg aat caa aat gag gca gcc caa gag ctc ggt att   595
Val Arg Ser Gly Leu Asn Gln Asn Glu Ala Ala Gln Glu Leu Gly Ile
150                 155                 160                 165

tcc aag cag gca atg tcg cag cga ttg cag gcg gca ggt tgg cag gcg   643
Ser Lys Gln Ala Met Ser Gln Arg Leu Gln Ala Ala Gly Trp Gln Ala
                170                 175                 180

gaa tct gct ggt tgg caa ttg gcc gta aac ctc atc gag cag gct ggc   691
Glu Ser Ala Gly Trp Gln Leu Ala Val Asn Leu Ile Glu Gln Ala Gly
            185                 190                 195

aag cgc tagcaggcga tttaagagcc tga                                720
Lys Arg
```

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<210> 1614
<211> 199
<212> PRT
<213> Corynebacterium glutamicum

<400> 1614

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Met Trp Ala Leu His Ala Arg Tyr Arg Gly Arg Asp Thr Arg Arg Ala
  1               5                  10                  15

Glu Leu Val Lys Arg Phe Ala Glu Ala Leu Ser Thr Leu Glu Gly Ala
             20                  25                  30

Gly Gln Phe Glu Val Ile Gly Val Glu Asp Ile Arg Ala His Ile Thr
         35                  40                  45

Ser Pro Leu Thr Thr Cys Asp Val Val Met Ala Leu Leu Ala Ala Gly
     50                  55                  60
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```
Asp Trp Ala Ile Gly Ile Gly Val Ile Pro Thr Val Asp Gly Thr Val
 65                  70                  75                  80

Asp Glu Ser Asp Glu Ala Ile Ile Glu Gln Val Lys Lys Ile Ser Ser
                85                  90                  95

Asp Ala Leu Arg Pro Thr Ala Lys Ala Gly Thr Val Lys Val Arg Ile
            100                 105                 110

Ala Gly Thr Lys Arg Asp Asn Thr Gln Ala Phe Asn Ile Ser Ala Ala
        115                 120                 125

Phe Thr Leu Ile Gly Gln Val Leu Ser Lys Arg Thr Ile Glu Gly Arg
    130                 135                 140

Glu Ala Thr Ala Leu Val Arg Ser Gly Leu Asn Gln Asn Glu Ala Ala
145                 150                 155                 160

Gln Glu Leu Gly Ile Ser Lys Gln Ala Met Ser Gln Arg Leu Gln Ala
                165                 170                 175

Ala Gly Trp Gln Ala Glu Ser Ala Gly Trp Gln Leu Ala Val Asn Leu
            180                 185                 190

Ile Glu Gln Ala Gly Lys Arg
        195


<210> 1615
<211> 549
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(526)
<223> RXA00153

<400> 1615
cctcgatttg agtaaagagg acgtcctcgc ctgatttttc gggtgtgttt ttgcgtggcg 60

agccctgcct ggcccttcca aattatgtag ggtggcctgc gtg gga gca ata att   115
                                            Val Gly Ala Ile Ile
                                              1               5

tgg ttt atc gga gca ttg gtt ctt gct ggc ttg gaa ttg gca gta ggt   163
Trp Phe Ile Gly Ala Leu Val Leu Ala Gly Leu Glu Leu Ala Val Gly
                10                  15                  20

gag ttc acc tta ttg atg ctc ggc ggt gca gct ttg gca acc gcc ggc   211
Glu Phe Thr Leu Leu Met Leu Gly Gly Ala Ala Leu Ala Thr Ala Gly
            25                  30                  35

gtg gca ctc atc ggt gtc cca gta tgg gct gaa ttt gtc acc ttc gcg   259
Val Ala Leu Ile Gly Val Pro Val Trp Ala Glu Phe Val Thr Phe Ala
        40                  45                  50

gtg gcc tca gct gct cta ctg atg ttc att agg ccg gcc att aga aag   307
Val Ala Ser Ala Ala Leu Leu Met Phe Ile Arg Pro Ala Ile Arg Lys
    55                  60                  65
```

```
cgt ctg ctg aaa cca aag gtt ctg gac tct tca cca cga gca ctt gtt   355
Arg Leu Leu Lys Pro Lys Val Leu Asp Ser Ser Pro Arg Ala Leu Val
 70                  75                  80                  85

ggc cac cgt gct gaa gtg ctc gaa gat gtc gga gcg acc agc ggg cag   403
Gly His Arg Ala Glu Val Leu Glu Asp Val Gly Ala Thr Ser Gly Gln
                90                  95                 100

gtc cgc ctg gat ggt tca att tgg tcc gcc cgc agc atg gat ccc aca   451
Val Arg Leu Asp Gly Ser Ile Trp Ser Ala Arg Ser Met Asp Pro Thr
            105                 110                 115

cac acc ttc gcg gaa ggt gaa att gtc agt gtc att gat atc caa ggc   499
His Thr Phe Ala Glu Gly Glu Ile Val Ser Val Ile Asp Ile Gln Gly
        120                 125                 130

acg acc gcg att gta tgg aaa gaa gcc taaattttta acaatcaaat         546
Thr Thr Ala Ile Val Trp Lys Glu Ala
    135                 140

agt                                                               549
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<210> 1616
<211> 142
<212> PRT
<213> Corynebacterium glutamicum

<400> 1616

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Val Gly Ala Ile Ile Trp Phe Ile Gly Ala Leu Val Leu Ala Gly Leu
  1               5                  10                  15

Glu Leu Ala Val Gly Glu Phe Thr Leu Leu Met Leu Gly Gly Ala Ala
             20                  25                  30

Leu Ala Thr Ala Gly Val Ala Leu Ile Gly Val Pro Val Trp Ala Glu
         35                  40                  45

Phe Val Thr Phe Ala Val Ala Ser Ala Ala Leu Leu Met Phe Ile Arg
     50                  55                  60

Pro Ala Ile Arg Lys Arg Leu Leu Lys Pro Lys Val Leu Asp Ser Ser
 65                  70                  75                  80

Pro Arg Ala Leu Val Gly His Arg Ala Glu Val Leu Glu Asp Val Gly
                85                  90                  95

Ala Thr Ser Gly Gln Val Arg Leu Asp Gly Ser Ile Trp Ser Ala Arg
            100                 105                 110

Ser Met Asp Pro Thr His Thr Phe Ala Glu Gly Glu Ile Val Ser Val
        115                 120                 125

Ile Asp Ile Gln Gly Thr Thr Ala Ile Val Trp Lys Glu Ala
    130                 135                 140
```

<210> 1617
<211> 906
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(883)
<223> RXA00155

<400> 1617
gttgcgggag tgtccaccaa aaatattgcc tgcatagggg tctgaaaaac tcatagctca 60

ccaccctagt caaagcactg cactacactt ccctaacact atg gaa att cga gca 115
Met Glu Ile Arg Ala
1 5

aac gtt tat tca ccg ctt caa aat act gcc gtc tgg cta ggt gcg tgg 163
Asn Val Tyr Ser Pro Leu Gln Asn Thr Ala Val Trp Leu Gly Ala Trp
10 15 20

ctc tat gaa tta gtg ccc acc gaa gat gtc atc gat gcg ttc gtc gat 211
Leu Tyr Glu Leu Val Pro Thr Glu Asp Val Ile Asp Ala Phe Val Asp
25 30 35

ctc ggc ggc ccg cac acc ttc ggc gac ggc ggg ctg ctc gat atg ctg 259
Leu Gly Gly Pro His Thr Phe Gly Asp Gly Gly Leu Leu Asp Met Leu
40 45 50

cga act tta aaa gaa tta aca agc acg ctt atc gac gcc ccc ttc cac 307
Arg Thr Leu Lys Glu Leu Thr Ser Thr Leu Ile Asp Ala Pro Phe His
55 60 65

ggt ccg att tta act ctc gca ctc agc ggc cca ggc caa gtg ccg gcg 355
Gly Pro Ile Leu Thr Leu Ala Leu Ser Gly Pro Gly Gln Val Pro Ala
70 75 80 85

ttg ccg gca ggt tca cgc gct gcg gtc ttg gcc tcc gcc tcg aag gag 403
Leu Pro Ala Gly Ser Arg Ala Ala Val Leu Ala Ser Ala Ser Lys Glu
90 95 100

ggg gcg ttg gtg ctg ggc ggc gtc gat aag cag cat tct tgg gcg ctt 451
Gly Ala Leu Val Leu Gly Gly Val Asp Lys Gln His Ser Trp Ala Leu
105 110 115

att cct acg cgc ggt aag gat gcc act gag tgg aat ttg gtg gag gtg 499
Ile Pro Thr Arg Gly Lys Asp Ala Thr Glu Trp Asn Leu Val Glu Val
120 125 130

gag ggc ttt ttg ccg gcg att gcg act gtc tcg ccc ggt gag gcg gat 547
Glu Gly Phe Leu Pro Ala Ile Ala Thr Val Ser Pro Gly Glu Ala Asp
135 140 145

cag ctg ctc cgt cag gcg aca gat cag gcg gca aat atc att gag tta 595
Gln Leu Leu Arg Gln Ala Thr Asp Gln Ala Ala Asn Ile Ile Glu Leu
150 155 160 165

agt ggc tac gct tca ctt gcg ccg aaa tct ttg aag aat ccg cga cta 643
Ser Gly Tyr Ala Ser Leu Ala Pro Lys Ser Leu Lys Asn Pro Arg Leu
170 175 180

acc gtg ggc atg ctg tca gat ttt tac gac acc ccg ggg ctt ccc tat 691
Thr Val Gly Met Leu Ser Asp Phe Tyr Asp Thr Pro Gly Leu Pro Tyr
185 190 195

```
gca gtc cca gag agg tcg gcg aag ctt ttt gcg cgc gca gat cgc gtg   739
Ala Val Pro Glu Arg Ser Ala Lys Leu Phe Ala Arg Ala Asp Arg Val
        200                 205                 210

gct gcc atc gca gag acc gtg cag gaa acc atc ggc gat cac agc ctg   787
Ala Ala Ile Ala Glu Thr Val Gln Glu Thr Ile Gly Asp His Ser Leu
    215                 220                 225

gat cca cag ttg att ttc ctg tgg agc cat att cgg acc gcg cgc atg   835
Asp Pro Gln Leu Ile Phe Leu Trp Ser His Ile Arg Thr Ala Arg Met
230                 235                 240                 245

gct ggg gtg agt tat gcc ctc gca gag ttt gcg agg gac tat cac tcc   883
Ala Gly Val Ser Tyr Ala Leu Ala Glu Phe Ala Arg Asp Tyr His Ser
                250                 255                 260

tagttggcag ctggcgccgc tga                                        906


<210> 1618
<211> 261
<212> PRT
<213> Corynebacterium glutamicum

<400> 1618
Met Glu Ile Arg Ala Asn Val Tyr Ser Pro Leu Gln Asn Thr Ala Val
  1               5                  10                  15

Trp Leu Gly Ala Trp Leu Tyr Glu Leu Val Pro Thr Glu Asp Val Ile
             20                  25                  30

Asp Ala Phe Val Asp Leu Gly Gly Pro His Thr Phe Gly Asp Gly Gly
         35                  40                  45

Leu Leu Asp Met Leu Arg Thr Leu Lys Glu Leu Thr Ser Thr Leu Ile
     50                  55                  60

Asp Ala Pro Phe His Gly Pro Ile Leu Thr Leu Ala Leu Ser Gly Pro
 65                  70                  75                  80

Gly Gln Val Pro Ala Leu Pro Ala Gly Ser Arg Ala Ala Val Leu Ala
                 85                  90                  95

Ser Ala Ser Lys Glu Gly Ala Leu Val Leu Gly Gly Val Asp Lys Gln
            100                 105                 110

His Ser Trp Ala Leu Ile Pro Thr Arg Gly Lys Asp Ala Thr Glu Trp
        115                 120                 125

Asn Leu Val Glu Val Glu Gly Phe Leu Pro Ala Ile Ala Thr Val Ser
    130                 135                 140

Pro Gly Glu Ala Asp Gln Leu Leu Arg Gln Ala Thr Asp Gln Ala Ala
145                 150                 155                 160

Asn Ile Ile Glu Leu Ser Gly Tyr Ala Ser Leu Ala Pro Lys Ser Leu
                165                 170                 175

Lys Asn Pro Arg Leu Thr Val Gly Met Leu Ser Asp Phe Tyr Asp Thr
            180                 185                 190
```

```
Pro Gly Leu Pro Tyr Ala Val Pro Glu Arg Ser Ala Lys Leu Phe Ala
        195                 200                 205

Arg Ala Asp Arg Val Ala Ala Ile Ala Glu Thr Val Gln Glu Thr Ile
    210                 215                 220

Gly Asp His Ser Leu Asp Pro Gln Leu Ile Phe Leu Trp Ser His Ile
225                 230                 235                 240

Arg Thr Ala Arg Met Ala Gly Val Ser Tyr Ala Leu Ala Glu Phe Ala
                245                 250                 255

Arg Asp Tyr His Ser
            260


<210> 1619
<211> 1305
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1282)
<223> RXA00159

<400> 1619
cttagggggt aaccccaccc ctgtacaagt tttcgtgcta ccaaacacgc cgtgctaggg 60

gtgtcgcatg gtgcaatgat ccccgctaac ctgggattcc atg gag aat gtt agt   115
                                            Met Glu Asn Val Ser
                                              1               5

tcc gtc acg tcg gat ggt tcg gta gcg gat gtg cat gcc gaa cgg tgg   163
Ser Val Thr Ser Asp Gly Ser Val Ala Asp Val His Ala Glu Arg Trp
                10                  15                  20

caa gaa ttg ctc gca cgt ttg gat gcc gat gcg ccg gat att gcg gag   211
Gln Glu Leu Leu Ala Arg Leu Asp Ala Asp Ala Pro Asp Ile Ala Glu
            25                  30                  35

ggc acc gcc gca aag ttg ctc gct acg atc ccg ggc tat gag ctc gtt   259
Gly Thr Ala Ala Lys Leu Leu Ala Thr Ile Pro Gly Tyr Glu Leu Val
        40                  45                  50

gac gcg ggg ccg atc agg gag tcg tcg ata cgc aat acg gcc ttg att   307
Asp Ala Gly Pro Ile Arg Glu Ser Ser Ile Arg Asn Thr Ala Leu Ile
    55                  60                  65

att cgc gtg att aac gcg ggc acc gag cca aag gcc gag gac ttg cct   355
Ile Arg Val Ile Asn Ala Gly Thr Glu Pro Lys Ala Glu Asp Leu Pro
70                  75                  80                  85

gag gct tta agg ctt gcc gac gaa cgt ata gcg caa aat gtg ccg ctg   403
Glu Ala Leu Arg Leu Ala Asp Glu Arg Ile Ala Gln Asn Val Pro Leu
                90                  95                  100

gga agt gtg ctg cac ggt ttt cgg atg tct ctg ggg gaa att ctg gag   451
Gly Ser Val Leu His Gly Phe Arg Met Ser Leu Gly Glu Ile Leu Glu
            105                 110                 115
```

```
cat ttg gtg cag ttg ggc ccg gaa tac aat att gat ccc ggc aga atg   499
His Leu Val Gln Leu Gly Pro Glu Tyr Asn Ile Asp Pro Gly Arg Met
        120                 125                 130

ctg cgc tgg tcc aca ctg atg tgg gcg gtc aat gat gcc ttt tct acg   547
Leu Arg Trp Ser Thr Leu Met Trp Ala Val Asn Asp Ala Phe Ser Thr
    135                 140                 145

cgt gcc aca agg gtg tac cgc gat cac gag gtc gcc acg gcg atc gcc   595
Arg Ala Thr Arg Val Tyr Arg Asp His Glu Val Ala Thr Ala Ile Ala
150                 155                 160                 165

gat tcg gtg cga agg tca gaa tgg atc ggc aaa gcg gtc tcg gaa ggc   643
Asp Ser Val Arg Arg Ser Glu Trp Ile Gly Lys Ala Val Ser Glu Gly
                170                 175                 180

tct gaa ctg tca gag ctt tta tgg ggt gct gcg atg tat gac gtt ccc   691
Ser Glu Leu Ser Glu Leu Leu Trp Gly Ala Ala Met Tyr Asp Val Pro
            185                 190                 195

gcc gac act cct cta aga gca ttg gca gcc acc tca cct gat cat gcg   739
Ala Asp Thr Pro Leu Arg Ala Leu Ala Ala Thr Ser Pro Asp His Ala
        200                 205                 210

aaa gct gaa aca cag atc cag aag tgg act cag cgc gcc gga gtg cgg   787
Lys Ala Glu Thr Gln Ile Gln Lys Trp Thr Gln Arg Ala Gly Val Arg
    215                 220                 225

gtg ctg gca tcg gtg cag cca agc gtg atc gtg ggg atc gtg att ggg   835
Val Leu Ala Ser Val Gln Pro Ser Val Ile Val Gly Ile Val Ile Gly
230                 235                 240                 245

gag ccg aag cga aac gtg gac ggc cct ggt ttt gct gtg ggt ttg ggt   883
Glu Pro Lys Arg Asn Val Asp Gly Pro Gly Phe Ala Val Gly Leu Gly
                250                 255                 260

agg gca gag gtg ctc tca aag ctg gcg gac tca tat aag gat gca tcc   931
Arg Ala Glu Val Leu Ser Lys Leu Ala Asp Ser Tyr Lys Asp Ala Ser
            265                 270                 275

ctt gta ttg aag gct gcc gat aat ctg aaa ctt aat gag gtg cag cgg   979
Leu Val Leu Lys Ala Ala Asp Asn Leu Lys Leu Asn Glu Val Gln Arg
        280                 285                 290

gca caa gat ttg tca tgg aag ttg gct atc cat gca agc cca cgg gtg   1027
Ala Gln Asp Leu Ser Trp Lys Leu Ala Ile His Ala Ser Pro Arg Val
    295                 300                 305

acg gag att ctt gcg cag aaa tat gtg aag cca cta agg gaa tct ggc   1075
Thr Glu Ile Leu Ala Gln Lys Tyr Val Lys Pro Leu Arg Glu Ser Gly
310                 315                 320                 325

gag ttt gct cat gag atc gtg gaa tct ttg cgg gca tat gtg gac aac   1123
Glu Phe Ala His Glu Ile Val Glu Ser Leu Arg Ala Tyr Val Asp Asn
                330                 335                 340

cag atg aat att cct gct gct gcg cgc agt att cct gtg cat gtg aat   1171
Gln Met Asn Ile Pro Ala Ala Ala Arg Ser Ile Pro Val His Val Asn
            345                 350                 355

acg ctt cgc tat cgg ttg cgc cgg ttt gag gag tta acg ggc tgc tat   1219
```

```
Thr Leu Arg Tyr Arg Leu Arg Arg Phe Glu Glu Leu Thr Gly Cys Tyr
        360                 365                 370

ttg gag gat aca tcc acg gtc att gaa gtg tcg tgg gtg ctg gaa gtc   1267
Leu Glu Asp Thr Ser Thr Val Ile Glu Val Ser Trp Val Leu Glu Val
    375                 380                 385

ttt ggc cgg gag ctg tagaaaattg cacctatata tat                     1305
Phe Gly Arg Glu Leu
390
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<210> 1620
<211> 394
<212> PRT
<213> Corynebacterium glutamicum

<400> 1620

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Met Glu Asn Val Ser Ser Val Thr Ser Asp Gly Ser Val Ala Asp Val
  1               5                  10                  15

His Ala Glu Arg Trp Gln Glu Leu Leu Ala Arg Leu Asp Ala Asp Ala
             20                  25                  30

Pro Asp Ile Ala Glu Gly Thr Ala Ala Lys Leu Leu Ala Thr Ile Pro
         35                  40                  45

Gly Tyr Glu Leu Val Asp Ala Gly Pro Ile Arg Glu Ser Ser Ile Arg
     50                  55                  60

Asn Thr Ala Leu Ile Ile Arg Val Ile Asn Ala Gly Thr Glu Pro Lys
 65                  70                  75                  80

Ala Glu Asp Leu Pro Glu Ala Leu Arg Leu Ala Asp Glu Arg Ile Ala
                 85                  90                  95

Gln Asn Val Pro Leu Gly Ser Val Leu His Gly Phe Arg Met Ser Leu
            100                 105                 110

Gly Glu Ile Leu Glu His Leu Val Gln Leu Gly Pro Glu Tyr Asn Ile
        115                 120                 125

Asp Pro Gly Arg Met Leu Arg Trp Ser Thr Leu Met Trp Ala Val Asn
    130                 135                 140

Asp Ala Phe Ser Thr Arg Ala Thr Arg Val Tyr Arg Asp His Glu Val
145                 150                 155                 160

Ala Thr Ala Ile Ala Asp Ser Val Arg Arg Ser Glu Trp Ile Gly Lys
                165                 170                 175

Ala Val Ser Glu Gly Ser Glu Leu Ser Glu Leu Leu Trp Gly Ala Ala
            180                 185                 190

Met Tyr Asp Val Pro Ala Asp Thr Pro Leu Arg Ala Leu Ala Ala Thr
        195                 200                 205

Ser Pro Asp His Ala Lys Ala Glu Thr Gln Ile Gln Lys Trp Thr Gln
    210                 215                 220

Arg Ala Gly Val Arg Val Leu Ala Ser Val Gln Pro Ser Val Ile Val
```

```
225                 230                 235                 240

Gly Ile Val Ile Gly Glu Pro Lys Arg Asn Val Asp Gly Pro Gly Phe
                245                 250                 255

Ala Val Gly Leu Gly Arg Ala Glu Val Leu Ser Lys Leu Ala Asp Ser
            260                 265                 270

Tyr Lys Asp Ala Ser Leu Val Leu Lys Ala Ala Asp Asn Leu Lys Leu
        275                 280                 285

Asn Glu Val Gln Arg Ala Gln Asp Leu Ser Trp Lys Leu Ala Ile His
    290                 295                 300

Ala Ser Pro Arg Val Thr Glu Ile Leu Ala Gln Lys Tyr Val Lys Pro
305                 310                 315                 320

Leu Arg Glu Ser Gly Glu Phe Ala His Glu Ile Val Glu Ser Leu Arg
                325                 330                 335

Ala Tyr Val Asp Asn Gln Met Asn Ile Pro Ala Ala Ala Arg Ser Ile
            340                 345                 350

Pro Val His Val Asn Thr Leu Arg Tyr Arg Leu Arg Arg Phe Glu Glu
        355                 360                 365

Leu Thr Gly Cys Tyr Leu Glu Asp Thr Ser Thr Val Ile Glu Val Ser
    370                 375                 380

Trp Val Leu Glu Val Phe Gly Arg Glu Leu
385                 390


<210> 1621
<211> 585
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(562)
<223> RXA00161

<400> 1621
ttactataca tggtgtagtc ccaaattaac taatgcgggt gaccaactgc accgtaaaaa 60

aaattcgctt atcgtaaatc agcaggtaga ataacactct atg agc gag cca ggg   115
                                              Met Ser Glu Pro Gly
                                                1               5

cca tcc ggg gtt aaa gaa aag aag aaa gta aag gca agt cac att gtc   163
Pro Ser Gly Val Lys Glu Lys Lys Lys Val Lys Ala Ser His Ile Val
                10                  15                  20

ttt ctt ctc att tgt ttt atc gca gcc tgc gcg ttg gcg tgg tgg cag   211
Phe Leu Leu Ile Cys Phe Ile Ala Ala Cys Ala Leu Ala Trp Trp Gln
            25                  30                  35

tgg tca aga ttc cag tcc ggg tct gga act ttc caa aac ctt ggc tat   259
Trp Ser Arg Phe Gln Ser Gly Ser Gly Thr Phe Gln Asn Leu Gly Tyr
        40                  45                  50
```

```
gcc ttc cag tgg cct ctt atc gga gca ttc ttt gtt tat gcc tac cgc   307
Ala Phe Gln Trp Pro Leu Ile Gly Ala Phe Phe Val Tyr Ala Tyr Arg
     55                  60                  65

aag tat ttg cag tat gag aat gag tcc att gag tta gaa aac atg gaa   355
Lys Tyr Leu Gln Tyr Glu Asn Glu Ser Ile Glu Leu Glu Asn Met Glu
 70                  75                  80                  85

gcc aaa atg atg gcg gag caa ggc aaa aca cca gtt gcg caa tca gag   403
Ala Lys Met Met Ala Glu Gln Gly Lys Thr Pro Val Ala Gln Ser Glu
                 90                  95                 100

cag gaa gat agc ttc gtt cag ctc tct cac cgt ccg agc ctg gtg gaa   451
Gln Glu Asp Ser Phe Val Gln Leu Ser His Arg Pro Ser Leu Val Glu
            105                 110                 115

gat gac agc gtc aag gaa atc gac gaa tcc ttc ctg ccg tct cgc ccg   499
Asp Asp Ser Val Lys Glu Ile Asp Glu Ser Phe Leu Pro Ser Arg Pro
        120                 125                 130

acg atg gat gtg gaa gag ttc aac agg ttg aat gat ccg cat gca cgg   547
Thr Met Asp Val Glu Glu Phe Asn Arg Leu Asn Asp Pro His Ala Arg
    135                 140                 145

aga cgt cga aaa gca taaacctgga acttttccgg gcc                    585
Arg Arg Arg Lys Ala
150
```

Do not add any new matter to this page

<210> 1622
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 1622

```
Met Ser Glu Pro Gly Pro Ser Gly Val Lys Glu Lys Lys Lys Val Lys
  1               5                  10                  15

Ala Ser His Ile Val Phe Leu Leu Ile Cys Phe Ile Ala Ala Cys Ala
             20                  25                  30

Leu Ala Trp Trp Gln Trp Ser Arg Phe Gln Ser Gly Ser Gly Thr Phe
         35                  40                  45

Gln Asn Leu Gly Tyr Ala Phe Gln Trp Pro Leu Ile Gly Ala Phe Phe
     50                  55                  60

Val Tyr Ala Tyr Arg Lys Tyr Leu Gln Tyr Glu Asn Glu Ser Ile Glu
 65                  70                  75                  80

Leu Glu Asn Met Glu Ala Lys Met Met Ala Glu Gln Gly Lys Thr Pro
                 85                  90                  95

Val Ala Gln Ser Glu Gln Glu Asp Ser Phe Val Gln Leu Ser His Arg
            100                 105                 110

Pro Ser Leu Val Glu Asp Asp Ser Val Lys Glu Ile Asp Glu Ser Phe
        115                 120                 125

Leu Pro Ser Arg Pro Thr Met Asp Val Glu Glu Phe Asn Arg Leu Asn
```

```
    130                 135                 140

Asp Pro His Ala Arg Arg Arg Arg Lys Ala
145                 150


<210> 1623
<211> 2196
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2173)
<223> RXA00169

<400> 1623
tttgctgtgt ctaagtgtgt ggggtaattg taatataatt ggtagaattt tctctaatta 60

atattttatt aacttacgga gaaagtttat gataaatatg atg tcg ttg ggt aat   115
                                          Met Ser Leu Gly Asn
                                            1               5

cca gca gca atg ctc gct gcg tac aac acc agc acg cag gtg gca ccg   163
Pro Ala Ala Met Leu Ala Ala Tyr Asn Thr Ser Thr Gln Val Ala Pro
                10                  15                  20

cag cca cag ctg gga cca cgt gct gga gaa gtt caa ctc agt agc gaa   211
Gln Pro Gln Leu Gly Pro Arg Ala Gly Glu Val Gln Leu Ser Ser Glu
            25                  30                  35

cag caa gcc atg att gat tat gta ctt gct ggc aaa gat gtc att gtt   259
Gln Gln Ala Met Ile Asp Tyr Val Leu Ala Gly Lys Asp Val Ile Val
        40                  45                  50

gat gcc acc gta ggc tcg ggc aaa act acc gct att caa cga ctg tgt   307
Asp Ala Thr Val Gly Ser Gly Lys Thr Thr Ala Ile Gln Arg Leu Cys
    55                  60                  65

tcg atc atg ggt gca gac cat gac gtg ctg tat ttg acg tat tcg aag   355
Ser Ile Met Gly Ala Asp His Asp Val Leu Tyr Leu Thr Tyr Ser Lys
70                  75                  80                  85

ttg ttg aag gtc gat gca cag cag cgc gtt cgt ggc gcc aag gtg cag   403
Leu Leu Lys Val Asp Ala Gln Gln Arg Val Arg Gly Ala Lys Val Gln
                90                  95                  100

aac tat cac ggc att gtc tat ccg cat cta ctc aag gcc ggc atc aag   451
Asn Tyr His Gly Ile Val Tyr Pro His Leu Leu Lys Ala Gly Ile Lys
            105                 110                 115

tgt ggt att agc gag tcg att cgg gag ttt aac aag aac ttc aaa cac   499
Cys Gly Ile Ser Glu Ser Ile Arg Glu Phe Asn Lys Asn Phe Lys His
        120                 125                 130

att tct cgc acg ttc ccc agt tac gac ctg ctg gtt att gat gag tac   547
Ile Ser Arg Thr Phe Pro Ser Tyr Asp Leu Leu Val Ile Asp Glu Tyr
    135                 140                 145

cag gac atc aat gag gac tat gca gaa ctg ctg cgc aac att aag tct   595
Gln Asp Ile Asn Glu Asp Tyr Ala Glu Leu Leu Arg Asn Ile Lys Ser
```

```
150                 155                 160                 165

gtg aat ccg ctt atg cag att gtc atg gtg ggt gat ttg gaa caa aaa   643
Val Asn Pro Leu Met Gln Ile Val Met Val Gly Asp Leu Glu Gln Lys
                170                 175                 180

gtc cgg tct gac acc acg tta gat cca caa gaa ttt gca gca caa ttg   691
Val Arg Ser Asp Thr Thr Leu Asp Pro Gln Glu Phe Ala Ala Gln Leu
            185                 190                 195

tgt gaa gat cca gtc ttc gcg ccg ttt aca cag tcg ttt cga att ggc   739
Cys Glu Asp Pro Val Phe Ala Pro Phe Thr Gln Ser Phe Arg Ile Gly
        200                 205                 210

gag gct atg gca gcg ggt ttg gct gat gcc tgg aat aaa ccg att gtg   787
Glu Ala Met Ala Ala Gly Leu Ala Asp Ala Trp Asn Lys Pro Ile Val
    215                 220                 225

ggt gcc aat acc gca cag cag att gaa tat agg tct ttc gct gag gca   835
Gly Ala Asn Thr Ala Gln Gln Ile Glu Tyr Arg Ser Phe Ala Glu Ala
230                 235                 240                 245

gtg gtg ttg atc caa agc acc gag ccg agc aaa ctg ttg tgt ttg ggt   883
Val Val Leu Ile Gln Ser Thr Glu Pro Ser Lys Leu Leu Cys Leu Gly
                250                 255                 260

agc cgc aat ggg cag atg tca gat gcg ctt aat gtc gtg gag agg aag   931
Ser Arg Asn Gly Gln Met Ser Asp Ala Leu Asn Val Val Glu Arg Lys
            265                 270                 275

tcg ccg gca aag ttc aat aag aaa act gtg ttc gcc tct att cgc gat   979
Ser Pro Ala Lys Phe Asn Lys Lys Thr Val Phe Ala Ser Ile Arg Asp
        280                 285                 290

ggt gat tcc cag att gca cac cct aat gac gct gcg gtg ttt acc acc   1027
Gly Asp Ser Gln Ile Ala His Pro Asn Asp Ala Ala Val Phe Thr Thr
    295                 300                 305

ttt gat tcc agt aaa ggt cta gag cgc gat acc tgc gtg gtc ttt gac   1075
Phe Asp Ser Ser Lys Gly Leu Glu Arg Asp Thr Cys Val Val Phe Asp
310                 315                 320                 325

tat gac gaa gaa ttc tgg gac atg cgt ctt ggt tac ccc aat gtt gat   1123
Tyr Asp Glu Glu Phe Trp Asp Met Arg Leu Gly Tyr Pro Asn Val Asp
                330                 335                 340

cca gtg gtc atg cgc aat gtg ttt ttg gtg gca gca tca cgc ggt aaa   1171
Pro Val Val Met Arg Asn Val Phe Leu Val Ala Ala Ser Arg Gly Lys
            345                 350                 355

aac aag gtt gtt ttt gta cgt agc gat tct ctt caa gca gcg tat gag   1219
Asn Lys Val Val Phe Val Arg Ser Asp Ser Leu Gln Ala Ala Tyr Glu
        360                 365                 370

gct ggt gcg gac tgg gct gca ggg ctc gct gtg ggt gtg gtg gac aac   1267
Ala Gly Ala Asp Trp Ala Ala Gly Leu Ala Val Gly Val Val Asp Asn
    375                 380                 385

aat act gag gtt gca cct gag gta gat gcc cat acg ccg gca gaa gaa   1315
Asn Thr Glu Val Ala Pro Glu Val Asp Ala His Thr Pro Ala Glu Glu
390                 395                 400                 405
```

```
agt aag ggt gat gtg ggt gag gtt cag tca cag att gag cgc atg atg   1363
Ser Lys Gly Asp Val Gly Glu Val Gln Ser Gln Ile Glu Arg Met Met
                410                 415                 420

ggt ttt atc cct gtt tca gtg ttt aaa gaa cta cct gag ttg gcg ccg   1411
Gly Phe Ile Pro Val Ser Val Phe Lys Glu Leu Pro Glu Leu Ala Pro
            425                 430                 435

agc gaa tat gcg cga ccg atc tct gtg act gaa gcc ttt gat ttt aag   1459
Ser Glu Tyr Ala Arg Pro Ile Ser Val Thr Glu Ala Phe Asp Phe Lys
        440                 445                 450

tac gca gag aat gtc gaa gca tgt ttt gac ctg ctt gat gtc aag cgt   1507
Tyr Ala Glu Asn Val Glu Ala Cys Phe Asp Leu Leu Asp Val Lys Arg
    455                 460                 465

ctc gac aac ggc aag ggt gca gcc att gag gtc aat cgc agt gac ggg   1555
Leu Asp Asn Gly Lys Gly Ala Ala Ile Glu Val Asn Arg Ser Asp Gly
470                 475                 480                 485

ctt att gat ctc tca ccc aca gtg gga aac ttt cag gaa gca gtg ttc   1603
Leu Ile Asp Leu Ser Pro Thr Val Gly Asn Phe Gln Glu Ala Val Phe
                490                 495                 500

ttc aag gac tac aac gtt cat aca gca cta tcg gcg tac ccg agt cag   1651
Phe Lys Asp Tyr Asn Val His Thr Ala Leu Ser Ala Tyr Pro Ser Gln
            505                 510                 515

ttc gcg aaa aat ctt aaa cgt ttg gtg aag aaa aac aat agc gta tgg   1699
Phe Ala Lys Asn Leu Lys Arg Leu Val Lys Lys Asn Asn Ser Val Trp
        520                 525                 530

cgt aac tgc ctt att gtc aca gca gcg tcc aca gag cag atg cgg tat   1747
Arg Asn Cys Leu Ile Val Thr Ala Ala Ser Thr Glu Gln Met Arg Tyr
    535                 540                 545

gtc gat cag gtg cgc agc tct atc ccg gtt gct gcg gag aag gca ttg   1795
Val Asp Gln Val Arg Ser Ser Ile Pro Val Ala Ala Glu Lys Ala Leu
550                 555                 560                 565

gtc tca cgg ctg agt acg agg ctg aat gct gat tca cgt aat cag att   1843
Val Ser Arg Leu Ser Thr Arg Leu Asn Ala Asp Ser Arg Asn Gln Ile
                570                 575                 580

cca ctg atc ctt gac ggc gag gca gta cag agc aaa gta gtg cgc acg   1891
Pro Leu Ile Leu Asp Gly Glu Ala Val Gln Ser Lys Val Val Arg Thr
            585                 590                 595

cca atg tct ttt gca ggt gtc gca gat gcg gtg cac aag ggt gtg ctt   1939
Pro Met Ser Phe Ala Gly Val Ala Asp Ala Val His Lys Gly Val Leu
        600                 605                 610

tat gaa ttg aaa ttc gtc tct gag ttg aca cat ccg atg ttt ttg cag   1987
Tyr Glu Leu Lys Phe Val Ser Glu Leu Thr His Pro Met Phe Leu Gln
    615                 620                 625

ctc gca atg tat ttg gtc atg tct ggg atg aag gac ggt att ttg tgg   2035
Leu Ala Met Tyr Leu Val Met Ser Gly Met Lys Asp Gly Ile Leu Trp
630                 635                 640                 645
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aac acc cgg aca gat gag gcg tgg cag gtg cgt gtt cct gac ccg aag   2083
Asn Thr Arg Thr Asp Glu Ala Trp Gln Val Arg Val Pro Asp Pro Lys
                650                 655                 660

cgt ttt ctt aat gct gtg gtg ttg tgt gtc tcc aag cag gat tac cgg   2131
Arg Phe Leu Asn Ala Val Val Leu Cys Val Ser Lys Gln Asp Tyr Arg
            665                 670                 675

gtc ggt aac ttt gat ctg ccg agc act ggt gga ggt gcg cgc           2173
Val Gly Asn Phe Asp Leu Pro Ser Thr Gly Gly Gly Ala Arg
        680                 685                 690

taaatggtgt tgatgtgtgg ggt                                        2196


<210> 1624
<211> 691
<212> PRT
<213> Corynebacterium glutamicum

<400> 1624
Met Ser Leu Gly Asn Pro Ala Ala Met Leu Ala Ala Tyr Asn Thr Ser
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Thr Gln Val Ala Pro Gln Pro Gln Leu Gly Pro Arg Ala Gly Glu Val
             20                  25                  30

Gln Leu Ser Ser Glu Gln Gln Ala Met Ile Asp Tyr Val Leu Ala Gly
         35                  40                  45

Lys Asp Val Ile Val Asp Ala Thr Val Gly Ser Gly Lys Thr Thr Ala
     50                  55                  60

Ile Gln Arg Leu Cys Ser Ile Met Gly Ala Asp His Asp Val Leu Tyr
 65                  70                  75                  80

Leu Thr Tyr Ser Lys Leu Leu Lys Val Asp Ala Gln Gln Arg Val Arg
                 85                  90                  95

Gly Ala Lys Val Gln Asn Tyr His Gly Ile Val Tyr Pro His Leu Leu
            100                 105                 110

Lys Ala Gly Ile Lys Cys Gly Ile Ser Glu Ser Ile Arg Glu Phe Asn
        115                 120                 125

Lys Asn Phe Lys His Ile Ser Arg Thr Phe Pro Ser Tyr Asp Leu Leu
    130                 135                 140

Val Ile Asp Glu Tyr Gln Asp Ile Asn Glu Asp Tyr Ala Glu Leu Leu
145                 150                 155                 160

Arg Asn Ile Lys Ser Val Asn Pro Leu Met Gln Ile Val Met Val Gly
                165                 170                 175

Asp Leu Glu Gln Lys Val Arg Ser Asp Thr Thr Leu Asp Pro Gln Glu
            180                 185                 190

Phe Ala Ala Gln Leu Cys Glu Asp Pro Val Phe Ala Pro Phe Thr Gln
        195                 200                 205

Ser Phe Arg Ile Gly Glu Ala Met Ala Ala Gly Leu Ala Asp Ala Trp
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    210                 215                 220

Asn Lys Pro Ile Val Gly Ala Asn Thr Ala Gln Gln Ile Glu Tyr Arg
225                 230                 235                 240

Ser Phe Ala Glu Ala Val Val Leu Ile Gln Ser Thr Glu Pro Ser Lys
                245                 250                 255

Leu Leu Cys Leu Gly Ser Arg Asn Gly Gln Met Ser Asp Ala Leu Asn
            260                 265                 270

Val Val Glu Arg Lys Ser Pro Ala Lys Phe Asn Lys Lys Thr Val Phe
        275                 280                 285

Ala Ser Ile Arg Asp Gly Asp Ser Gln Ile Ala His Pro Asn Asp Ala
    290                 295                 300

Ala Val Phe Thr Thr Phe Asp Ser Ser Lys Gly Leu Glu Arg Asp Thr
305                 310                 315                 320

Cys Val Val Phe Asp Tyr Asp Glu Glu Phe Trp Asp Met Arg Leu Gly
                325                 330                 335

Tyr Pro Asn Val Asp Pro Val Val Met Arg Asn Val Phe Leu Val Ala
            340                 345                 350

Ala Ser Arg Gly Lys Asn Lys Val Val Phe Val Arg Ser Asp Ser Leu
        355                 360                 365

Gln Ala Ala Tyr Glu Ala Gly Ala Asp Trp Ala Ala Gly Leu Ala Val
    370                 375                 380

Gly Val Val Asp Asn Asn Thr Glu Val Ala Pro Glu Val Asp Ala His
385                 390                 395                 400

Thr Pro Ala Glu Glu Ser Lys Gly Asp Val Gly Glu Val Gln Ser Gln
                405                 410                 415

Ile Glu Arg Met Met Gly Phe Ile Pro Val Ser Val Phe Lys Glu Leu
            420                 425                 430

Pro Glu Leu Ala Pro Ser Glu Tyr Ala Arg Pro Ile Ser Val Thr Glu
        435                 440                 445

Ala Phe Asp Phe Lys Tyr Ala Glu Asn Val Glu Ala Cys Phe Asp Leu
    450                 455                 460

Leu Asp Val Lys Arg Leu Asp Asn Gly Lys Gly Ala Ala Ile Glu Val
465                 470                 475                 480

Asn Arg Ser Asp Gly Leu Ile Asp Leu Ser Pro Thr Val Gly Asn Phe
                485                 490                 495

Gln Glu Ala Val Phe Phe Lys Asp Tyr Asn Val His Thr Ala Leu Ser
            500                 505                 510

Ala Tyr Pro Ser Gln Phe Ala Lys Asn Leu Lys Arg Leu Val Lys Lys
        515                 520                 525

Asn Asn Ser Val Trp Arg Asn Cys Leu Ile Val Thr Ala Ala Ser Thr
    530                 535                 540
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Glu Gln Met Arg Tyr Val Asp Gln Val Arg Ser Ser Ile Pro Val Ala
545                 550                 555                 560

Ala Glu Lys Ala Leu Val Ser Arg Leu Ser Thr Arg Leu Asn Ala Asp
                565                 570                 575

Ser Arg Asn Gln Ile Pro Leu Ile Leu Asp Gly Glu Ala Val Gln Ser
            580                 585                 590

Lys Val Val Arg Thr Pro Met Ser Phe Ala Gly Val Ala Asp Ala Val
        595                 600                 605

His Lys Gly Val Leu Tyr Glu Leu Lys Phe Val Ser Glu Leu Thr His
    610                 615                 620

Pro Met Phe Leu Gln Leu Ala Met Tyr Leu Val Met Ser Gly Met Lys
625                 630                 635                 640

Asp Gly Ile Leu Trp Asn Thr Arg Thr Asp Glu Ala Trp Gln Val Arg
                645                 650                 655

Val Pro Asp Pro Lys Arg Phe Leu Asn Ala Val Val Leu Cys Val Ser
            660                 665                 670

Lys Gln Asp Tyr Arg Val Gly Asn Phe Asp Leu Pro Ser Thr Gly Gly
        675                 680                 685

Gly Ala Arg
    690
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Sequence Listing - 2006-12-22 17:44:44 - 10/599,207

<210> 1625
<211> 1977
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1954)
<223> RXA00170

<400> 1625
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taagcggttg gtacgaagac tagtgggtgt ttctgctgtc atg ttg ctg gcc atc 115
                                              Met Leu Leu Ala Ile
                                                1   5

ggg gtt gca tct ccg gta gct caa gca caa gtg gaa gat caa ttt gag 163
Gly Val Ala Ser Pro Val Ala Gln Ala Gln Val Glu Asp Gln Phe Glu
                10   15   20

ctt gta aaa gaa atc agt gat gag cag ttt gct gat gat ggt gtt gac 211
Leu Val Lys Glu Ile Ser Asp Glu Gln Phe Ala Asp Asp Gly Val Asp
            25   30   35

tat gtt ccc aat agg aat gct ccg act gtt aag gaa caa ctt gag gat 259
Tyr Val Pro Asn Arg Asn Ala Pro Thr Val Lys Glu Gln Leu Glu Asp
        40   45   50

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ttc gaa tca gca cat cca gaa gta gtc att gag tat cac gag cac gtc   307
Phe Glu Ser Ala His Pro Glu Val Val Ile Glu Tyr His Glu His Val
     55                  60                  65

aac gat agt aaa gac aat gtt gag gaa ctt ccg cta cct aag cgg gac   355
Asn Asp Ser Lys Asp Asn Val Glu Glu Leu Pro Leu Pro Lys Arg Asp
 70                  75                  80                  85

atc gtt gca ggg gaa atg cgc tca gat gtc atc gag tta ccg gag ggg   403
Ile Val Ala Gly Glu Met Arg Ser Asp Val Ile Glu Leu Pro Glu Gly
                90                  95                 100

gtg agc aag gac gaa gct gat cag gtg gag gtt gcg gaa gcg cga ctt   451
Val Ser Lys Asp Glu Ala Asp Gln Val Glu Val Ala Glu Ala Arg Leu
            105                 110                 115

aat gag ggc gca cga ttg atg gct gca act ggg tgt gag gct atg tgg   499
Asn Glu Gly Ala Arg Leu Met Ala Ala Thr Gly Cys Glu Ala Met Trp
        120                 125                 130

cca aca ggt ttc tca gtt tgt ggc cgg att ctt gac gct tat cgg cag   547
Pro Thr Gly Phe Ser Val Cys Gly Arg Ile Leu Asp Ala Tyr Arg Gln
    135                 140                 145

gtt gga ggt cag ttg tca tgg ctt ggg cca cca aag tca aac gag ttg   595
Val Gly Gly Gln Leu Ser Trp Leu Gly Pro Pro Lys Ser Asn Glu Leu
150                 155                 160                 165

acc aat ccc gac ggt gtt ggc aaa aga agt gaa ttt gtt ggg ggt gcc   643
Thr Asn Pro Asp Gly Val Gly Lys Arg Ser Glu Phe Val Gly Gly Ala
                170                 175                 180

atc tat tgg cat cca gac aca ggc gct tat gca gtg acc ctg gac ggt   691
Ile Tyr Trp His Pro Asp Thr Gly Ala Tyr Ala Val Thr Leu Asp Gly
            185                 190                 195

ttg agg cag tgg ggg acc ttg aac tgg gaa tca ggg cca ttg ggg tac   739
Leu Arg Gln Trp Gly Thr Leu Asn Trp Glu Ser Gly Pro Leu Gly Tyr
        200                 205                 210

cca acc tct ggt ccg atg gat aca aac tat ccc ctt act cag cga cag   787
Pro Thr Ser Gly Pro Met Asp Thr Asn Tyr Pro Leu Thr Gln Arg Gln
    215                 220                 225

act ttt caa ggt ggt gac aac tat tac aac cca ttg act ggc ggt gct   835
Thr Phe Gln Gly Gly Asp Asn Tyr Tyr Asn Pro Leu Thr Gly Gly Ala
230                 235                 240                 245

gtg tgg ggc gat att aaa cag cgc tac gaa gaa ctt ggc ggc tcg aat   883
Val Trp Gly Asp Ile Lys Gln Arg Tyr Glu Glu Leu Gly Gly Ser Asn
                250                 255                 260

cat gcc att ggc atc ccg atc act aat gag cta cct agc ggt act gag   931
His Ala Ile Gly Ile Pro Ile Thr Asn Glu Leu Pro Ser Gly Thr Glu
            265                 270                 275

tat ttt tac aat aat ttc ttc aat gga aca att tcg tgg cga aat gat   979
Tyr Phe Tyr Asn Asn Phe Phe Asn Gly Thr Ile Ser Trp Arg Asn Asp
        280                 285                 290

cgt cag aca cgg ttt atg tat ttg gct acg cag cgg gtg tgg gat gcg   1027
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Arg Gln Thr Arg Phe Met Tyr Leu Ala Thr Gln Arg Val Trp Asp Ala
    295                 300                 305

ttg ggt cgg gag acg ggt cgt tta ggt ttt cct gaa gca gat gaa aca   1075
Leu Gly Arg Glu Thr Gly Arg Leu Gly Phe Pro Glu Ala Asp Glu Thr
310                 315                 320                 325

cct gag gtt tct ggt cta ttc cat gtg gtg aat ttt gcg gag cgc ggg   1123
Pro Glu Val Ser Gly Leu Phe His Val Val Asn Phe Ala Glu Arg Gly
                330                 335                 340

gtg att gcg tgg aat gga atc cta ggc gcc aga gag ctg tat ggt gat   1171
Val Ile Ala Trp Asn Gly Ile Leu Gly Ala Arg Glu Leu Tyr Gly Asp
            345                 350                 355

gtt tac tcc ctg tgg ctg caa tac caa aat acc gat act cct tta ggg   1219
Val Tyr Ser Leu Trp Leu Gln Tyr Gln Asn Thr Asp Thr Pro Leu Gly
        360                 365                 370

tgg ccg ata cca tca ttg aca tca tta aat gag tca ctc gaa caa gaa   1267
Trp Pro Ile Pro Ser Leu Thr Ser Leu Asn Glu Ser Leu Glu Gln Glu
    375                 380                 385

ttc acc aga ggt gtt gtt tta ggc tca ggt gat gca ctg aca tgg att   1315
Phe Thr Arg Gly Val Val Leu Gly Ser Gly Asp Ala Leu Thr Trp Ile
390                 395                 400                 405

cct gac gat gaa gaa aga agt ttg gag gat ttc ctc cca att gga agt   1363
Pro Asp Asp Glu Glu Arg Ser Leu Glu Asp Phe Leu Pro Ile Gly Ser
                410                 415                 420

agc ggc tca tcc tca tcg agc caa gag atg acc ctg ttt tcc cag cgt   1411
Ser Gly Ser Ser Ser Ser Ser Gln Glu Met Thr Leu Phe Ser Gln Arg
            425                 430                 435

gca caa tac gtg gat tgc aag aat ctt ccc gat tta gat gag cag aga   1459
Ala Gln Tyr Val Asp Cys Lys Asn Leu Pro Asp Leu Asp Glu Gln Arg
        440                 445                 450

aaa act gaa aac aac att gaa aag aat ggt ggc ccg atc aaa aaa gag   1507
Lys Thr Glu Asn Asn Ile Glu Lys Asn Gly Gly Pro Ile Lys Lys Glu
    455                 460                 465

tat agt tcg cga ggt ttc ccc acc gag ttc aga ttt gtc gtg aga aaa   1555
Tyr Ser Ser Arg Gly Phe Pro Thr Glu Phe Arg Phe Val Val Arg Lys
470                 475                 480                 485

ggg cat tat gac cgt tac agg aat gaa ggc tgg gga tat tta aaa aac   1603
Gly His Tyr Asp Arg Tyr Arg Asn Glu Gly Trp Gly Tyr Leu Lys Asn
                490                 495                 500

tat tgc aaa cac aac ttc gcc aac cac gct atg gct gag gcc gta gta   1651
Tyr Cys Lys His Asn Phe Ala Asn His Ala Met Ala Glu Ala Val Val
            505                 510                 515

gat aaa gcg gtg att gat tat ggc tca tcg cca gga acc agc tat tac   1699
Asp Lys Ala Val Ile Asp Tyr Gly Ser Ser Pro Gly Thr Ser Tyr Tyr
        520                 525                 530

aag ttc gag aaa acg gtg tac ttt cta gat tgc aga act tat aca ttc   1747
Lys Phe Glu Lys Thr Val Tyr Phe Leu Asp Cys Arg Thr Tyr Thr Phe
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    535                 540                 545

aat aag aac tca gga tgt aaa gaa atg cac gct ccg caa tgg gtg act   1795
Asn Lys Asn Ser Gly Cys Lys Glu Met His Ala Pro Gln Trp Val Thr
550                 555                 560                 565

att att tac aat cct cat act ttc act gga gca aat tcg aac aga ccc   1843
Ile Ile Tyr Asn Pro His Thr Phe Thr Gly Ala Asn Ser Asn Arg Pro
                570                 575                 580

aag ggg gta att tca gca tgg tgt aat tca acc cca cct ggt gga atc   1891
Lys Gly Val Ile Ser Ala Trp Cys Asn Ser Thr Pro Pro Gly Gly Ile
            585                 590                 595

gaa cac gag cct gaa att tcc caa tgt cct gat cat gtg aat ctt tat   1939
Glu His Glu Pro Glu Ile Ser Gln Cys Pro Asp His Val Asn Leu Tyr
        600                 605                 610

aat aag ctt cgc ata tgacagaacc ccatcaactg tgc                     1977
Asn Lys Leu Arg Ile
    615
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<210> 1626
<211> 618
<212> PRT
<213> Corynebacterium glutamicum

<400> 1626

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Met Leu Leu Ala Ile Gly Val Ala Ser Pro Val Ala Gln Ala Gln Val
  1               5                  10                  15

Glu Asp Gln Phe Glu Leu Val Lys Glu Ile Ser Asp Glu Gln Phe Ala
             20                  25                  30

Asp Asp Gly Val Asp Tyr Val Pro Asn Arg Asn Ala Pro Thr Val Lys
         35                  40                  45

Glu Gln Leu Glu Asp Phe Glu Ser Ala His Pro Glu Val Val Ile Glu
     50                  55                  60

Tyr His Glu His Val Asn Asp Ser Lys Asp Asn Val Glu Glu Leu Pro
 65                  70                  75                  80

Leu Pro Lys Arg Asp Ile Val Ala Gly Glu Met Arg Ser Asp Val Ile
                 85                  90                  95

Glu Leu Pro Glu Gly Val Ser Lys Asp Glu Ala Asp Gln Val Glu Val
            100                 105                 110

Ala Glu Ala Arg Leu Asn Glu Gly Ala Arg Leu Met Ala Ala Thr Gly
        115                 120                 125

Cys Glu Ala Met Trp Pro Thr Gly Phe Ser Val Cys Gly Arg Ile Leu
    130                 135                 140

Asp Ala Tyr Arg Gln Val Gly Gly Gln Leu Ser Trp Leu Gly Pro Pro
145                 150                 155                 160

Lys Ser Asn Glu Leu Thr Asn Pro Asp Gly Val Gly Lys Arg Ser Glu
                165                 170                 175
```

```
Phe Val Gly Gly Ala Ile Tyr Trp His Pro Asp Thr Gly Ala Tyr Ala
            180                 185                 190

Val Thr Leu Asp Gly Leu Arg Gln Trp Gly Thr Leu Asn Trp Glu Ser
        195                 200                 205

Gly Pro Leu Gly Tyr Pro Thr Ser Gly Pro Met Asp Thr Asn Tyr Pro
    210                 215                 220

Leu Thr Gln Arg Gln Thr Phe Gln Gly Gly Asp Asn Tyr Tyr Asn Pro
225                 230                 235                 240

Leu Thr Gly Gly Ala Val Trp Gly Asp Ile Lys Gln Arg Tyr Glu Glu
                245                 250                 255

Leu Gly Gly Ser Asn His Ala Ile Gly Ile Pro Ile Thr Asn Glu Leu
            260                 265                 270

Pro Ser Gly Thr Glu Tyr Phe Tyr Asn Asn Phe Phe Asn Gly Thr Ile
        275                 280                 285

Ser Trp Arg Asn Asp Arg Gln Thr Arg Phe Met Tyr Leu Ala Thr Gln
    290                 295                 300

Arg Val Trp Asp Ala Leu Gly Arg Glu Thr Gly Arg Leu Gly Phe Pro
305                 310                 315                 320

Glu Ala Asp Glu Thr Pro Glu Val Ser Gly Leu Phe His Val Val Asn
                325                 330                 335

Phe Ala Glu Arg Gly Val Ile Ala Trp Asn Gly Ile Leu Gly Ala Arg
            340                 345                 350

Glu Leu Tyr Gly Asp Val Tyr Ser Leu Trp Leu Gln Tyr Gln Asn Thr
        355                 360                 365

Asp Thr Pro Leu Gly Trp Pro Ile Pro Ser Leu Thr Ser Leu Asn Glu
    370                 375                 380

Ser Leu Glu Gln Glu Phe Thr Arg Gly Val Val Leu Gly Ser Gly Asp
385                 390                 395                 400

Ala Leu Thr Trp Ile Pro Asp Asp Glu Glu Arg Ser Leu Glu Asp Phe
                405                 410                 415

Leu Pro Ile Gly Ser Ser Gly Ser Ser Ser Ser Ser Gln Glu Met Thr
            420                 425                 430

Leu Phe Ser Gln Arg Ala Gln Tyr Val Asp Cys Lys Asn Leu Pro Asp
        435                 440                 445

Leu Asp Glu Gln Arg Lys Thr Glu Asn Asn Ile Glu Lys Asn Gly Gly
    450                 455                 460

Pro Ile Lys Lys Glu Tyr Ser Ser Arg Gly Phe Pro Thr Glu Phe Arg
465                 470                 475                 480

Phe Val Val Arg Lys Gly His Tyr Asp Arg Tyr Arg Asn Glu Gly Trp
                485                 490                 495
```

```
Gly Tyr Leu Lys Asn Tyr Cys Lys His Asn Phe Ala Asn His Ala Met
            500                 505                 510

Ala Glu Ala Val Val Asp Lys Ala Val Ile Asp Tyr Gly Ser Ser Pro
        515                 520                 525

Gly Thr Ser Tyr Tyr Lys Phe Glu Lys Thr Val Tyr Phe Leu Asp Cys
    530                 535                 540

Arg Thr Tyr Thr Phe Asn Lys Asn Ser Gly Cys Lys Glu Met His Ala
545                 550                 555                 560

Pro Gln Trp Val Thr Ile Ile Tyr Asn Pro His Thr Phe Thr Gly Ala
                565                 570                 575

Asn Ser Asn Arg Pro Lys Gly Val Ile Ser Ala Trp Cys Asn Ser Thr
            580                 585                 590

Pro Pro Gly Gly Ile Glu His Glu Pro Glu Ile Ser Gln Cys Pro Asp
        595                 600                 605

His Val Asn Leu Tyr Asn Lys Leu Arg Ile
    610                 615
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<210> 1627
<211> 456
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(433)
<223> RXA00173

<400> 1627

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gagagccgta aggcagctat tcgcgacgct attctcgcct atg tca aca aca atc   115
                                              Met Ser Thr Thr Ile
                                                1               5

aag gct gct gca ccc tac agc ctt cat gcc cat gat ctc gaa cag ctt   163
Lys Ala Ala Ala Pro Tyr Ser Leu His Ala His Asp Leu Glu Gln Leu
                10                  15                  20

gct gta gat ctc act tta gtt acc acc ttt gat agc aat gct gca gtt   211
Ala Val Asp Leu Thr Leu Val Thr Thr Phe Asp Ser Asn Ala Ala Val
            25                  30                  35

gat gtc acg cca aca cat aca gaa gca cct ggt ttt acc ctg cat gag   259
Asp Val Thr Pro Thr His Thr Glu Ala Pro Gly Phe Thr Leu His Glu
        40                  45                  50

ggc acc gat act gcg cct atg gct cca acc ctg gtc gta cct att tcc   307
Gly Thr Asp Thr Ala Pro Met Ala Pro Thr Leu Val Val Pro Ile Ser
    55                  60                  65

agc gac atc tcc aca gcc gtt tcg gaa ata tct aca tta gtg cag cag   355
Ser Asp Ile Ser Thr Ala Val Ser Glu Ile Ser Thr Leu Val Gln Gln
70                  75                  80                  85
```

```
gct cgc acc gac gca gca agc gcc att cat gaa gca gaa gct gaa ttt   403
Ala Arg Thr Asp Ala Ala Ser Ala Ile His Glu Ala Glu Ala Glu Phe
                 90                  95                 100

tac aac caa ctt gct gcg gtc ctt gct cag tgatttaatg tggccgacac     453
Tyr Asn Gln Leu Ala Ala Val Leu Ala Gln
            105                 110

acc                                                               456


<210> 1628
<211> 111
<212> PRT
<213> Corynebacterium glutamicum

<400> 1628
Met Ser Thr Thr Ile Lys Ala Ala Ala Pro Tyr Ser Leu His Ala His
  1               5                  10                  15

Asp Leu Glu Gln Leu Ala Val Asp Leu Thr Leu Val Thr Thr Phe Asp
             20                  25                  30

Ser Asn Ala Ala Val Asp Val Thr Pro Thr His Thr Glu Ala Pro Gly
         35                  40                  45

Phe Thr Leu His Glu Gly Thr Asp Thr Ala Pro Met Ala Pro Thr Leu
     50                  55                  60

Val Val Pro Ile Ser Ser Asp Ile Ser Thr Ala Val Ser Glu Ile Ser
 65                  70                  75                  80

Thr Leu Val Gln Gln Ala Arg Thr Asp Ala Ala Ser Ala Ile His Glu
                 85                  90                  95

Ala Glu Ala Glu Phe Tyr Asn Gln Leu Ala Ala Val Leu Ala Gln
            100                 105                 110


<210> 1629
<211> 408
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(385)
<223> RXA00174

<400> 1629
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taagccactg ggaatcataa aaaagaaagt agcactagct atg cct aat cac cca   115
                                              Met Pro Asn His Pro
                                                1               5

cct att tcc acc ttc gat gac cgt cgc tct gct atg cgc gaa ggc att   163
Pro Ile Ser Thr Phe Asp Asp Arg Arg Ser Ala Met Arg Glu Gly Ile
            10                  15                  20
```

act gat tac ctt gcc aat aca aat gca aat ggg tta ggc ggt tac agc 211
Thr Asp Tyr Leu Ala Asn Thr Asn Ala Asn Gly Leu Gly Gly Tyr Ser
25 30 35

atc agc gac acc cac ctc gac aat ctt gct gag aaa ttc acc cgc aca 259
Ile Ser Asp Thr His Leu Asp Asn Leu Ala Glu Lys Phe Thr Arg Thr
40 45 50

cat ggt gaa gca cag tac gat gcc ggc ttt gat ccc aat gat ctt gaa 307
His Gly Glu Ala Gln Tyr Asp Ala Gly Phe Asp Pro Asn Asp Leu Glu
55 60 65

cca gag act ttt gtt cgt gac att gag atg agc tgg gat gag cgt gct 355
Pro Glu Thr Phe Val Arg Asp Ile Glu Met Ser Trp Asp Glu Arg Ala
70 75 80 85

att gat cgt gcc ctg atc cac aca caa ctg tgaagaaaga agccgcaatg 405
Ile Asp Arg Ala Leu Ile His Thr Gln Leu
90 95

tcc 408

<210> 1630
<211> 95
<212> PRT
<213> Corynebacterium glutamicum

<400> 1630
Met Pro Asn His Pro Pro Ile Ser Thr Phe Asp Asp Arg Arg Ser Ala
1 5 10 15

Met Arg Glu Gly Ile Thr Asp Tyr Leu Ala Asn Thr Asn Ala Asn Gly
20 25 30

Leu Gly Gly Tyr Ser Ile Ser Asp Thr His Leu Asp Asn Leu Ala Glu
35 40 45

Lys Phe Thr Arg Thr His Gly Glu Ala Gln Tyr Asp Ala Gly Phe Asp
50 55 60

Pro Asn Asp Leu Glu Pro Glu Thr Phe Val Arg Asp Ile Glu Met Ser
65 70 75 80

Trp Asp Glu Arg Ala Ile Asp Arg Ala Leu Ile His Thr Gln Leu
85 90 95

<210> 1631
<211> 753
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(730)
<223> RXA00175

<400> 1631
agctcgacag ccgtaaagaa gttgtaggtc tttttcgctt gggatactga tgctctccca 60

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agcgaacatg ggcgggagcc catgtcgggg tgttgtgcga atg gct gtg tgt caa   115
                                             Met Ala Val Cys Gln
                                               1               5

cta cct cag cct gag aaa aca aca ctt ata aag aaa gac ctt tta ctc   163
Leu Pro Gln Pro Glu Lys Thr Thr Leu Ile Lys Lys Asp Leu Leu Leu
                 10                  15                  20

atg act tct aca act aac tcc acc gcc atg ttc aac gac cac ctt atc   211
Met Thr Ser Thr Thr Asn Ser Thr Ala Met Phe Asn Asp His Leu Ile
             25                  30                  35

cct atg gca gag ctt gat gaa caa gct ctg cgc gac agc gtt ggt tct   259
Pro Met Ala Glu Leu Asp Glu Gln Ala Leu Arg Asp Ser Val Gly Ser
         40                  45                  50

tgg gca cag tac aag cac ccg ctt gac cag cgc aaa gaa cca gag ctc   307
Trp Ala Gln Tyr Lys His Pro Leu Asp Gln Arg Lys Glu Pro Glu Leu
     55                  60                  65

gtc ctt att cgt cgc gtc aac agc tca gag cgt gtg tgg gtc tta agt   355
Val Leu Ile Arg Arg Val Asn Ser Ser Glu Arg Val Trp Val Leu Ser
 70                  75                  80                  85

ttc act gac ctg cgt gct gat gca ggt ctt gtg cct cgt agc aca ccg   403
Phe Thr Asp Leu Arg Ala Asp Ala Gly Leu Val Pro Arg Ser Thr Pro
                 90                  95                 100

aat gct gac ccc tcc aat atc cgc aat acc att ttc tct gtc gct gtc   451
Asn Ala Asp Pro Ser Asn Ile Arg Asn Thr Ile Phe Ser Val Ala Val
            105                 110                 115

cgc gat ctt gtc ctt gat cgc tca ctt ccc cgg ctg ctt aac ctc aac   499
Arg Asp Leu Val Leu Asp Arg Ser Leu Pro Arg Leu Leu Asn Leu Asn
        120                 125                 130

ggg caa cca cca gca ggt gaa tgg gaa gaa ggc ttt gtc tac gtc gat   547
Gly Gln Pro Pro Ala Gly Glu Trp Glu Glu Gly Phe Val Tyr Val Asp
    135                 140                 145

tat gac cag agc gac acc gta gat ggc tac ctc att gag cac agc gaa   595
Tyr Asp Gln Ser Asp Thr Val Asp Gly Tyr Leu Ile Glu His Ser Glu
150                 155                 160                 165

cct gtc tcc att gaa agt caa acc acc ggt gaa atg cac tat ttc gat   643
Pro Val Ser Ile Glu Ser Gln Thr Thr Gly Glu Met His Tyr Phe Asp
                170                 175                 180

aag gtg cca ggc ggt gtg gct gtt acc aac aat ccc gat ggc act gaa   691
Lys Val Pro Gly Gly Val Ala Val Thr Asn Asn Pro Asp Gly Thr Glu
            185                 190                 195

caa ggt gat gca cgc cgc tgg gta agc cac tgg gaa tca taaaaaagaa    740
Gln Gly Asp Ala Arg Arg Trp Val Ser His Trp Glu Ser
        200                 205                 210

agtagcacta gct                                                   753


<210> 1632
<211> 210
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<212> PRT
<213> Corynebacterium glutamicum

<400> 1632
Met Ala Val Cys Gln Leu Pro Gln Pro Glu Lys Thr Thr Leu Ile Lys
1 5 10 15

Lys Asp Leu Leu Leu Met Thr Ser Thr Thr Asn Ser Thr Ala Met Phe
20 25 30

Asn Asp His Leu Ile Pro Met Ala Glu Leu Asp Glu Gln Ala Leu Arg
35 40 45

Asp Ser Val Gly Ser Trp Ala Gln Tyr Lys His Pro Leu Asp Gln Arg
50 55 60

Lys Glu Pro Glu Leu Val Leu Ile Arg Arg Val Asn Ser Ser Glu Arg
65 70 75 80

Val Trp Val Leu Ser Phe Thr Asp Leu Arg Ala Asp Ala Gly Leu Val
85 90 95

Pro Arg Ser Thr Pro Asn Ala Asp Pro Ser Asn Ile Arg Asn Thr Ile
100 105 110

Phe Ser Val Ala Val Arg Asp Leu Val Leu Asp Arg Ser Leu Pro Arg
115 120 125

Leu Leu Asn Leu Asn Gly Gln Pro Pro Ala Gly Glu Trp Glu Glu Gly
130 135 140

Phe Val Tyr Val Asp Tyr Asp Gln Ser Asp Thr Val Asp Gly Tyr Leu
145 150 155 160

Ile Glu His Ser Glu Pro Val Ser Ile Glu Ser Gln Thr Thr Gly Glu
165 170 175

Met His Tyr Phe Asp Lys Val Pro Gly Gly Val Ala Val Thr Asn Asn
180 185 190

Pro Asp Gly Thr Glu Gln Gly Asp Ala Arg Arg Trp Val Ser His Trp
195 200 205

Glu Ser
210

<210> 1633
<211> 582
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(559)
<223> RXA00179

<400> 1633
gcgggttcgc caaaccttgg tgatctcgtt agtgtatgta tcaagcattt tctttttgcc 60

caaccataat tgaaaggtcc accagcccgt gaccaccatc atg atc gct att cac 115

```
                                                  Met Ile Ala Ile His
                                                    1               5

gct att gca gca atc ctg ttc cta gga cca gca aca gta gct aac tct   163
Ala Ile Ala Ala Ile Leu Phe Leu Gly Pro Ala Thr Val Ala Asn Ser
                10                  15                  20

cag ttc cac gtc cgc gcg tac gat gca cac aac ggc aac acc caa gcc   211
Gln Phe His Val Arg Ala Tyr Asp Ala His Asn Gly Asn Thr Gln Ala
            25                  30                  35

gct ggc tcc gca aaa acc ctt ttc aag att tcc cag tcc tac ggc atg   259
Ala Gly Ser Ala Lys Thr Leu Phe Lys Ile Ser Gln Ser Tyr Gly Met
        40                  45                  50

ctg tcc ctg ctc gtg cct ttg ctg ggt atc gcc atc atg ctt ctc gat   307
Leu Ser Leu Leu Val Pro Leu Leu Gly Ile Ala Ile Met Leu Leu Asp
    55                  60                  65

tgg tct ttc tac aag tct gaa ggc cag ttc cac gca gca atc gct ctc   355
Trp Ser Phe Tyr Lys Ser Glu Gly Gln Phe His Ala Ala Ile Ala Leu
70                  75                  80                  85

agt gtt atc acc tgg gcg ctg ctt ctc ttc gtt atc ttc cca cgc cag   403
Ser Val Ile Thr Trp Ala Leu Leu Leu Phe Val Ile Phe Pro Arg Gln
                90                  95                 100

aag aag atg atg ggt gct ctt gac ctt ctg gag gac gat gag cag gct   451
Lys Lys Met Met Gly Ala Leu Asp Leu Leu Glu Asp Asp Glu Gln Ala
            105                 110                 115

gca aag act tac gag atc gaa aac tgg gac aag gcg aag agc cag ctg   499
Ala Lys Thr Tyr Glu Ile Glu Asn Trp Asp Lys Ala Lys Ser Gln Leu
        120                 125                 130

tcc atg ttc ggc ggc atc tgg gct ctg ctg tgg gtc atc atc gct gtg   547
Ser Met Phe Gly Gly Ile Trp Ala Leu Leu Trp Val Ile Ile Ala Val
    135                 140                 145

ctg atg ttc atc taacacatct caaattgcca aaa                        582
Leu Met Phe Ile
150
```

Application Number: 2004800430400

<2l0> 1634
<211> 153
<212> PRT
<213> Corynebacterium glutamicum

<400> 1634

```
Met Ile Ala Ile His Ala Ile Ala Ala Ile Leu Phe Leu Gly Pro Ala
  1               5                  10                  15

Thr Val Ala Asn Ser Gln Phe His Val Arg Ala Tyr Asp Ala His Asn
            20                  25                  30

Gly Asn Thr Gln Ala Ala Gly Ser Ala Lys Thr Leu Phe Lys Ile Ser
        35                  40                  45

Gln Ser Tyr Gly Met Leu Ser Leu Leu Val Pro Leu Leu Gly Ile Ala
    50                  55                  60
```

```
Ile Met Leu Leu Asp Trp Ser Phe Tyr Lys Ser Glu Gly Gln Phe His
 65                  70                  75                  80

Ala Ala Ile Ala Leu Ser Val Ile Thr Trp Ala Leu Leu Leu Phe Val
                 85                  90                  95

Ile Phe Pro Arg Gln Lys Lys Met Met Gly Ala Leu Asp Leu Leu Glu
            100                 105                 110

Asp Asp Glu Gln Ala Ala Lys Thr Tyr Glu Ile Glu Asn Trp Asp Lys
        115                 120                 125

Ala Lys Ser Gln Leu Ser Met Phe Gly Gly Ile Trp Ala Leu Leu Trp
    130                 135                 140

Val Ile Ile Ala Val Leu Met Phe Ile
145                 150


<210> 1635
<211> 663
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(640)
<223> RXA00180

<400> 1635
aaacgaggat gttgatttcg ctgacgcagc tcagaagctt tcgaaagaaa gttaagcctt 60

agagggaacc aaacgccaag gcgatgagtc taacccgagt atg aag aac ttt att   115
                                              Met Lys Asn Phe Ile
                                                1               5

cgg gta ctc atc gcc ttt agt gtt ttc ctc tgt ata tat acc gtt gct   163
Arg Val Leu Ile Ala Phe Ser Val Phe Leu Cys Ile Tyr Thr Val Ala
                10                  15                  20

ccc cac att ggc cga ggt cct gga gac ctc gca cca gtt aca gca atc   211
Pro His Ile Gly Arg Gly Pro Gly Asp Leu Ala Pro Val Thr Ala Ile
            25                  30                  35

ccc caa cga gcc aca gtc cta ggc tat gac aga gcc tcc atg ttt ggc   259
Pro Gln Arg Ala Thr Val Leu Gly Tyr Asp Arg Ala Ser Met Phe Gly
        40                  45                  50

gga tgg ttg ggt ggc gtg cgg gaa ggc atc gtg gat gaa gcc ggc gac   307
Gly Trp Leu Gly Gly Val Arg Glu Gly Ile Val Asp Glu Ala Gly Asp
    55                  60                  65

act gat cca tac tcc ggg aat cga tta gac ctc tct agt gcc gag gtg   355
Thr Asp Pro Tyr Ser Gly Asn Arg Leu Asp Leu Ser Ser Ala Glu Val
70                  75                  80                  85

gat cat att ctc ccg ctc agc gcc gcc tgg gat cta ggc gca cac cgg   403
Asp His Ile Leu Pro Leu Ser Ala Ala Trp Asp Leu Gly Ala His Arg
                90                  95                 100
```

```
tgg agc gct ggc gag aga atc agc ttt gcc aac gac ccc ctc aac ctc   451
Trp Ser Ala Gly Glu Arg Ile Ser Phe Ala Asn Asp Pro Leu Asn Leu
            105                 110                 115

gtg ctc gtc tca aaa gct gag aac caa gaa aaa tcc gat caa ctt ccc   499
Val Leu Val Ser Lys Ala Glu Asn Gln Glu Lys Ser Asp Gln Leu Pro
        120                 125                 130

agc gag tgg ctc ccc tct gat cga agt gca cga tgt tgg tac gtg gaa   547
Ser Glu Trp Leu Pro Ser Asp Arg Ser Ala Arg Cys Trp Tyr Val Glu
    135                 140                 145

cgc ctt ttc gcc gtg gcc aac gca tac gaa ctt ccg tta cca gaa aac   595
Arg Leu Phe Ala Val Ala Asn Ala Tyr Glu Leu Pro Leu Pro Glu Asn
150                 155                 160                 165

gac att cgg gtt gga cga aaa cag tgc ggg ttc gcc aaa cct tgg       640
Asp Ile Arg Val Gly Arg Lys Gln Cys Gly Phe Ala Lys Pro Trp
                170                 175                 180

tgatctcgtt agtgtatgta tca                                        663
```

<210> 1636
<211> 180
<212> PRT
<213> Corynebacterium glutamicum

<400> 1636

```
Met Lys Asn Phe Ile Arg Val Leu Ile Ala Phe Ser Val Phe Leu Cys
  1               5                  10                  15

Ile Tyr Thr Val Ala Pro His Ile Gly Arg Gly Pro Gly Asp Leu Ala
             20                  25                  30

Pro Val Thr Ala Ile Pro Gln Arg Ala Thr Val Leu Gly Tyr Asp Arg
         35                  40                  45

Ala Ser Met Phe Gly Gly Trp Leu Gly Gly Val Arg Glu Gly Ile Val
     50                  55                  60

Asp Glu Ala Gly Asp Thr Asp Pro Tyr Ser Gly Asn Arg Leu Asp Leu
 65                  70                  75                  80

Ser Ser Ala Glu Val Asp His Ile Leu Pro Leu Ser Ala Ala Trp Asp
                 85                  90                  95

Leu Gly Ala His Arg Trp Ser Ala Gly Glu Arg Ile Ser Phe Ala Asn
            100                 105                 110

Asp Pro Leu Asn Leu Val Leu Val Ser Lys Ala Glu Asn Gln Glu Lys
        115                 120                 125

Ser Asp Gln Leu Pro Ser Glu Trp Leu Pro Ser Asp Arg Ser Ala Arg
    130                 135                 140

Cys Trp Tyr Val Glu Arg Leu Phe Ala Val Ala Asn Ala Tyr Glu Leu
145                 150                 155                 160

Pro Leu Pro Glu Asn Asp Ile Arg Val Gly Arg Lys Gln Cys Gly Phe
                165                 170                 175
```

```
Ala Lys Pro Trp
            180


<210> 1637
<211> 975
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(952)
<223> RXA00183

<400> 1637
ctggccagcg ccatcgtggg cgagggcgaa ggctggatca ccgaactcaa cccagaagaa 60

ttggctatgc tgatgagtta ccgcgaaaag gagggtgcag atg act gaa tca cgc   115
                                        Met Thr Glu Ser Arg
                                          1               5

cgc gtg aaa atg gat aac gtt att tac gcc aat ttt ggc agc aaa cag   163
Arg Val Lys Met Asp Asn Val Ile Tyr Ala Asn Phe Gly Ser Lys Gln
                 10                  15                  20

cgc gta tct act cct gat gac cgc acc cag gtg att aat aaa tca cga   211
Arg Val Ser Thr Pro Asp Asp Arg Thr Gln Val Ile Asn Lys Ser Arg
             25                  30                  35

cac aaa caa ttc agc cca gcg ggt act cgt acc gtg atg ttg acg gag   259
His Lys Gln Phe Ser Pro Ala Gly Thr Arg Thr Val Met Leu Thr Glu
         40                  45                  50

aaa aac gcc gac agc gga cga cgg tcc cgc ggt gag cag tac tac cga   307
Lys Asn Ala Asp Ser Gly Arg Arg Ser Arg Gly Glu Gln Tyr Tyr Arg
     55                  60                  65

aac ggc aat gtc acc ggc atg act gtg ctg gaa ggc cgc gtg gaa tgc   355
Asn Gly Asn Val Thr Gly Met Thr Val Leu Glu Gly Arg Val Glu Cys
 70                  75                  80                  85

act gtc gcg ggc tcc caa aac gag ccg ttt gtt acc aca gtg acc ttc   403
Thr Val Ala Gly Ser Gln Asn Glu Pro Phe Val Thr Thr Val Thr Phe
                 90                  95                 100

cca tac cga agc tcg gaa aaa ctc cgc gaa gcc tac gca gct att gcg   451
Pro Tyr Arg Ser Ser Glu Lys Leu Arg Glu Ala Tyr Ala Ala Ile Ala
            105                 110                 115

gat act ccc aat ggc ctg cgg ctt gtg cgt gat ggc cat ctg acc tcc   499
Asp Thr Pro Asn Gly Leu Arg Leu Val Arg Asp Gly His Leu Thr Ser
        120                 125                 130

tcc atg ctg gat cac ttg gtg gga agt cct gat gag tcg att tat ttt   547
Ser Met Leu Asp His Leu Val Gly Ser Pro Asp Glu Ser Ile Tyr Phe
    135                 140                 145

gac tgc acc tgc ccc gac cga tcg ctt gtg tgt aaa cat gcc gtt gcc   595
Asp Cys Thr Cys Pro Asp Arg Ser Leu Val Cys Lys His Ala Val Ala
150                 155                 160                 165
```

```
agc gcg tat cac gtt gcc gag aag atg acc gcg aac ccc ggt ctg atc   643
Ser Ala Tyr His Val Ala Glu Lys Met Thr Ala Asn Pro Gly Leu Ile
                170                 175                 180

ttg gat att cgt ggt caa ggg atg gct gga tta gaa gca ctg att cgg   691
Leu Asp Ile Arg Gly Gln Gly Met Ala Gly Leu Glu Ala Leu Ile Arg
            185                 190                 195

acc tat cac acc aag gtt gaa act gaa cct gaa gac aat gac agt ttt   739
Thr Tyr His Thr Lys Val Glu Thr Glu Pro Glu Asp Asn Asp Ser Phe
        200                 205                 210

tgg aac ggc agg gaa ctt cct gct ttg cct gat cca aag att gcc cct   787
Trp Asn Gly Arg Glu Leu Pro Ala Leu Pro Asp Pro Lys Ile Ala Pro
    215                 220                 225

gct atc gac gat tcc gat atc aac tac ctc cac aag gct tta agg atg   835
Ala Ile Asp Asp Ser Asp Ile Asn Tyr Leu His Lys Ala Leu Arg Met
230                 235                 240                 245

gtc tca tac acc tcc ctg gag cag ctt cgt gcg gtc agt gat att gaa   883
Val Ser Tyr Thr Ser Leu Glu Gln Leu Arg Ala Val Ser Asp Ile Glu
                250                 255                 260

gat atg tac gag att ttg gta gcc aac cac cct gat aac cag caa gtg   931
Asp Met Tyr Glu Ile Leu Val Ala Asn His Pro Asp Asn Gln Gln Val
            265                 270                 275

tat gag gaa gaa gac act gat taaccagggc ttatggttgt ggt            975
Tyr Glu Glu Glu Asp Thr Asp
        280
```

<210> 1638
<211> 284
<212> PRT
<213> Corynebacterium glutamicum

<400> 1638

```
Met Thr Glu Ser Arg Arg Val Lys Met Asp Asn Val Ile Tyr Ala Asn
  1               5                  10                  15

Phe Gly Ser Lys Gln Arg Val Ser Thr Pro Asp Asp Arg Thr Gln Val
             20                  25                  30

Ile Asn Lys Ser Arg His Lys Gln Phe Ser Pro Ala Gly Thr Arg Thr
         35                  40                  45

Val Met Leu Thr Glu Lys Asn Ala Asp Ser Gly Arg Arg Ser Arg Gly
     50                  55                  60

Glu Gln Tyr Tyr Arg Asn Gly Asn Val Thr Gly Met Thr Val Leu Glu
 65                  70                  75                  80

Gly Arg Val Glu Cys Thr Val Ala Gly Ser Gln Asn Glu Pro Phe Val
                 85                  90                  95

Thr Thr Val Thr Phe Pro Tyr Arg Ser Ser Glu Lys Leu Arg Glu Ala
            100                 105                 110
```

```
Tyr Ala Ala Ile Ala Asp Thr Pro Asn Gly Leu Arg Leu Val Arg Asp
        115                 120                 125

Gly His Leu Thr Ser Ser Met Leu Asp His Leu Val Gly Ser Pro Asp
    130                 135                 140

Glu Ser Ile Tyr Phe Asp Cys Thr Cys Pro Asp Arg Ser Leu Val Cys
145                 150                 155                 160

Lys His Ala Val Ala Ser Ala Tyr His Val Ala Glu Lys Met Thr Ala
                165                 170                 175

Asn Pro Gly Leu Ile Leu Asp Ile Arg Gly Gln Gly Met Ala Gly Leu
            180                 185                 190

Glu Ala Leu Ile Arg Thr Tyr His Thr Lys Val Glu Thr Glu Pro Glu
        195                 200                 205

Asp Asn Asp Ser Phe Trp Asn Gly Arg Glu Leu Pro Ala Leu Pro Asp
    210                 215                 220

Pro Lys Ile Ala Pro Ala Ile Asp Asp Ser Asp Ile Asn Tyr Leu His
225                 230                 235                 240

Lys Ala Leu Arg Met Val Ser Tyr Thr Ser Leu Glu Gln Leu Arg Ala
                245                 250                 255

Val Ser Asp Ile Glu Asp Met Tyr Glu Ile Leu Val Ala Asn His Pro
            260                 265                 270

Asp Asn Gln Gln Val Tyr Glu Glu Glu Asp Thr Asp
        275                 280
```

<210> 1639
<211> 2751
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2728)
<223> RXA00185

<400> 1639

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attgcgagag ctcgctgact ctgtggtcaa tggtgcagcg ccggaagaag accgcgatgc 60

gctcaaccta ttgttccgac taagccggga ggtctaagac atg cgt att cat gaa   115
                                                Met Arg Ile His Glu
                                                  1               5

atc atc att gac aat ttc cga gcc atc gaa cat cta gaa ctt cgt gac   163
Ile Ile Ile Asp Asn Phe Arg Ala Ile Glu His Leu Glu Leu Arg Asp
                 10                  15                  20

att cct gac cag ggc gtt atc gtg atc cac ggt gac aat gag caa ggc   211
Ile Pro Asp Gln Gly Val Ile Val Ile His Gly Asp Asn Glu Gln Gly
             25                  30                  35

aaa tct tca atc ctt gaa gcc ata aaa aca gtt ctg aat agt aaa cac   259
Lys Ser Ser Ile Leu Glu Ala Ile Lys Thr Val Leu Asn Ser Lys His
```

```
         40                  45                  50

aga acc acc agc aag acg atc aag gcc att cag cct gtt gac cgt gat   307
Arg Thr Thr Ser Lys Thr Ile Lys Ala Ile Gln Pro Val Asp Arg Asp
     55                  60                  65

gtt ccc atc agc atc acc ctc gag gca acc gta ggc acg gtt cga ttc   355
Val Pro Ile Ser Ile Thr Leu Glu Ala Thr Val Gly Thr Val Arg Phe
 70                  75                  80                  85

cgc ata cac aaa cgc ttc cta aaa tcc aca gcc gca gaa ctg caa gtc   403
Arg Ile His Lys Arg Phe Leu Lys Ser Thr Ala Ala Glu Leu Gln Val
                 90                  95                 100

atc gag cca cgt cca tcc aac cac cgt gga cta gaa gcc gaa gct gca   451
Ile Glu Pro Arg Pro Ser Asn His Arg Gly Leu Glu Ala Glu Ala Ala
            105                 110                 115

ctg gca gaa ata ctg gaa agc cat ttg gac acc tct ttg ctt gac gca   499
Leu Ala Glu Ile Leu Glu Ser His Leu Asp Thr Ser Leu Leu Asp Ala
        120                 125                 130

ttg ttt atg aaa cag ggt gaa gta gaa gca ggt atc agc gct gta gga   547
Leu Phe Met Lys Gln Gly Glu Val Glu Ala Gly Ile Ser Ala Val Gly
    135                 140                 145

att cct acc ctg acc agc gct ttg aac gct caa aat ggc aat acc gaa   595
Ile Pro Thr Leu Thr Ser Ala Leu Asn Ala Gln Asn Gly Asn Thr Glu
150                 155                 160                 165

gat gcc acc gaa gac acc gca ctc atg gag gct gta gaa aag gaa tac   643
Asp Ala Thr Glu Asp Thr Ala Leu Met Glu Ala Val Glu Lys Glu Tyr
                170                 175                 180

cta aag ttc tac acc aac tcc gga aag gcg aat acg agg ttc cta cag   691
Leu Lys Phe Tyr Thr Asn Ser Gly Lys Ala Asn Thr Arg Phe Leu Gln
            185                 190                 195

ttt tcc aaa cag gtg gaa acc ctt cgt act gat ttg gat gag gct aac   739
Phe Ser Lys Gln Val Glu Thr Leu Arg Thr Asp Leu Asp Glu Ala Asn
        200                 205                 210

gct gaa gta gca aag ctc tcc tcc cat gtt gac cga gtt aaa cga ttg   787
Ala Glu Val Ala Lys Leu Ser Ser His Val Asp Arg Val Lys Arg Leu
    215                 220                 225

gaa att gat cgg gat cag gcc aca gca cag tta ccc aag gca gag gaa   835
Glu Ile Asp Arg Asp Gln Ala Thr Ala Gln Leu Pro Lys Ala Glu Glu
230                 235                 240                 245

gaa ctc gca ggg agg aaa gca gaa ctg gag gaa gcc caa aag gtt aag   883
Glu Leu Ala Gly Arg Lys Ala Glu Leu Glu Glu Ala Gln Lys Val Lys
                250                 255                 260

gct caa gcc acg gaa atc ctt gcg cag ttt tcc cgg gcg gaa gaa cag   931
Ala Gln Ala Thr Glu Ile Leu Ala Gln Phe Ser Arg Ala Glu Glu Gln
            265                 270                 275

tta gag cag gca aca gga gct cag aaa cga cgt aaa gaa ctc cgc aat   979
Leu Glu Gln Ala Thr Gly Ala Gln Lys Arg Arg Lys Glu Leu Arg Asn
        280                 285                 290
```

```
aag ctg gaa tta gca cag aca gaa gtc gaa aag gct gaa gca ggg caa   1027
Lys Leu Glu Leu Ala Gln Thr Glu Val Glu Lys Ala Glu Ala Gly Gln
    295                 300                 305

gag aac ctg gcg caa gaa gct tcc cgt gaa gca gaa gaa ttc cta gcc   1075
Glu Asn Leu Ala Gln Glu Ala Ser Arg Glu Ala Glu Glu Phe Leu Ala
310                 315                 320                 325

tta agt gaa aag ttc gag gca gcg cgc gca gct gaa act ctg gcc gtt   1123
Leu Ser Glu Lys Phe Glu Ala Ala Arg Ala Ala Glu Thr Leu Ala Val
                330                 335                 340

gaa aag gtg aaa gca gca cgt caa tcg gtt gct gga atc aaa aac cgt   1171
Glu Lys Val Lys Ala Ala Arg Gln Ser Val Ala Gly Ile Lys Asn Arg
            345                 350                 355

gac cgt aaa gaa cac ctc acg gtt atg ctt ggt gaa ctt gat cga att   1219
Asp Arg Lys Glu His Leu Thr Val Met Leu Gly Glu Leu Asp Arg Ile
        360                 365                 370

ggg cag cgc ctc tac gaa ttg cgc agc gtc cag cac tca tcg gtg cgt   1267
Gly Gln Arg Leu Tyr Glu Leu Arg Ser Val Gln His Ser Ser Val Arg
    375                 380                 385

gtg agc cag cgt gat att gat gct ctg caa aag gcg atc acc gag gtc   1315
Val Ser Gln Arg Asp Ile Asp Ala Leu Gln Lys Ala Ile Thr Glu Val
390                 395                 400                 405

gat atc caa agg acg ctc gtt gaa gcg cag cag gga agt att acc ctc   1363
Asp Ile Gln Arg Thr Leu Val Glu Ala Gln Gln Gly Ser Ile Thr Leu
                410                 415                 420

agt gct tcc aca ccc acc gac att caa cta ggt gat gac acc gtt tca   1411
Ser Ala Ser Thr Pro Thr Asp Ile Gln Leu Gly Asp Asp Thr Val Ser
            425                 430                 435

gct acc gac gct gga acc aca gtt gcc ctc gac cga gaa ctc acc gtc   1459
Ala Thr Asp Ala Gly Thr Thr Val Ala Leu Asp Arg Glu Leu Thr Val
        440                 445                 450

gtg gtc ggc gat gtc acc ttg gtg att aac cca gga aaa aca gca gcg   1507
Val Val Gly Asp Val Thr Leu Val Ile Asn Pro Gly Lys Thr Ala Ala
    455                 460                 465

gaa agt cgc acc gat ttt gaa tcc gcc gag gca gca ttg gcg gag ctg   1555
Glu Ser Arg Thr Asp Phe Glu Ser Ala Glu Ala Ala Leu Ala Glu Leu
470                 475                 480                 485

ctt gat caa ctc gac gtc tca gac ttg gac cag ctc agg gaa cgt ttc   1603
Leu Asp Gln Leu Asp Val Ser Asp Leu Asp Gln Leu Arg Glu Arg Phe
                490                 495                 500

act gcc caa gag caa cga gac gcg gat att gca gaa ctg gtt cgc gaa   1651
Thr Ala Gln Glu Gln Arg Asp Ala Asp Ile Ala Glu Leu Val Arg Glu
            505                 510                 515

caa cag cgc atg agc ggt ggg aca gaa aca aca gtt tta cgt gcc gag   1699
Gln Gln Arg Met Ser Gly Gly Thr Glu Thr Thr Val Leu Arg Ala Glu
        520                 525                 530
```

```
cta gaa ggc ctg cac gtc cca gag gat cta gac cca tca att tct gtg   1747
Leu Glu Gly Leu His Val Pro Glu Asp Leu Asp Pro Ser Ile Ser Val
    535                 540                 545

gat gat gcg caa act cag ttg aat gag gca gaa gag tcc aga gag ctc   1795
Asp Asp Ala Gln Thr Gln Leu Asn Glu Ala Glu Glu Ser Arg Glu Leu
550                 555                 560                 565

gct gcg gag gcg cat aaa cac gca aat gca gca ctt gat gga ttg cgt   1843
Ala Ala Glu Ala His Lys His Ala Asn Ala Ala Leu Asp Gly Leu Arg
                570                 575                 580

tcg cgt ccc gta gat aaa gct ctg aca gtt ttc aac gct cag ctc gca   1891
Ser Arg Pro Val Asp Lys Ala Leu Thr Val Phe Asn Ala Gln Leu Ala
            585                 590                 595

gca ctg cag aga aac ctc tct tcc gca caa gtt gaa tta gac cgt gca   1939
Ala Leu Gln Arg Asn Leu Ser Ser Ala Gln Val Glu Leu Asp Arg Ala
        600                 605                 610

gtg gca gaa acc tcg gat gac gaa gtt gat gct gct gta cag cgg tgc   1987
Val Ala Glu Thr Ser Asp Asp Glu Val Asp Ala Ala Val Gln Arg Cys
    615                 620                 625

gct gaa gct cta gct ggg gtg cgg gta cag aag cag gag att gaa cag   2035
Ala Glu Ala Leu Ala Gly Val Arg Val Gln Lys Gln Glu Ile Glu Gln
630                 635                 640                 645

gtc ttg gca aaa acc aac cca gac atg gct caa cgc tta tgt gat gct   2083
Val Leu Ala Lys Thr Asn Pro Asp Met Ala Gln Arg Leu Cys Asp Ala
                650                 655                 660

gct gaa gca aat gtg cga tcg tat aaa acg gca gtg tct gat gcc acc   2131
Ala Glu Ala Asn Val Arg Ser Tyr Lys Thr Ala Val Ser Asp Ala Thr
            665                 670                 675

aca gag ttg gtg cgc ctg gaa ggc ctc atc ggt gta gct gca ggt gcg   2179
Thr Glu Leu Val Arg Leu Glu Gly Leu Ile Gly Val Ala Ala Gly Ala
        680                 685                 690

aaa gaa cga cta gat aaa gtt aag tct gcg ctg aca gca gct gaa aac   2227
Lys Glu Arg Leu Asp Lys Val Lys Ser Ala Leu Thr Ala Ala Glu Asn
    695                 700                 705

cgg ttt gaa tca gaa caa cgt cgc gcc cac gct gca cgt cgc ctc tat   2275
Arg Phe Glu Ser Glu Gln Arg Arg Ala His Ala Ala Arg Arg Leu Tyr
710                 715                 720                 725

gcc ctc atg gtg ttc tac cgt gat gaa tcc cga aag cgc tac gca gca   2323
Ala Leu Met Val Phe Tyr Arg Asp Glu Ser Arg Lys Arg Tyr Ala Ala
                730                 735                 740

ccc ttc gcg gac aaa cta tcc agg ctg gca gca tcc gta ttt gga gaa   2371
Pro Phe Ala Asp Lys Leu Ser Arg Leu Ala Ala Ser Val Phe Gly Glu
            745                 750                 755

tca gca gac ttt gat ctt gat gat gag ctg aag atc tcc agt cgt tcc   2419
Ser Ala Asp Phe Asp Leu Asp Asp Glu Leu Lys Ile Ser Ser Arg Ser
        760                 765                 770

ata gga cca cga aca gtg gac ctt gcc aat ctt tct ggc ggc gca aag   2467
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Ile Gly Pro Arg Thr Val Asp Leu Ala Asn Leu Ser Gly Gly Ala Lys
    775                 780                 785

gaa cag ctg gca atc ctc acc cgc ttt gct atc gca gaa ttg gta gca   2515
Glu Gln Leu Ala Ile Leu Thr Arg Phe Ala Ile Ala Glu Leu Val Ala
790                 795                 800                 805

gaa tcc tcc gcg caa ggt gct gtg cct gtg ttt att gat gat gca ttg   2563
Glu Ser Ser Ala Gln Gly Ala Val Pro Val Phe Ile Asp Asp Ala Leu
                810                 815                 820

ggg agc aca gac cca gag cga ctg acc cgc ata tct act ctg ttt agt   2611
Gly Ser Thr Asp Pro Glu Arg Leu Thr Arg Ile Ser Thr Leu Phe Ser
            825                 830                 835

gat gca ggc aag gac tct cag gtg ttt gtt ctc acc tgt gtt cca gac   2659
Asp Ala Gly Lys Asp Ser Gln Val Phe Val Leu Thr Cys Val Pro Asp
        840                 845                 850

cgg tac aac tat gta gag gtc acc caa aag cac agc atc gag tca ttg   2707
Arg Tyr Asn Tyr Val Glu Val Thr Gln Lys His Ser Ile Glu Ser Leu
    855                 860                 865

aaa act gcc aac gct ctg ctg tagctgagca aaaagccaag caa             2751
Lys Thr Ala Asn Ala Leu Leu
870                 875


<210> 1640
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Met Arg Ile His Glu Ile Ile Ile Asp Asn Phe Arg Ala Ile Glu His
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Leu Glu Leu Arg Asp Ile Pro Asp Gln Gly Val Ile Val Ile His Gly
             20                  25                  30

Asp Asn Glu Gln Gly Lys Ser Ser Ile Leu Glu Ala Ile Lys Thr Val
         35                  40                  45

Leu Asn Ser Lys His Arg Thr Thr Ser Lys Thr Ile Lys Ala Ile Gln
     50                  55                  60

Pro Val Asp Arg Asp Val Pro Ile Ser Ile Thr Leu Glu Ala Thr Val
 65                  70                  75                  80

Gly Thr Val Arg Phe Arg Ile His Lys Arg Phe Leu Lys Ser Thr Ala
                 85                  90                  95

Ala Glu Leu Gln Val Ile Glu Pro Arg Pro Ser Asn His Arg Gly Leu
            100                 105                 110

Glu Ala Glu Ala Ala Leu Ala Glu Ile Leu Glu Ser His Leu Asp Thr
        115                 120                 125

Ser Leu Leu Asp Ala Leu Phe Met Lys Gln Gly Glu Val Glu Ala Gly
    130                 135                 140
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Ile Ser Ala Val Gly Ile Pro Thr Leu Thr Ser Ala Leu Asn Ala Gln
145                 150                 155                 160

Asn Gly Asn Thr Glu Asp Ala Thr Glu Asp Thr Ala Leu Met Glu Ala
                165                 170                 175

Val Glu Lys Glu Tyr Leu Lys Phe Tyr Thr Asn Ser Gly Lys Ala Asn
            180                 185                 190

Thr Arg Phe Leu Gln Phe Ser Lys Gln Val Glu Thr Leu Arg Thr Asp
        195                 200                 205

Leu Asp Glu Ala Asn Ala Glu Val Ala Lys Leu Ser Ser His Val Asp
    210                 215                 220

Arg Val Lys Arg Leu Glu Ile Asp Arg Asp Gln Ala Thr Ala Gln Leu
225                 230                 235                 240

Pro Lys Ala Glu Glu Glu Leu Ala Gly Arg Lys Ala Glu Leu Glu Glu
                245                 250                 255

Ala Gln Lys Val Lys Ala Gln Ala Thr Glu Ile Leu Ala Gln Phe Ser
            260                 265                 270

Arg Ala Glu Glu Gln Leu Glu Gln Ala Thr Gly Ala Gln Lys Arg Arg
        275                 280                 285

Lys Glu Leu Arg Asn Lys Leu Glu Leu Ala Gln Thr Glu Val Glu Lys
    290                 295                 300

Ala Glu Ala Gly Gln Glu Asn Leu Ala Gln Glu Ala Ser Arg Glu Ala
305                 310                 315                 320

Glu Glu Phe Leu Ala Leu Ser Glu Lys Phe Glu Ala Ala Arg Ala Ala
                325                 330                 335

Glu Thr Leu Ala Val Glu Lys Val Lys Ala Ala Arg Gln Ser Val Ala
            340                 345                 350

Gly Ile Lys Asn Arg Asp Arg Lys Glu His Leu Thr Val Met Leu Gly
        355                 360                 365

Glu Leu Asp Arg Ile Gly Gln Arg Leu Tyr Glu Leu Arg Ser Val Gln
    370                 375                 380

His Ser Ser Val Arg Val Ser Gln Arg Asp Ile Asp Ala Leu Gln Lys
385                 390                 395                 400

Ala Ile Thr Glu Val Asp Ile Gln Arg Thr Leu Val Glu Ala Gln Gln
                405                 410                 415

Gly Ser Ile Thr Leu Ser Ala Ser Thr Pro Thr Asp Ile Gln Leu Gly
            420                 425                 430

Asp Asp Thr Val Ser Ala Thr Asp Ala Gly Thr Thr Val Ala Leu Asp
        435                 440                 445

Arg Glu Leu Thr Val Val Val Gly Asp Val Thr Leu Val Ile Asn Pro
    450                 455                 460

Gly Lys Thr Ala Ala Glu Ser Arg Thr Asp Phe Glu Ser Ala Glu Ala
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465                 470                 475                 480

Ala Leu Ala Glu Leu Leu Asp Gln Leu Asp Val Ser Asp Leu Asp Gln
                485                 490                 495

Leu Arg Glu Arg Phe Thr Ala Gln Glu Gln Arg Asp Ala Asp Ile Ala
            500                 505                 510

Glu Leu Val Arg Glu Gln Gln Arg Met Ser Gly Gly Thr Glu Thr Thr
        515                 520                 525

Val Leu Arg Ala Glu Leu Glu Gly Leu His Val Pro Glu Asp Leu Asp
    530                 535                 540

Pro Ser Ile Ser Val Asp Asp Ala Gln Thr Gln Leu Asn Glu Ala Glu
545                 550                 555                 560

Glu Ser Arg Glu Leu Ala Ala Glu Ala His Lys His Ala Asn Ala Ala
                565                 570                 575

Leu Asp Gly Leu Arg Ser Arg Pro Val Asp Lys Ala Leu Thr Val Phe
            580                 585                 590

Asn Ala Gln Leu Ala Ala Leu Gln Arg Asn Leu Ser Ser Ala Gln Val
        595                 600                 605

Glu Leu Asp Arg Ala Val Ala Glu Thr Ser Asp Asp Glu Val Asp Ala
    610                 615                 620

Ala Val Gln Arg Cys Ala Glu Ala Leu Ala Gly Val Arg Val Gln Lys
625                 630                 635                 640

Gln Glu Ile Glu Gln Val Leu Ala Lys Thr Asn Pro Asp Met Ala Gln
                645                 650                 655

Arg Leu Cys Asp Ala Ala Glu Ala Asn Val Arg Ser Tyr Lys Thr Ala
            660                 665                 670

Val Ser Asp Ala Thr Thr Glu Leu Val Arg Leu Glu Gly Leu Ile Gly
        675                 680                 685

Val Ala Ala Gly Ala Lys Glu Arg Leu Asp Lys Val Lys Ser Ala Leu
    690                 695                 700

Thr Ala Ala Glu Asn Arg Phe Glu Ser Glu Gln Arg Arg Ala His Ala
705                 710                 715                 720

Ala Arg Arg Leu Tyr Ala Leu Met Val Phe Tyr Arg Asp Glu Ser Arg
                725                 730                 735

Lys Arg Tyr Ala Ala Pro Phe Ala Asp Lys Leu Ser Arg Leu Ala Ala
            740                 745                 750

Ser Val Phe Gly Glu Ser Ala Asp Phe Asp Leu Asp Asp Glu Leu Lys
        755                 760                 765

Ile Ser Ser Arg Ser Ile Gly Pro Arg Thr Val Asp Leu Ala Asn Leu
    770                 775                 780

Ser Gly Gly Ala Lys Glu Gln Leu Ala Ile Leu Thr Arg Phe Ala Ile
785                 790                 795                 800
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Ala Glu Leu Val Ala Glu Ser Ser Ala Gln Gly Ala Val Pro Val Phe
                805                 810                 815

Ile Asp Asp Ala Leu Gly Ser Thr Asp Pro Glu Arg Leu Thr Arg Ile
            820                 825                 830

Ser Thr Leu Phe Ser Asp Ala Gly Lys Asp Ser Gln Val Phe Val Leu
        835                 840                 845

Thr Cys Val Pro Asp Arg Tyr Asn Tyr Val Glu Val Thr Gln Lys His
    850                 855                 860

Ser Ile Glu Ser Leu Lys Thr Ala Asn Ala Leu Leu
865                 870                 875


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<223> RXA00199

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gtacactccg cagcagcgca cgcgttatcg ccagctgctc atg gaa gat ctt gag   115
                                            Met Glu Asp Leu Glu
                                              1               5

att ttt gat cgg cat ttg cag cat tcc gat ttt gag gat cag ggt tcc   163
Ile Phe Asp Arg His Leu Gln His Ser Asp Phe Glu Asp Gln Gly Ser
                10                  15                  20

atc ggc ctc gag ttg gaa ctc aac ctc gtg gat aag cat atg caa cct   211
Ile Gly Leu Glu Leu Glu Leu Asn Leu Val Asp Lys His Met Gln Pro
            25                  30                  35

gct ttg gca ggc cac gcg gtg ctt tcc cat tta gac gat gag tac cag   259
Ala Leu Ala Gly His Ala Val Leu Ser His Leu Asp Asp Glu Tyr Gln
        40                  45                  50

tcg gag atc ggt aac ttt aat gtt gaa atg aac cac ccg cca cta tcc   307
Ser Glu Ile Gly Asn Phe Asn Val Glu Met Asn His Pro Pro Leu Ser
    55                  60                  65

gtt aaa ggc gat gct tta cga cgc ctc gag caa ggc atc acc tcg cgt   355
Val Lys Gly Asp Ala Leu Arg Arg Leu Glu Gln Gly Ile Thr Ser Arg
70                  75                  80                  85

cta ggt cgc gtg cgc gcg gcc gcc aca tcg gag aac gtg aac gtg gcg   403
Leu Gly Arg Val Arg Ala Ala Ala Thr Ser Glu Asn Val Asn Val Ala
                90                  95                  100

atg atc ggc acg ctg ccc acc atc acc cca gaa ttc ctc gaa gat ccg   451
Met Ile Gly Thr Leu Pro Thr Ile Thr Pro Glu Phe Leu Glu Asp Pro
            105                 110                 115
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gca tgg atg acc caa gaa aac cgc tac cgt gcg ctg agc aat gcg gtg   499
Ala Trp Met Thr Gln Glu Asn Arg Tyr Arg Ala Leu Ser Asn Ala Val
        120                 125                 130

atg gaa tcg cgt ggc gag tta gtg cac atc aac atc gcc gac cgt gaa   547
Met Glu Ser Arg Gly Glu Leu Val His Ile Asn Ile Ala Asp Arg Glu
    135                 140                 145

caa atc atc cac gat ttc act gat ctc gcc ccc gaa tca act tgc acg   595
Gln Ile Ile His Asp Phe Thr Asp Leu Ala Pro Glu Ser Thr Cys Thr
150                 155                 160                 165

tct att cag ttg cac ctg caa tta gca ccc aat aag ttt gct gca gcg   643
Ser Ile Gln Leu His Leu Gln Leu Ala Pro Asn Lys Phe Ala Ala Ala
                170                 175                 180

tgg aat gcg tcg caa gca ata gct ggt gtt caa gca gct ctt tcc gcc   691
Trp Asn Ala Ser Gln Ala Ile Ala Gly Val Gln Ala Ala Leu Ser Ala
            185                 190                 195

aac tcc cca ctt ttc cta ggc cgt cgg gtg tgg cat gaa agc cgc att   739
Asn Ser Pro Leu Phe Leu Gly Arg Arg Val Trp His Glu Ser Arg Ile
        200                 205                 210

cca gtg ttt caa caa gct atc gat acg cgt act cct gaa ctt gtg aat   787
Pro Val Phe Gln Gln Ala Ile Asp Thr Arg Thr Pro Glu Leu Val Asn
    215                 220                 225

caa gga gtc cgc ccc aga gta tgg ttc ggc gaa cga tgg atc acc agt   835
Gln Gly Val Arg Pro Arg Val Trp Phe Gly Glu Arg Trp Ile Thr Ser
230                 235                 240                 245

gtt ttt gat ctt ttc gaa gaa aac gta cgc tac ttc tcc cct ctc atc   883
Val Phe Asp Leu Phe Glu Glu Asn Val Arg Tyr Phe Ser Pro Leu Ile
                250                 255                 260

gca gaa tcc cgc gcc ctg tct ggc aca cca atg atg aag gga aaa tcc   931
Ala Glu Ser Arg Ala Leu Ser Gly Thr Pro Met Met Lys Gly Lys Ser
            265                 270                 275

ccc gca ctc cac tac ctc aat ctc cac aac gga acg gtg tgg cgc tgg   979
Pro Ala Leu His Tyr Leu Asn Leu His Asn Gly Thr Val Trp Arg Trp
        280                 285                 290

aac cga ccc att tac gca ccg ggg gaa gag cgc tct cat ctg cgt ttg   1027
Asn Arg Pro Ile Tyr Ala Pro Gly Glu Glu Arg Ser His Leu Arg Leu
    295                 300                 305

gaa aac cgt ctc cta cct gca ggt ccc acc ccc atc gac atc acc gcc   1075
Glu Asn Arg Leu Leu Pro Ala Gly Pro Thr Pro Ile Asp Ile Thr Ala
310                 315                 320                 325

gat gcc gct ttc tac tac ggt ttg gtt aaa tat ctg gcc gag gaa aac   1123
Asp Ala Ala Phe Tyr Tyr Gly Leu Val Lys Tyr Leu Ala Glu Glu Asn
                330                 335                 340

cgc cct gtc tgg tca cgt ctc cta ttc cct gat gcg gaa aag aac ttc   1171
Arg Pro Val Trp Ser Arg Leu Leu Phe Pro Asp Ala Glu Lys Asn Phe
            345                 350                 355
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caa tcc ggt gca cgt tca ggg ctg ttc gcc cgc atg acc tgg cca acc   1219
Gln Ser Gly Ala Arg Ser Gly Leu Phe Ala Arg Met Thr Trp Pro Thr
        360                 365                 370

ctc gga caa gtc aac gtt gcg aat ctg gtc caa gag cac ctc atc cct   1267
Leu Gly Gln Val Asn Val Ala Asn Leu Val Gln Glu His Leu Ile Pro
    375                 380                 385

caa gcc aga atc gga ctg gaa cga ctc gaa gta aac aaa gac ctt atc   1315
Gln Ala Arg Ile Gly Leu Glu Arg Leu Glu Val Asn Lys Asp Leu Ile
390                 395                 400                 405

gac caa tac ctg ggc atc atc acc gaa cgc gcg aag tcc cgc caa aac   1363
Asp Gln Tyr Leu Gly Ile Ile Thr Glu Arg Ala Lys Ser Arg Gln Asn
                410                 415                 420

ggt gcc acc tgg cag ttg cgt agc ctc aac aag ctg gaa gca cac gga   1411
Gly Ala Thr Trp Gln Leu Arg Ser Leu Asn Lys Leu Glu Ala His Gly
            425                 430                 435

agc atg ccg ggt tcc gat gct cga aaa gca ggt ctt gca gca atg ttg   1459
Ser Met Pro Gly Ser Asp Ala Arg Lys Ala Gly Leu Ala Ala Met Leu
        440                 445                 450

caa cag tat tta cag aat caa gaa agc ggc caa cct gtc cac aca tgg   1507
Gln Gln Tyr Leu Gln Asn Gln Glu Ser Gly Gln Pro Val His Thr Trp
    455                 460                 465

gct att ggt tcg taaaacggca aggaaagata ata                        1542
Ala Ile Gly Ser
470
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<210> 1642
<211> 473
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<213> Corynebacterium glutamicum

<400> 1642

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Met Glu Asp Leu Glu Ile Phe Asp Arg His Leu Gln His Ser Asp Phe
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Glu Asp Gln Gly Ser Ile Gly Leu Glu Leu Glu Leu Asn Leu Val Asp
             20                  25                  30

Lys His Met Gln Pro Ala Leu Ala Gly His Ala Val Leu Ser His Leu
         35                  40                  45

Asp Asp Glu Tyr Gln Ser Glu Ile Gly Asn Phe Asn Val Glu Met Asn
     50                  55                  60

His Pro Pro Leu Ser Val Lys Gly Asp Ala Leu Arg Arg Leu Glu Gln
 65                  70                  75                  80

Gly Ile Thr Ser Arg Leu Gly Arg Val Arg Ala Ala Ala Thr Ser Glu
                 85                  90                  95

Asn Val Asn Val Ala Met Ile Gly Thr Leu Pro Thr Ile Thr Pro Glu
            100                 105                 110

Phe Leu Glu Asp Pro Ala Trp Met Thr Gln Glu Asn Arg Tyr Arg Ala
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        115                 120                 125

Leu Ser Asn Ala Val Met Glu Ser Arg Gly Glu Leu Val His Ile Asn
    130                 135                 140

Ile Ala Asp Arg Glu Gln Ile Ile His Asp Phe Thr Asp Leu Ala Pro
145                 150                 155                 160

Glu Ser Thr Cys Thr Ser Ile Gln Leu His Leu Gln Leu Ala Pro Asn
                165                 170                 175

Lys Phe Ala Ala Ala Trp Asn Ala Ser Gln Ala Ile Ala Gly Val Gln
            180                 185                 190

Ala Ala Leu Ser Ala Asn Ser Pro Leu Phe Leu Gly Arg Arg Val Trp
        195                 200                 205

His Glu Ser Arg Ile Pro Val Phe Gln Gln Ala Ile Asp Thr Arg Thr
    210                 215                 220

Pro Glu Leu Val Asn Gln Gly Val Arg Pro Arg Val Trp Phe Gly Glu
225                 230                 235                 240

Arg Trp Ile Thr Ser Val Phe Asp Leu Phe Glu Glu Asn Val Arg Tyr
                245                 250                 255

Phe Ser Pro Leu Ile Ala Glu Ser Arg Ala Leu Ser Gly Thr Pro Met
            260                 265                 270

Met Lys Gly Lys Ser Pro Ala Leu His Tyr Leu Asn Leu His Asn Gly
        275                 280                 285

Thr Val Trp Arg Trp Asn Arg Pro Ile Tyr Ala Pro Gly Glu Glu Arg
    290                 295                 300

Ser His Leu Arg Leu Glu Asn Arg Leu Leu Pro Ala Gly Pro Thr Pro
305                 310                 315                 320

Ile Asp Ile Thr Ala Asp Ala Ala Phe Tyr Tyr Gly Leu Val Lys Tyr
                325                 330                 335

Leu Ala Glu Glu Asn Arg Pro Val Trp Ser Arg Leu Leu Phe Pro Asp
            340                 345                 350

Ala Glu Lys Asn Phe Gln Ser Gly Ala Arg Ser Gly Leu Phe Ala Arg
        355                 360                 365

Met Thr Trp Pro Thr Leu Gly Gln Val Asn Val Ala Asn Leu Val Gln
    370                 375                 380

Glu His Leu Ile Pro Gln Ala Arg Ile Gly Leu Glu Arg Leu Glu Val
385                 390                 395                 400

Asn Lys Asp Leu Ile Asp Gln Tyr Leu Gly Ile Ile Thr Glu Arg Ala
                405                 410                 415

Lys Ser Arg Gln Asn Gly Ala Thr Trp Gln Leu Arg Ser Leu Asn Lys
            420                 425                 430

Leu Glu Ala His Gly Ser Met Pro Gly Ser Asp Ala Arg Lys Ala Gly
        435                 440                 445
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Leu Ala Ala Met Leu Gln Gln Tyr Leu Gln Asn Gln Glu Ser Gly Gln
    450                 455                 460

Pro Val His Thr Trp Ala Ile Gly Ser
465                 470


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<213> Corynebacterium glutamicum

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<223> RXA00200

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cac tac gcc gga gtc acc gag att cct gaa tac cga atc tcc cca gac   48
His Tyr Ala Gly Val Thr Glu Ile Pro Glu Tyr Arg Ile Ser Pro Asp
  1               5                  10                  15

cac ggc gga aaa tcc acc ctc tcc cca ttc caa gac tgg gca ggc ggc   96
His Gly Gly Lys Ser Thr Leu Ser Pro Phe Gln Asp Trp Ala Gly Gly
             20                  25                  30

gga tcc atg ggc acg gcc gaa gca gta aac aac gcc tac gaa atc ccg   144
Gly Ser Met Gly Thr Ala Glu Ala Val Asn Asn Ala Tyr Glu Ile Pro
         35                  40                  45

tcc tac ctc cgc aac gac tgg ggc cgc gac tgg ggt tcc atc gaa cgc   192
Ser Tyr Leu Arg Asn Asp Trp Gly Arg Asp Trp Gly Ser Ile Glu Arg
     50                  55                  60

tac tcg ctg cgc acc aac tcc aac ggc gat gca cct aag gtt gca gac   240
Tyr Ser Leu Arg Thr Asn Ser Asn Gly Asp Ala Pro Lys Val Ala Asp
 65                  70                  75                  80

atc aac ctt gaa acc atc caa cgt tcc gga ctc tgg aat cca ggg cat   288
Ile Asn Leu Glu Thr Ile Gln Arg Ser Gly Leu Trp Asn Pro Gly His
                 85                  90                  95

atg aag gta gat gaa taagaccttc agtactggaa gtt                    326
Met Lys Val Asp Glu
            100


<210> 1644
<211> 101
<212> PRT
<213> Corynebacterium glutamicum

<400> 1644
His Tyr Ala Gly Val Thr Glu Ile Pro Glu Tyr Arg Ile Ser Pro Asp
  1               5                  10                  15

His Gly Gly Lys Ser Thr Leu Ser Pro Phe Gln Asp Trp Ala Gly Gly
             20                  25                  30

Gly Ser Met Gly Thr Ala Glu Ala Val Asn Asn Ala Tyr Glu Ile Pro
```

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         35                  40                  45

Ser Tyr Leu Arg Asn Asp Trp Gly Arg Asp Trp Gly Ser Ile Glu Arg
     50                  55                  60

Tyr Ser Leu Arg Thr Asn Ser Asn Gly Asp Ala Pro Lys Val Ala Asp
 65                  70                  75                  80

Ile Asn Leu Glu Thr Ile Gln Arg Ser Gly Leu Trp Asn Pro Gly His
                 85                  90                  95

Met Lys Val Asp Glu
            100


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<212> DNA
<213> Corynebacterium glutamicum

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<223> RXA00207

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aaacccccgc ggaaaaattt tgtctctaga ctggctcacc atg gaa atg aaa ttg   115
                                              Met Glu Met Lys Leu
                                                1               5

aaa aag gca tcc cag gtc agc act gcc acc gtc gtc gca gca ggt ttg   163
Lys Lys Ala Ser Gln Val Ser Thr Ala Thr Val Val Ala Ala Gly Leu
                10                  15                  20

atc ggc ggt tgg ttg act gcc cgt gaa tcc ggc att cgc cca ctg ggc   211
Ile Gly Gly Trp Leu Thr Ala Arg Glu Ser Gly Ile Arg Pro Leu Gly
            25                  30                  35

acc att cca ttg gca gca tcc gga gcg ctt gct gca cga agc tgg aat   259
Thr Ile Pro Leu Ala Ala Ser Gly Ala Leu Ala Ala Arg Ser Trp Asn
        40                  45                  50

gaa aag aag ggt cct gca gta gct act ggc ctg ctg gca acc tac gtt   307
Glu Lys Lys Gly Pro Ala Val Ala Thr Gly Leu Leu Ala Thr Tyr Val
    55                  60                  65

ggt gca ttt ggc ctg tcc cac cca ctt gcc aag aag att ggc gcg tgg   355
Gly Ala Phe Gly Leu Ser His Pro Leu Ala Lys Lys Ile Gly Ala Trp
70                  75                  80                  85

cct gca gtt ctt act gtg acc gct ggc gct gct gcg att gct tac gca   403
Pro Ala Val Leu Thr Val Thr Ala Gly Ala Ala Ala Ile Ala Tyr Ala
                90                  95                  100

gta tct gac tcc cag taataattac ggtaaaaaaa ctt                    441
Val Ser Asp Ser Gln
            105
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Met Glu Met Lys Leu Lys Lys Ala Ser Gln Val Ser Thr Ala Thr Val
1 5 10 15

Val Ala Ala Gly Leu Ile Gly Gly Trp Leu Thr Ala Arg Glu Ser Gly
20 25 30

Ile Arg Pro Leu Gly Thr Ile Pro Leu Ala Ala Ser Gly Ala Leu Ala
35 40 45

Ala Arg Ser Trp Asn Glu Lys Lys Gly Pro Ala Val Ala Thr Gly Leu
50 55 60

Leu Ala Thr Tyr Val Gly Ala Phe Gly Leu Ser His Pro Leu Ala Lys
65 70 75 80

Lys Ile Gly Ala Trp Pro Ala Val Leu Thr Val Thr Ala Gly Ala Ala
85 90 95

Ala Ile Ala Tyr Ala Val Ser Asp Ser Gln
100 105

<210> 1647
<211> 786
<212> DNA
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<220>
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<222> (101)..(763)
<223> RXA00211

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tgagccaaaa tcaataaggt gtttttcagc ctgaggtaaa aatacggtgg tactgtcgaa 60

accaatcatc ccctagtttt gaaaagaagg aagcgagcca atg tca ttc ctg atc 115
Met Ser Phe Leu Ile
1 5

cgc gtc ctg ttg tcc gac acc cca ggc agc ctc gcg tta ctc gct gaa 163
Arg Val Leu Leu Ser Asp Thr Pro Gly Ser Leu Ala Leu Leu Ala Glu
10 15 20

gcc ctt ggg att gta gag gcc aat att caa tcc gtg gac gtg gtg gaa 211
Ala Leu Gly Ile Val Glu Ala Asn Ile Gln Ser Val Asp Val Val Glu
25 30 35

cgc ttc ccc aat ggc acg gtc atg gac gat ctg gtg atc tcc atc cct 259
Arg Phe Pro Asn Gly Thr Val Met Asp Asp Leu Val Ile Ser Ile Pro
40 45 50

cgc gat gtc atg gca gac acc atc atc acc gca gct gaa gaa gtc gac 307
Arg Asp Val Met Ala Asp Thr Ile Ile Thr Ala Ala Glu Glu Val Asp
55 60 65

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ggc gtg gag att gat tcc atc cgc cca ttc tcc ggg act gtt gac cgc   355
Gly Val Glu Ile Asp Ser Ile Arg Pro Phe Ser Gly Thr Val Asp Arg
 70                  75                  80                  85

cgc gga cag atc caa atg ctg gct gct gtt gct cac caa cgc cgc gat   403
Arg Gly Gln Ile Gln Met Leu Ala Ala Val Ala His Gln Arg Arg Asp
                90                  95                 100

atc acc gca gcg atg gaa gaa atg gtc gat gtc atc ccc cgc acc atg   451
Ile Thr Ala Ala Met Glu Glu Met Val Asp Val Ile Pro Arg Thr Met
            105                 110                 115

acc tct ggt tgg gct ttg gtc att gat cta aaa gga ccc atc act cgc   499
Thr Ser Gly Trp Ala Leu Val Ile Asp Leu Lys Gly Pro Ile Thr Arg
        120                 125                 130

atc gct ggt tcc cta gca gcg ccc gaa gat gac ggc acc gtt ccg gag   547
Ile Ala Gly Ser Leu Ala Ala Pro Glu Asp Asp Gly Thr Val Pro Glu
    135                 140                 145

aac atc gtt ctc aaa gaa gct cgc atg ctc aac ccg gaa aac gat ccg   595
Asn Ile Val Leu Lys Glu Ala Arg Met Leu Asn Pro Glu Asn Asp Pro
150                 155                 160                 165

tgg att cca gag tcc tgg aca ctg ctt gat tct tcc ctt gcc atc gct   643
Trp Ile Pro Glu Ser Trp Thr Leu Leu Asp Ser Ser Leu Ala Ile Ala
                170                 175                 180

ccg atc ggc aag cac ggc ctg gct ctg att atc ggt cgc cct ggt ggc   691
Pro Ile Gly Lys His Gly Leu Ala Leu Ile Ile Gly Arg Pro Gly Gly
            185                 190                 195

cct gat ttc ttg gcc agc gaa gtg gag cac tta ggc caa gtc ggt gac   739
Pro Asp Phe Leu Ala Ser Glu Val Glu His Leu Gly Gln Val Gly Asp
        200                 205                 210

att atc gga gca atg ctt caa aaa taatctgagc tgtttaaaaa atg         786
Ile Ile Gly Ala Met Leu Gln Lys
    215                 220
```

Sequence Listing.ST25.txt

<210> 1648
<211> 221
<212> PRT
<213> Corynebacterium glutamicum

<400> 1648

```
Met Ser Phe Leu Ile Arg Val Leu Leu Ser Asp Thr Pro Gly Ser Leu
  1               5                  10                  15

Ala Leu Leu Ala Glu Ala Leu Gly Ile Val Glu Ala Asn Ile Gln Ser
             20                  25                  30

Val Asp Val Val Glu Arg Phe Pro Asn Gly Thr Val Met Asp Asp Leu
         35                  40                  45

Val Ile Ser Ile Pro Arg Asp Val Met Ala Asp Thr Ile Ile Thr Ala
     50                  55                  60

Ala Glu Glu Val Asp Gly Val Glu Ile Asp Ser Ile Arg Pro Phe Ser
 65                  70                  75                  80
```

```
Gly Thr Val Asp Arg Arg Gly Gln Ile Gln Met Leu Ala Ala Val Ala
                85                  90                  95

His Gln Arg Arg Asp Ile Thr Ala Ala Met Glu Glu Met Val Asp Val
            100                 105                 110

Ile Pro Arg Thr Met Thr Ser Gly Trp Ala Leu Val Ile Asp Leu Lys
        115                 120                 125

Gly Pro Ile Thr Arg Ile Ala Gly Ser Leu Ala Ala Pro Glu Asp Asp
    130                 135                 140

Gly Thr Val Pro Glu Asn Ile Val Leu Lys Glu Ala Arg Met Leu Asn
145                 150                 155                 160

Pro Glu Asn Asp Pro Trp Ile Pro Glu Ser Trp Thr Leu Leu Asp Ser
                165                 170                 175

Ser Leu Ala Ile Ala Pro Ile Gly Lys His Gly Leu Ala Leu Ile Ile
            180                 185                 190

Gly Arg Pro Gly Gly Pro Asp Phe Leu Ala Ser Glu Val Glu His Leu
        195                 200                 205

Gly Gln Val Gly Asp Ile Ile Gly Ala Met Leu Gln Lys
    210                 215                 220


<210> 1649
<211> 1263
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1240)
<223> RXA00218

<400> 1649
tctaaactca cgctagactt ctaaaagatc taaagttcag ttccaacaca agccagcact 60

gcattccgca aacccgacta gaccatccaa ggtgtcttct atg tca gct cgc aat   115
                                              Met Ser Ala Arg Asn
                                                1               5

ccg ttc cgc ccc act ttc gga gtt tcc ccc acc gta ctt gca ggc cga   163
Pro Phe Arg Pro Thr Phe Gly Val Ser Pro Thr Val Leu Ala Gly Arg
                10                  15                  20

gac tca ctt cta cag tct ttc aaa ctt ggt ctc gcg gaa ggc ccc gga   211
Asp Ser Leu Leu Gln Ser Phe Lys Leu Gly Leu Ala Glu Gly Pro Gly
            25                  30                  35

agc ccc ttt aga gca ttg ctg att tcg gga tct cgt ggc atg ggt aaa   259
Ser Pro Phe Arg Ala Leu Leu Ile Ser Gly Ser Arg Gly Met Gly Lys
        40                  45                  50

act gtg ttg ctc aat gaa ttt gaa gat gca gct gcg tct caa ggg tgg   307
Thr Val Leu Leu Asn Glu Phe Glu Asp Ala Ala Ala Ser Gln Gly Trp
    55                  60                  65
```

```
atc acg ctg cgc gcc tat ccg gat aat tcc atg gtg gat ggc tta gtt   355
Ile Thr Leu Arg Ala Tyr Pro Asp Asn Ser Met Val Asp Gly Leu Val
 70                  75                  80                  85

aat tcc gcc atc ccg gag gcg cta cag aat ctt gac gga ccg cag tcc   403
Asn Ser Ala Ile Pro Glu Ala Leu Gln Asn Leu Asp Gly Pro Gln Ser
                90                  95                 100

aaa aga atg ctc agt ggt gtg gcc att cct ggt atc gct acg gtg acg   451
Lys Arg Met Leu Ser Gly Val Ala Ile Pro Gly Ile Ala Thr Val Thr
            105                 110                 115

gcc att gct gat cca acc aag aag gat ccc act ccc acg ctg att tcc   499
Ala Ile Ala Asp Pro Thr Lys Lys Asp Pro Thr Pro Thr Leu Ile Ser
        120                 125                 130

agg ctc cgc gag ttg gct act cgt ttg caa aag cac ggc tcc gga att   547
Arg Leu Arg Glu Leu Ala Thr Arg Leu Gln Lys His Gly Ser Gly Ile
    135                 140                 145

ttg atc acc ctt gat gaa ctc caa agc gcc aat gtg gat ctt ttg cat   595
Leu Ile Thr Leu Asp Glu Leu Gln Ser Ala Asn Val Asp Leu Leu His
150                 155                 160                 165

gtg ttg gcc act gcg gtc cag gat ctc cta cgg gat gat ttc gat atc   643
Val Leu Ala Thr Ala Val Gln Asp Leu Leu Arg Asp Asp Phe Asp Ile
                170                 175                 180

gca ttg gta gca gcg ggt ctg cca gag gga atc gat cgt ctt ctc cag   691
Ala Leu Val Ala Ala Gly Leu Pro Glu Gly Ile Asp Arg Leu Leu Gln
            185                 190                 195

cat gag ggc aca acc ttt atc cgc cga gcc gaa aga atc ctg ctc aat   739
His Glu Gly Thr Thr Phe Ile Arg Arg Ala Glu Arg Ile Leu Leu Asn
        200                 205                 210

cct gtc aac cat gaa gat tcg gtg gag atg ttc ctg gat acc gct gcg   787
Pro Val Asn His Glu Asp Ser Val Glu Met Phe Leu Asp Thr Ala Ala
    215                 220                 225

gaa ggc caa cgc cac atg act tcc gag gcc gcc gaa ctc gcg gcg cag   835
Glu Gly Gln Arg His Met Thr Ser Glu Ala Ala Glu Leu Ala Ala Gln
230                 235                 240                 245

atc agc aag ggc tac ccc tac tcc atg cag ctg act ggt tct ctg gca   883
Ile Ser Lys Gly Tyr Pro Tyr Ser Met Gln Leu Thr Gly Ser Leu Ala
                250                 255                 260

tgg gcg cga agt act ctt gac aac tcc gat acc atc cag gcc gaa caa   931
Trp Ala Arg Ser Thr Leu Asp Asn Ser Asp Thr Ile Gln Ala Glu Gln
            265                 270                 275

gta gat gct gtc cgc gac gag gtt gtg cgc cgc atg ggc atg caa gtc   979
Val Asp Ala Val Arg Asp Glu Val Val Arg Arg Met Gly Met Gln Val
        280                 285                 290

cac gag cca agc ctg cac cag gtc cct gat ggt gag ctg acc att ttg   1027
His Glu Pro Ser Leu His Gln Val Pro Asp Gly Glu Leu Thr Ile Leu
    295                 300                 305
```

```
tac gcg att gcc caa ctg tca aaa aac ggc gag atg gtg tct act gga   1075
Tyr Ala Ile Ala Gln Leu Ser Lys Asn Gly Glu Met Val Ser Thr Gly
310                 315                 320                 325

gat atc gca cac ctc atg ggc gtc aag ccc aac gcc ttg tcg atg cag   1123
Asp Ile Ala His Leu Met Gly Val Lys Pro Asn Ala Leu Ser Met Gln
                330                 335                 340

aga aag caa ctt ctc agc aga ggt ctc gta gag gtt ccc aag tac ggt   1171
Arg Lys Gln Leu Leu Ser Arg Gly Leu Val Glu Val Pro Lys Tyr Gly
            345                 350                 355

ttc ctc aat ttc act ttg ccg tac atg cgc gag cac ctc ctc aac agc   1219
Phe Leu Asn Phe Thr Leu Pro Tyr Met Arg Glu His Leu Leu Asn Ser
        360                 365                 370

ccg cac cac cga cca atc aca taagacacaa gcactaaaac agc             1263
Pro His His Arg Pro Ile Thr
    375                 380
```

<210> 1650
<211> 380
<212> PRT
<213> Corynebacterium glutamicum

<400> 1650

```
Met Ser Ala Arg Asn Pro Phe Arg Pro Thr Phe Gly Val Ser Pro Thr
  1               5                  10                  15

Val Leu Ala Gly Arg Asp Ser Leu Leu Gln Ser Phe Lys Leu Gly Leu
             20                  25                  30

Ala Glu Gly Pro Gly Ser Pro Phe Arg Ala Leu Leu Ile Ser Gly Ser
         35                  40                  45

Arg Gly Met Gly Lys Thr Val Leu Leu Asn Glu Phe Glu Asp Ala Ala
     50                  55                  60

Ala Ser Gln Gly Trp Ile Thr Leu Arg Ala Tyr Pro Asp Asn Ser Met
 65                  70                  75                  80

Val Asp Gly Leu Val Asn Ser Ala Ile Pro Glu Ala Leu Gln Asn Leu
                 85                  90                  95

Asp Gly Pro Gln Ser Lys Arg Met Leu Ser Gly Val Ala Ile Pro Gly
            100                 105                 110

Ile Ala Thr Val Thr Ala Ile Ala Asp Pro Thr Lys Lys Asp Pro Thr
        115                 120                 125

Pro Thr Leu Ile Ser Arg Leu Arg Glu Leu Ala Thr Arg Leu Gln Lys
    130                 135                 140

His Gly Ser Gly Ile Leu Ile Thr Leu Asp Glu Leu Gln Ser Ala Asn
145                 150                 155                 160

Val Asp Leu Leu His Val Leu Ala Thr Ala Val Gln Asp Leu Leu Arg
                165                 170                 175

Asp Asp Phe Asp Ile Ala Leu Val Ala Ala Gly Leu Pro Glu Gly Ile
```

```
            180                 185                 190

Asp Arg Leu Leu Gln His Glu Gly Thr Thr Phe Ile Arg Arg Ala Glu
        195                 200                 205

Arg Ile Leu Leu Asn Pro Val Asn His Glu Asp Ser Val Glu Met Phe
    210                 215                 220

Leu Asp Thr Ala Ala Glu Gly Gln Arg His Met Thr Ser Glu Ala Ala
225                 230                 235                 240

Glu Leu Ala Ala Gln Ile Ser Lys Gly Tyr Pro Tyr Ser Met Gln Leu
                245                 250                 255

Thr Gly Ser Leu Ala Trp Ala Arg Ser Thr Leu Asp Asn Ser Asp Thr
            260                 265                 270

Ile Gln Ala Glu Gln Val Asp Ala Val Arg Asp Glu Val Val Arg Arg
        275                 280                 285

Met Gly Met Gln Val His Glu Pro Ser Leu His Gln Val Pro Asp Gly
    290                 295                 300

Glu Leu Thr Ile Leu Tyr Ala Ile Ala Gln Leu Ser Lys Asn Gly Glu
305                 310                 315                 320

Met Val Ser Thr Gly Asp Ile Ala His Leu Met Gly Val Lys Pro Asn
                325                 330                 335

Ala Leu Ser Met Gln Arg Lys Gln Leu Leu Ser Arg Gly Leu Val Glu
            340                 345                 350

Val Pro Lys Tyr Gly Phe Leu Asn Phe Thr Leu Pro Tyr Met Arg Glu
        355                 360                 365

His Leu Leu Asn Ser Pro His His Arg Pro Ile Thr
    370                 375                 380


<210> 1651
<211> 627
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(604)
<223> RXA00220

<400> 1651
agatcgtgcc gagtttccgg tttggatggg gtttgggatg ttaatgggag aggatcggcg 60

tgatcgtgcc ggttttcctt gcgttggtag tcttggggct atg agc gca ttc cac   115
                                              Met Ser Ala Phe His
                                                1               5

atc cga gcg gaa caa tcg cac gat atc agc gcg att cat gat gtt act   163
Ile Arg Ala Glu Gln Ser His Asp Ile Ser Ala Ile His Asp Val Thr
                10                  15                  20

gaa gcg gcc ttt aca gga att gag cat tca gat gga aca gag caa gat   211
```

```
Glu Ala Ala Phe Thr Gly Ile Glu His Ser Asp Gly Thr Glu Gln Asp
            25                  30                  35

ctc gtc gat aag ctt cgt gct gca aag gcg ctg agc ctt tcg ctc gtc   259
Leu Val Asp Lys Leu Arg Ala Ala Lys Ala Leu Ser Leu Ser Leu Val
        40                  45                  50

gct gag gcg gat ggc gag gtc att ggg cat att gct gcc tct gag gtg   307
Ala Glu Ala Asp Gly Glu Val Ile Gly His Ile Ala Ala Ser Glu Val
    55                  60                  65

ctg att ggc ggt ggg gtg cag ggc tgg ttt ggc att ggg cct gtc agt   355
Leu Ile Gly Gly Gly Val Gln Gly Trp Phe Gly Ile Gly Pro Val Ser
70                  75                  80                  85

gtt cgg ccc gat aag cag cag caa ggc gtg ggt att gcg ctg atg ggc   403
Val Arg Pro Asp Lys Gln Gln Gln Gly Val Gly Ile Ala Leu Met Gly
                90                  95                  100

agc gcg ctt gat cag ttg cgt gcg gag ggt gct ggc ggc atc gtg ttg   451
Ser Ala Leu Asp Gln Leu Arg Ala Glu Gly Ala Gly Gly Ile Val Leu
            105                 110                 115

ctg ggg gat ccg ggc tat tat cga cgc ttc ggt ttt gag gtc gtg ccc   499
Leu Gly Asp Pro Gly Tyr Tyr Arg Arg Phe Gly Phe Glu Val Val Pro
        120                 125                 130

ggg ctg gtc tat ccg gac gcg cca gcg gaa ttt ttt atg gct gtg tgt   547
Gly Leu Val Tyr Pro Asp Ala Pro Ala Glu Phe Phe Met Ala Val Cys
    135                 140                 145

ttg aat gct ccg gcg ttt ccg cag ggt gtt gtg gag tat cac tcg gca   595
Leu Asn Ala Pro Ala Phe Pro Gln Gly Val Val Glu Tyr His Ser Ala
150                 155                 160                 165

ttt gga ggg tagagacccc atcgtggcgg gcc                            627
Phe Gly Gly
```

<210> 1652
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 1652

```
Met Ser Ala Phe His Ile Arg Ala Glu Gln Ser His Asp Ile Ser Ala
  1               5                  10                  15

Ile His Asp Val Thr Glu Ala Ala Phe Thr Gly Ile Glu His Ser Asp
            20                  25                  30

Gly Thr Glu Gln Asp Leu Val Asp Lys Leu Arg Ala Ala Lys Ala Leu
        35                  40                  45

Ser Leu Ser Leu Val Ala Glu Ala Asp Gly Glu Val Ile Gly His Ile
    50                  55                  60

Ala Ala Ser Glu Val Leu Ile Gly Gly Gly Val Gln Gly Trp Phe Gly
65                  70                  75                  80
```

```
Ile Gly Pro Val Ser Val Arg Pro Asp Lys Gln Gln Gln Gly Val Gly
                 85                  90                  95

Ile Ala Leu Met Gly Ser Ala Leu Asp Gln Leu Arg Ala Glu Gly Ala
            100                 105                 110

Gly Gly Ile Val Leu Leu Gly Asp Pro Gly Tyr Tyr Arg Arg Phe Gly
        115                 120                 125

Phe Glu Val Val Pro Gly Leu Val Tyr Pro Asp Ala Pro Ala Glu Phe
    130                 135                 140

Phe Met Ala Val Cys Leu Asn Ala Pro Ala Phe Pro Gln Gly Val Val
145                 150                 155                 160

Glu Tyr His Ser Ala Phe Gly Gly
                165
```

Sequence Listing.txt

<210> 1653
<211> 843
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(820)
<223> RXA00230

<400> 1653

```
aggtcttacc gcccctcaaa tcctgcagat tttccgtcgt caatcaggga cgaaagtaca 60

tcctatctat ctagctccac tagcacagat aggaactccg ttg att cat gag caa   115
                                            Leu Ile His Glu Gln
                                              1               5

gac gtt cag aag ctg tta aac tac atc act tca cac ttt ggt gtt gac   163
Asp Val Gln Lys Leu Leu Asn Tyr Ile Thr Ser His Phe Gly Val Asp
                 10                  15                  20

cct gaa aga tgg ttt cat cct gaa ggc tac caa agc att gcc cta gcg   211
Pro Glu Arg Trp Phe His Pro Glu Gly Tyr Gln Ser Ile Ala Leu Ala
             25                  30                  35

att ctt gac tcc att tac tcg act ggt aat cgc tat aca ggt gta ctc   259
Ile Leu Asp Ser Ile Tyr Ser Thr Gly Asn Arg Tyr Thr Gly Val Leu
         40                  45                  50

aac ctt gtc aat cga tac tgc ggg ctg cgc gca aat gaa gga tca cac   307
Asn Leu Val Asn Arg Tyr Cys Gly Leu Arg Ala Asn Glu Gly Ser His
     55                  60                  65

cct gaa gcc gat act gcc act gat ctc atc gag aca ttc tac cgg tgg   355
Pro Glu Ala Asp Thr Ala Thr Asp Leu Ile Glu Thr Phe Tyr Arg Trp
 70                  75                  80                  85

gga ggg gtc gac gaa ttt gtt ctc aaa acg aat aat cgg tgg aga act   403
Gly Gly Val Asp Glu Phe Val Leu Lys Thr Asn Asn Arg Trp Arg Thr
                 90                  95                 100

tcc tcc aag att cac gca ccc tat aag gca tac gca gct ttg gaa gca   451
```

```
Ser Ser Lys Ile His Ala Pro Tyr Lys Ala Tyr Ala Ala Leu Glu Ala
            105                 110                 115

gca aag gta ctt gcg ggt cat tcc atc gaa tcc atc agc gat gtt gtc   499
Ala Lys Val Leu Ala Gly His Ser Ile Glu Ser Ile Ser Asp Val Val
        120                 125                 130

ggc agg ttc gat tcg cgc gaa agc cgt gaa cac tca gat atc gcg aga   547
Gly Arg Phe Asp Ser Arg Glu Ser Arg Glu His Ser Asp Ile Ala Arg
    135                 140                 145

gaa tgg ttg atg ata acc ggc caa agt agt gcg ttg acc tgg agt tac   595
Glu Trp Leu Met Ile Thr Gly Gln Ser Ser Ala Leu Thr Trp Ser Tyr
150                 155                 160                 165

ttc ctt atg ctc gta ggt gtc cca gga gtg aaa gca gac cga atg atc   643
Phe Leu Met Leu Val Gly Val Pro Gly Val Lys Ala Asp Arg Met Ile
                170                 175                 180

gtc cgt ttc gtc act cac gtg ctc gag cgt ccg aaa gag att tcc agg   691
Val Arg Phe Val Thr His Val Leu Glu Arg Pro Lys Glu Ile Ser Arg
            185                 190                 195

cac gaa gct tca cgg ttg att gag gaa gtt gcg gac att atg tgc gtc   739
His Glu Ala Ser Arg Leu Ile Glu Glu Val Ala Asp Ile Met Cys Val
        200                 205                 210

aac tac atc tac ctc gac cac acc atc tgg cgg ttc caa tca ggg cgc   787
Asn Tyr Ile Tyr Leu Asp His Thr Ile Trp Arg Phe Gln Ser Gly Arg
    215                 220                 225

ccc tac ctc caa gaa gac tcc tcc cct ttc gaa taaatccatc acatttcaca 840
Pro Tyr Leu Gln Glu Asp Ser Ser Pro Phe Glu
230                 235                 240

gtc                                                               843


<210> 1654
<211> 240
<212> PRT
<213> Corynebacterium glutamicum

<400> 1654
Leu Ile His Glu Gln Asp Val Gln Lys Leu Leu Asn Tyr Ile Thr Ser
  1               5                  10                  15

His Phe Gly Val Asp Pro Glu Arg Trp Phe His Pro Glu Gly Tyr Gln
             20                  25                  30

Ser Ile Ala Leu Ala Ile Leu Asp Ser Ile Tyr Ser Thr Gly Asn Arg
         35                  40                  45

Tyr Thr Gly Val Leu Asn Leu Val Asn Arg Tyr Cys Gly Leu Arg Ala
     50                  55                  60

Asn Glu Gly Ser His Pro Glu Ala Asp Thr Ala Thr Asp Leu Ile Glu
 65                  70                  75                  80

Thr Phe Tyr Arg Trp Gly Gly Val Asp Glu Phe Val Leu Lys Thr Asn
                 85                  90                  95
```

```
Asn Arg Trp Arg Thr Ser Ser Lys Ile His Ala Pro Tyr Lys Ala Tyr
            100                 105                 110

Ala Ala Leu Glu Ala Ala Lys Val Leu Ala Gly His Ser Ile Glu Ser
        115                 120                 125

Ile Ser Asp Val Val Gly Arg Phe Asp Ser Arg Glu Ser Arg Glu His
    130                 135                 140

Ser Asp Ile Ala Arg Glu Trp Leu Met Ile Thr Gly Gln Ser Ser Ala
145                 150                 155                 160

Leu Thr Trp Ser Tyr Phe Leu Met Leu Val Gly Val Pro Gly Val Lys
                165                 170                 175

Ala Asp Arg Met Ile Val Arg Phe Val Thr His Val Leu Glu Arg Pro
            180                 185                 190

Lys Glu Ile Ser Arg His Glu Ala Ser Arg Leu Ile Glu Glu Val Ala
        195                 200                 205

Asp Ile Met Cys Val Asn Tyr Ile Tyr Leu Asp His Thr Ile Trp Arg
    210                 215                 220

Phe Gln Ser Gly Arg Pro Tyr Leu Gln Glu Asp Ser Ser Pro Phe Glu
225                 230                 235                 240
```

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<210> 1655
<211> 517
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(517)
<223> RXA00233

<400> 1655

```
cgcctccagc agttgaggga gaagttccaa cacttgcacc aactgaggaa gcaactgtgc 60

aatagcgctt tagacacaga ctcatgacag aatagaagac atg agt gtg aat gaa   115
                                            Met Ser Val Asn Glu
                                              1               5

gca gat ctg aac gct gtc gaa gag caa ttg gga agg gcc cca cga ggt   163
Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly Arg Ala Pro Arg Gly
                 10                  15                  20

gtc ctc gat att tct tac cgc agc cct gat gga gta ccc ggt gtg gtg   211
Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly Val Pro Gly Val Val
             25                  30                  35

atg acc gca cca aaa ctg gat gac gga acc cca ttc cca acc ctg tac   259
Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro Phe Pro Thr Leu Tyr
         40                  45                  50
```

```
tac ttg aca gat cca cgc ctg acc acc gag gca tcc cgc ctc gag gtc   307
Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala Ser Arg Leu Glu Val
     55                  60                  65

gca ttg gta atg aag tgg atg act gat cgc ctt tcc acc gac gaa gag   355
Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu Ser Thr Asp Glu Glu
 70                  75                  80                  85

ctt cgt gcc gac tac cag cgc gcc cac gag cac ttc ctg gca aag cgc   403
Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His Phe Leu Ala Lys Arg
                90                  95                 100

aac gca att gaa gat ctc ggc acg gat ttt tcc ggc ggt ggc atg cct   451
Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser Gly Gly Gly Met Pro
            105                 110                 115

gac cga gtg aag tgc ctt cac gtc ctc att gac tat gca ctg gca gaa   499
Asp Arg Val Lys Cys Leu His Val Leu Ile Asp Tyr Ala Leu Ala Glu
        120                 125                 130

ggc cca cac cat ttc ctt                                          517
Gly Pro His His Phe Leu
    135
```

<210> 1656
<211> 139
<212> PRT
<213> Corynebacterium glutamicum

<400> 1656

```
Met Ser Val Asn Glu Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly
  1               5                  10                  15

Arg Ala Pro Arg Gly Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly
             20                  25                  30

Val Pro Gly Val Val Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro
         35                  40                  45

Phe Pro Thr Leu Tyr Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala
     50                  55                  60

Ser Arg Leu Glu Val Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu
 65                  70                  75                  80

Ser Thr Asp Glu Glu Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His
                 85                  90                  95

Phe Leu Ala Lys Arg Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser
            100                 105                 110

Gly Gly Gly Met Pro Asp Arg Val Lys Cys Leu His Val Leu Ile Asp
        115                 120                 125

Tyr Ala Leu Ala Glu Gly Pro His His Phe Leu
    130                 135
```

<210> 1657
<211> 663

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(640)
<223> RXA00234

<400> 1657
ttcagggcta aataaaagcg cttttcgacg cccggtaacc tcaaggttgc cgggcgtcgt 60

tgccttacta ctgttactgg tgtgactatg atcgaggatt atg gca aag cag aag 115
Met Ala Lys Gln Lys
1 5

aaa act cat aaa ggc ctt gtt cct gtc tca agc agg gaa cgt gct tca 163
Lys Thr His Lys Gly Leu Val Pro Val Ser Ser Arg Glu Arg Ala Ser
10 15 20

gag tca gtt tct gct acc cgc gcc cca ttt aga ttg ggt gcc gtc ggc 211
Glu Ser Val Ser Ala Thr Arg Ala Pro Phe Arg Leu Gly Ala Val Gly
25 30 35

atc ggt gca atc gca ctc gta gtt ctt ctc atc ctg ttt gtc atc gcg 259
Ile Gly Ala Ile Ala Leu Val Val Leu Leu Ile Leu Phe Val Ile Ala
40 45 50

att cct gtg cgt aac tat ttt cag ctg cgc tcc gac atc gcc caa aca 307
Ile Pro Val Arg Asn Tyr Phe Gln Leu Arg Ser Asp Ile Ala Gln Thr
55 60 65

gag gct tcc att gaa gcc aaa gaa caa cag atc aaa caa ctg gaa tct 355
Glu Ala Ser Ile Glu Ala Lys Glu Gln Gln Ile Lys Gln Leu Glu Ser
70 75 80 85

gac ctc aac agg tac caa tca gag gcg tac atc cgc gaa caa gca cgc 403
Asp Leu Asn Arg Tyr Gln Ser Glu Ala Tyr Ile Arg Glu Gln Ala Arg
90 95 100

ctg cgc cta ggc gtc att gaa cct gga gaa acc gcg ttc aga atc gtg 451
Leu Arg Leu Gly Val Ile Glu Pro Gly Glu Thr Ala Phe Arg Ile Val
105 110 115

gac cca gca cta gat acc gac acc tca gtc acc tct gac ggc aac gaa 499
Asp Pro Ala Leu Asp Thr Asp Thr Ser Val Thr Ser Asp Gly Asn Glu
120 125 130

gag aaa cca ctg gga gct tgg tat gaa aac ctc tgg gac tca gtc acc 547
Glu Lys Pro Leu Gly Ala Trp Tyr Glu Asn Leu Trp Asp Ser Val Thr
135 140 145

aag cca gaa gca ctc ggc gaa gag gaa att gcg cct cca gca gtt gag 595
Lys Pro Glu Ala Leu Gly Glu Glu Glu Ile Ala Pro Pro Ala Val Glu
150 155 160 165

gga gaa gtt cca aca ctt gca cca act gag gaa gca act gtg caa 640
Gly Glu Val Pro Thr Leu Ala Pro Thr Glu Glu Ala Thr Val Gln
170 175 180

tagcgcttta gacacagact cat 663

<210> 1658
<211> 180
<212> PRT
<213> Corynebacterium glutamicum

<400> 1658
Met Ala Lys Gln Lys Lys Thr His Lys Gly Leu Val Pro Val Ser Ser
1 5 10 15

Arg Glu Arg Ala Ser Glu Ser Val Ser Ala Thr Arg Ala Pro Phe Arg
20 25 30

Leu Gly Ala Val Gly Ile Gly Ala Ile Ala Leu Val Val Leu Leu Ile
35 40 45

Leu Phe Val Ile Ala Ile Pro Val Arg Asn Tyr Phe Gln Leu Arg Ser
50 55 60

Asp Ile Ala Gln Thr Glu Ala Ser Ile Glu Ala Lys Glu Gln Gln Ile
65 70 75 80

Lys Gln Leu Glu Ser Asp Leu Asn Arg Tyr Gln Ser Glu Ala Tyr Ile
85 90 95

Arg Glu Gln Ala Arg Leu Arg Leu Gly Val Ile Glu Pro Gly Glu Thr
100 105 110

Ala Phe Arg Ile Val Asp Pro Ala Leu Asp Thr Asp Thr Ser Val Thr
115 120 125

Ser Asp Gly Asn Glu Glu Lys Pro Leu Gly Ala Trp Tyr Glu Asn Leu
130 135 140

Trp Asp Ser Val Thr Lys Pro Glu Ala Leu Gly Glu Glu Glu Ile Ala
145 150 155 160

Pro Pro Ala Val Glu Gly Glu Val Pro Thr Leu Ala Pro Thr Glu Glu
165 170 175

Ala Thr Val Gln
180

<210> 1659
<211> 501
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(478)
<223> RXA00237

<400> 1659
actggtagaa gctttgatga tctacatcac aaatttacaa tgtgtggtga gttattcata 60

ttacccaagg acttaaacct taaaaggagc cctaaaaatc atg aag ctt tca cac 115
Met Lys Leu Ser His
1 5

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cgc atc gca gca atg gca gca acc gca ggc atc aca gtg gca gca ttc   163
Arg Ile Ala Ala Met Ala Ala Thr Ala Gly Ile Thr Val Ala Ala Phe
                10                  15                  20

gca gca cct gct tcc gca tcc gac ttc gca aac cta tcc tcc acc aac   211
Ala Ala Pro Ala Ser Ala Ser Asp Phe Ala Asn Leu Ser Ser Thr Asn
            25                  30                  35

aaa gaa ctg tcc cct cag tac aac tgg gtt gct tgc ggc atc ctt gag   259
Lys Glu Leu Ser Pro Gln Tyr Asn Trp Val Ala Cys Gly Ile Leu Glu
        40                  45                  50

ggt ggc ctc aaa gca gct ggc gtc ctt gaa gaa ggc cag tac aac cgc   307
Gly Gly Leu Lys Ala Ala Gly Val Leu Glu Glu Gly Gln Tyr Asn Arg
    55                  60                  65

gag ctc gca gaa gca atc gcc gca aag ggt gaa ggc ttc tgg acc act   355
Glu Leu Ala Glu Ala Ile Ala Ala Lys Gly Glu Gly Phe Trp Thr Thr
70                  75                  80                  85

cag ttc cca caa atc ggt gat tgg aac gaa gat cag gca gca gca ctt   403
Gln Phe Pro Gln Ile Gly Asp Trp Asn Glu Asp Gln Ala Ala Ala Leu
                90                  95                  100

gcc gac cgc gca caa acc tgt ggc cta gtt aag gct gac acc tac ctt   451
Ala Asp Arg Ala Gln Thr Cys Gly Leu Val Lys Ala Asp Thr Tyr Leu
            105                 110                 115

tct gag ctg tcc tcc aac ttc tct tcc taaaaggttc gggggtaacc         498
Ser Glu Leu Ser Ser Asn Phe Ser Ser
        120                 125

cca                                                               501
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<210> 1660
<211> 126
<212> PRT
<213> Corynebacterium glutamicum

<400> 1660

```
Met Lys Leu Ser His Arg Ile Ala Ala Met Ala Ala Thr Ala Gly Ile
  1               5                  10                  15

Thr Val Ala Ala Phe Ala Ala Pro Ala Ser Ala Ser Asp Phe Ala Asn
            20                  25                  30

Leu Ser Ser Thr Asn Lys Glu Leu Ser Pro Gln Tyr Asn Trp Val Ala
        35                  40                  45

Cys Gly Ile Leu Glu Gly Gly Leu Lys Ala Ala Gly Val Leu Glu Glu
    50                  55                  60

Gly Gln Tyr Asn Arg Glu Leu Ala Glu Ala Ile Ala Ala Lys Gly Glu
65                  70                  75                  80

Gly Phe Trp Thr Thr Gln Phe Pro Gln Ile Gly Asp Trp Asn Glu Asp
                85                  90                  95

Gln Ala Ala Ala Leu Ala Asp Arg Ala Gln Thr Cys Gly Leu Val Lys
            100                 105                 110
```

```
Ala Asp Thr Tyr Leu Ser Glu Leu Ser Ser Asn Phe Ser Ser
        115                 120                 125


<210> 1661
<211> 492
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(469)
<223> RXA00238

<400> 1661
aacagtcaca taaatcactt cagtaacgta tgattttgga ctgttgtggc ttttgccata 60

tttatttcat ttccatctca gtgatctctt aaggaaaccc atg aag aaa cta cgt   115
                                            Met Lys Lys Leu Arg
                                              1               5

ttc gcc acc atc gct gcc gct acc gtt gcc ctg act gcg agc ctt acc   163
Phe Ala Thr Ile Ala Ala Ala Thr Val Ala Leu Thr Ala Ser Leu Thr
                10                  15                  20

ccc tca gct tcc gca cag gat ttc aac caa atc atc gac aac ttt gat   211
Pro Ser Ala Ser Ala Gln Asp Phe Asn Gln Ile Ile Asp Asn Phe Asp
            25                  30                  35

tgc ggc atc ctt cag acc gct atc tac acc acc ggc ctg gct cac gag   259
Cys Gly Ile Leu Gln Thr Ala Ile Tyr Thr Thr Gly Leu Ala His Glu
         40                  45                  50

aac tcc act cgc tca gag ctc gcc gct aat ctg cgc aac tcc gca gct   307
Asn Ser Thr Arg Ser Glu Leu Ala Ala Asn Leu Arg Asn Ser Ala Ala
     55                  60                  65

gtc ggc caa cta gac ttc cca ttg aat atc gcg gct acc ggc tac tcc   355
Val Gly Gln Leu Asp Phe Pro Leu Asn Ile Ala Ala Thr Gly Tyr Ser
 70                  75                  80                  85

gag cgc atc gct aac cgc gca ctg acc tgc gga atc gtg aag gaa gat   403
Glu Arg Ile Ala Asn Arg Ala Leu Thr Cys Gly Ile Val Lys Glu Asp
                90                  95                 100

cca cag gac ttc ctc tcc cag ctg cag ctt ctg tcc tct aac cta tct   451
Pro Gln Asp Phe Leu Ser Gln Leu Gln Leu Leu Ser Ser Asn Leu Ser
            105                 110                 115

tct tcc ttc ttc act gct tagtttctct tgggcttttc ctt                 492
Ser Ser Phe Phe Thr Ala
        120


<210> 1662
<211> 123
<212> PRT
<213> Corynebacterium glutamicum

<400> 1662
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```
Met Lys Lys Leu Arg Phe Ala Thr Ile Ala Ala Ala Thr Val Ala Leu
  1               5                  10                  15

Thr Ala Ser Leu Thr Pro Ser Ala Ser Ala Gln Asp Phe Asn Gln Ile
             20                  25                  30

Ile Asp Asn Phe Asp Cys Gly Ile Leu Gln Thr Ala Ile Tyr Thr Thr
         35                  40                  45

Gly Leu Ala His Glu Asn Ser Thr Arg Ser Glu Leu Ala Ala Asn Leu
     50                  55                  60

Arg Asn Ser Ala Ala Val Gly Gln Leu Asp Phe Pro Leu Asn Ile Ala
 65                  70                  75                  80

Ala Thr Gly Tyr Ser Glu Arg Ile Ala Asn Arg Ala Leu Thr Cys Gly
                 85                  90                  95

Ile Val Lys Glu Asp Pro Gln Asp Phe Leu Ser Gln Leu Gln Leu Leu
            100                 105                 110

Ser Ser Asn Leu Ser Ser Ser Phe Phe Thr Ala
        115                 120
```

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<210> 1663
<211> 708
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(685)
<223> RXA00239

<400> 1663

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acaaagcgga tcagattaac aaggtccgtg acgctgtcga tgagcgcatt ggcaaaaaca 60

acggcggcga agagaatcca gccaactagt attaggcgtc atg cgc gtc gta gtt   115
                                            Met Arg Val Val Val
                                              1               5

gtt gat cct aaa cac ccc gtc ctt cca gtc tct ttc ctc gag gct gtt   163
Val Asp Pro Lys His Pro Val Leu Pro Val Ser Phe Leu Glu Ala Val
                 10                  15                  20

ctt ggg cgg ggt gaa cct gtt tct atc gat ccc gat ttt cca ttt gat   211
Leu Gly Arg Gly Glu Pro Val Ser Ile Asp Pro Asp Phe Pro Phe Asp
             25                  30                  35

att gaa aaa tgg ggg atc aag acg tcg aca agc gcc tcc tgg ttt atc   259
Ile Glu Lys Trp Gly Ile Lys Thr Ser Thr Ser Ala Ser Trp Phe Ile
         40                  45                  50

atc gca aaa ccg caa agc acg ctg ctt atc gac gcg ccc ctc aac cct   307
Ile Ala Lys Pro Gln Ser Thr Leu Leu Ile Asp Ala Pro Leu Asn Pro
     55                  60                  65

ttg cat gag gcc gtc ggc gtc atg cgg gcg gcc gtg ggc cgc ggc gag   355
Leu His Glu Ala Val Gly Val Met Arg Ala Ala Val Gly Arg Gly Glu
 70                  75                  80                  85
```

```
tgg gaa cgc acg caa acc cat gag agt ttg att ccg tat ctg gaa gaa   403
Trp Glu Arg Thr Gln Thr His Glu Ser Leu Ile Pro Tyr Leu Glu Glu
                 90                  95                 100

gaa tcg cag gag ttt att gaa gcg att cat ggt ggc gat gat gag cac   451
Glu Ser Gln Glu Phe Ile Glu Ala Ile His Gly Gly Asp Asp Glu His
            105                 110                 115

atg aaa agc gaa ctg ggg gat gtt ttg ctg cag gtg ctt ttt cat gca   499
Met Lys Ser Glu Leu Gly Asp Val Leu Leu Gln Val Leu Phe His Ala
        120                 125                 130

gaa atc gcc gcc cgt cag ggt cga ttc gac att ttt gac gtg gcg gcg   547
Glu Ile Ala Ala Arg Gln Gly Arg Phe Asp Ile Phe Asp Val Ala Ala
    135                 140                 145

agt ttc gta gcc aag atg caa tct cgt tcg ccg tac ctg ttc gac ggc   595
Ser Phe Val Ala Lys Met Gln Ser Arg Ser Pro Tyr Leu Phe Asp Gly
150                 155                 160                 165

tct acc gga att gtg gac acc gac gag cag cag cgg ctg tgg gct caa   643
Ser Thr Gly Ile Val Asp Thr Asp Glu Gln Gln Arg Leu Trp Ala Gln
                170                 175                 180

gga aaa gcc caa gag aaa cta agc agt gaa gaa gga aga aga           685
Gly Lys Ala Gln Glu Lys Leu Ser Ser Glu Glu Gly Arg Arg
            185                 190                 195

taggttagag gacagaagct gca                                        708


<210> 1664
<211> 195
<212> PRT
<213> Corynebacterium glutamicum

<400> 1664
Met Arg Val Val Val Val Asp Pro Lys His Pro Val Leu Pro Val Ser
  1               5                  10                  15

Phe Leu Glu Ala Val Leu Gly Arg Gly Glu Pro Val Ser Ile Asp Pro
             20                  25                  30

Asp Phe Pro Phe Asp Ile Glu Lys Trp Gly Ile Lys Thr Ser Thr Ser
         35                  40                  45

Ala Ser Trp Phe Ile Ile Ala Lys Pro Gln Ser Thr Leu Leu Ile Asp
     50                  55                  60

Ala Pro Leu Asn Pro Leu His Glu Ala Val Gly Val Met Arg Ala Ala
 65                  70                  75                  80

Val Gly Arg Gly Glu Trp Glu Arg Thr Gln Thr His Glu Ser Leu Ile
                 85                  90                  95

Pro Tyr Leu Glu Glu Glu Ser Gln Glu Phe Ile Glu Ala Ile His Gly
            100                 105                 110

Gly Asp Asp Glu His Met Lys Ser Glu Leu Gly Asp Val Leu Leu Gln
        115                 120                 125
```

```
Val Leu Phe His Ala Glu Ile Ala Ala Arg Gln Gly Arg Phe Asp Ile
    130                 135                 140

Phe Asp Val Ala Ala Ser Phe Val Ala Lys Met Gln Ser Arg Ser Pro
145                 150                 155                 160

Tyr Leu Phe Asp Gly Ser Thr Gly Ile Val Asp Thr Asp Glu Gln Gln
                165                 170                 175

Arg Leu Trp Ala Gln Gly Lys Ala Gln Glu Lys Leu Ser Ser Glu Glu
            180                 185                 190

Gly Arg Arg
        195


<210> 1665
<211> 333
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(310)
<223> RXA00240

<400> 1665
tcatttaacg tagttgacgt acggcgaagt cgctaaactt cgcgtaatct tggggccaat 60

taatcaagtg cagatgaatt gtttagaaag gctggagacc atg ggt att ttt gac   115
                                            Met Gly Ile Phe Asp
                                              1               5

gaa gct aag aag aag gca acc gaa ttc ctc gac tct gat tca ggc gag   163
Glu Ala Lys Lys Lys Ala Thr Glu Phe Leu Asp Ser Asp Ser Gly Glu
                10                  15                  20

cag aag tcc gat gga ctg ctg gat aag gcc gca gac aaa gct aag ggt   211
Gln Lys Ser Asp Gly Leu Leu Asp Lys Ala Ala Asp Lys Ala Lys Gly
            25                  30                  35

ctc ctc ggt gaa gac aaa gcg gat cag att aac aag gtc cgt gac gct   259
Leu Leu Gly Glu Asp Lys Ala Asp Gln Ile Asn Lys Val Arg Asp Ala
        40                  45                  50

gtc gat gag cgc att ggc aaa aac aac ggc ggc gaa gag aat cca gcc   307
Val Asp Glu Arg Ile Gly Lys Asn Asn Gly Gly Glu Glu Asn Pro Ala
    55                  60                  65

aac tagtattagg cgtcatgcgc gtc                                    333
Asn
 70


<210> 1666
<211> 70
<212> PRT
<213> Corynebacterium glutamicum

<400> 1666
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Met Gly Ile Phe Asp Glu Ala Lys Lys Lys Ala Thr Glu Phe Leu Asp
  1               5                  10                  15

Ser Asp Ser Gly Glu Gln Lys Ser Asp Gly Leu Leu Asp Lys Ala Ala
             20                  25                  30

Asp Lys Ala Lys Gly Leu Leu Gly Glu Asp Lys Ala Asp Gln Ile Asn
         35                  40                  45

Lys Val Arg Asp Ala Val Asp Glu Arg Ile Gly Lys Asn Asn Gly Gly
     50                  55                  60

Glu Glu Asn Pro Ala Asn
 65                  70


<210> 1667
<211> 759
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(736)
<223> RXA00244

<400> 1667
agtgggaaag tgatgatgcc acacaccgcc ggcggattac aggatggcag ttcatcaggg 60

gtttaaacag tgaagatttg gcagaaagcg agatggataa atg aat gat cag ctg   115
                                            Met Asn Asp Gln Leu
                                              1               5

tgg gaa ggc gac act gga acg ctg act ttt ggg tcc agg aaa gct ctg   163
Trp Glu Gly Asp Thr Gly Thr Leu Thr Phe Gly Ser Arg Lys Ala Leu
                 10                  15                  20

gtg caa tta ctc aaa ggt ccc atg gtg aat gct ttg cag cat gtt gaa   211
Val Gln Leu Leu Lys Gly Pro Met Val Asn Ala Leu Gln His Val Glu
             25                  30                  35

gtg tgg cgg gct atc acc aca gat caa gat gcg ctc aat gct gtg ctt   259
Val Trp Arg Ala Ile Thr Thr Asp Gln Asp Ala Leu Asn Ala Val Leu
         40                  45                  50

aac aat ttg ttc ctc gag ttg gtt ctt gat gag gat gcg ggt gtt gca   307
Asn Asn Leu Phe Leu Glu Leu Val Leu Asp Glu Asp Ala Gly Val Ala
     55                  60                  65

ttt act cgg cct gcc aat ggt aga caa gaa gta ttg gtt gga aat aac   355
Phe Thr Arg Pro Ala Asn Gly Arg Gln Glu Val Leu Val Gly Asn Asn
 70                  75                  80                  85

aaa act gaa gcg atg ccc aaa gtg ctg cgc acg gag acg ctg tcg cat   403
Lys Thr Glu Ala Met Pro Lys Val Leu Arg Thr Glu Thr Leu Ser His
                 90                  95                 100

ttt gat acg ttg atc att ttg att ctg cgc caa gaa ctc acc atg gcg   451
Phe Asp Thr Leu Ile Ile Leu Ile Leu Arg Gln Glu Leu Thr Met Ala
             105                 110                 115
```

```
cca ccg ggg gaa cga gtc att gtg gat cgt gaa gaa atc cgc gaa caa   499
Pro Pro Gly Glu Arg Val Ile Val Asp Arg Glu Glu Ile Arg Glu Gln
        120                 125                 130

gtg ttg ctc tac cgc gtt gat gaa gag cga gat gaa gcc aaa cta gct   547
Val Leu Leu Tyr Arg Val Asp Glu Glu Arg Asp Glu Ala Lys Leu Ala
    135                 140                 145

aag cga ttc gac gct gca ttt agg cgc atc gtg gat tat tca tta gct   595
Lys Arg Phe Asp Ala Ala Phe Arg Arg Ile Val Asp Tyr Ser Leu Ala
150                 155                 160                 165

aaa aag aca gag aca cct gaa cgt ttt gag gtc tca cca gca ctg cgc   643
Lys Lys Thr Glu Thr Pro Glu Arg Phe Glu Val Ser Pro Ala Leu Arg
                170                 175                 180

cag att ttt gat gcc gac act gtg gca ggt gtg cgc gct gag tac gaa   691
Gln Ile Phe Asp Ala Asp Thr Val Ala Gly Val Arg Ala Glu Tyr Glu
            185                 190                 195

aaa ttt aac aaa gca gcc cat gat gga aat gaa gag gaa cag aag        736
Lys Phe Asn Lys Ala Ala His Asp Gly Asn Glu Glu Glu Gln Lys
        200                 205                 210

tgaccagcga acaagcttta gat                                         759


<210> 1668
<211> 212
<212> PRT
<213> Corynebacterium glutamicum

<400> 1668
Met Asn Asp Gln Leu Trp Glu Gly Asp Thr Gly Thr Leu Thr Phe Gly
  1               5                  10                  15

Ser Arg Lys Ala Leu Val Gln Leu Leu Lys Gly Pro Met Val Asn Ala
             20                  25                  30

Leu Gln His Val Glu Val Trp Arg Ala Ile Thr Thr Asp Gln Asp Ala
         35                  40                  45

Leu Asn Ala Val Leu Asn Asn Leu Phe Leu Glu Leu Val Leu Asp Glu
     50                  55                  60

Asp Ala Gly Val Ala Phe Thr Arg Pro Ala Asn Gly Arg Gln Glu Val
 65                  70                  75                  80

Leu Val Gly Asn Asn Lys Thr Glu Ala Met Pro Lys Val Leu Arg Thr
                 85                  90                  95

Glu Thr Leu Ser His Phe Asp Thr Leu Ile Ile Leu Ile Leu Arg Gln
            100                 105                 110

Glu Leu Thr Met Ala Pro Pro Gly Glu Arg Val Ile Val Asp Arg Glu
        115                 120                 125

Glu Ile Arg Glu Gln Val Leu Leu Tyr Arg Val Asp Glu Glu Arg Asp
    130                 135                 140

Glu Ala Lys Leu Ala Lys Arg Phe Asp Ala Ala Phe Arg Arg Ile Val
```

```
145                 150                 155                 160

Asp Tyr Ser Leu Ala Lys Lys Thr Glu Thr Pro Glu Arg Phe Glu Val
                165                 170                 175

Ser Pro Ala Leu Arg Gln Ile Phe Asp Ala Asp Thr Val Ala Gly Val
            180                 185                 190

Arg Ala Glu Tyr Glu Lys Phe Asn Lys Ala Ala His Asp Gly Asn Glu
        195                 200                 205

Glu Glu Gln Lys
    210


<210> 1669
<211> 1608
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1585)
<223> RXA00245

<400> 1669
atgacctttg tttgaagttg gtgcggtgat gggggagtgt gaccggattc gaacaggaat 60

gtacgacacg tgtccacccc ttctggaata gtcaattggc atg acc gtt gta tcg   115
                                        Met Thr Val Val Ser
                                          1               5

cac gcg ctt ggg ttt aag cga ttt agg cag gaa tcc ctg gag ctg tct   163
His Ala Leu Gly Phe Lys Arg Phe Arg Gln Glu Ser Leu Glu Leu Ser
                10                  15                  20

ttg ttg cgc agt gac aac ttt ccg gtg gtg ctc gcc gtg gta gcg cag   211
Leu Leu Arg Ser Asp Asn Phe Pro Val Val Leu Ala Val Val Ala Gln
            25                  30                  35

tat ttt ccg cag ggg gct atc gct aag ccg gcc tca gag ctg tat cag   259
Tyr Phe Pro Gln Gly Ala Ile Ala Lys Pro Ala Ser Glu Leu Tyr Gln
        40                  45                  50

ctg ctc agc gat gat ttt cgg gtg ctg cgt gaa gaa gga ttt gag ctg   307
Leu Leu Ser Asp Asp Phe Arg Val Leu Arg Glu Glu Gly Phe Glu Leu
    55                  60                  65

ccg aaa agc ccg tcg gat tat gtg agt gat tgg gtg aag tcc cgg tgg   355
Pro Lys Ser Pro Ser Asp Tyr Val Ser Asp Trp Val Lys Ser Arg Trp
70                  75                  80                  85

ttt gtg cgt cgt ccg ggt agt tcg cag act ggt gag acc gtg gaa ccg   403
Phe Val Arg Arg Pro Gly Ser Ser Gln Thr Gly Glu Thr Val Glu Pro
                90                  95                  100

agt gaa gag ctg ttg gcg gtg ctg gat tcg gtg cag cgg tgg gat aac   451
Ser Glu Glu Leu Leu Ala Val Leu Asp Ser Val Gln Arg Trp Asp Asn
            105                 110                 115

ccg cat cga agc att tcg gcg tct cga att gaa tcg ttg acg cag gcg   499
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Pro His Arg Ser Ile Ser Ala Ser Arg Ile Glu Ser Leu Thr Gln Ala
        120                 125                 130

ttg cag act ttg gcg ttg gaa tcg gac ccc agc aca gcg aaa cgt tta   547
Leu Gln Thr Leu Ala Leu Glu Ser Asp Pro Ser Thr Ala Lys Arg Leu
    135                 140                 145

gct gag tta gag cgt gaa cgc gac agg att gaa cgc cag att gaa gcg   595
Ala Glu Leu Glu Arg Glu Arg Asp Arg Ile Glu Arg Gln Ile Glu Ala
150                 155                 160                 165

gtc cac gct ggt gaa ttt gaa gtc ctc acc acc gtg cag att ggt gat   643
Val His Ala Gly Glu Phe Glu Val Leu Thr Thr Val Gln Ile Gly Asp
                170                 175                 180

cgg gta gca gat att ttg gat cta gca gca tct att cct gca gat ttc   691
Arg Val Ala Asp Ile Leu Asp Leu Ala Ala Ser Ile Pro Ala Asp Phe
            185                 190                 195

gcc agg gta agg cat gag ctg agc gat ctg aac cgg aag ctg cgc agg   739
Ala Arg Val Arg His Glu Leu Ser Asp Leu Asn Arg Lys Leu Arg Arg
        200                 205                 210

cag ttg ctt gat cct gaa gat tcc cgt ggt gat gtt ttg gaa gag atc   787
Gln Leu Leu Asp Pro Glu Asp Ser Arg Gly Asp Val Leu Glu Glu Ile
    215                 220                 225

ttc agg gga gtt gat ctg att ggg gat tcc gat gcg ggg cgc agc ttc   835
Phe Arg Gly Val Asp Leu Ile Gly Asp Ser Asp Ala Gly Arg Ser Phe
230                 235                 240                 245

aat agt ttc ttt gat gtt ttg ctc gat cgg gaa cgc tca agt ctg att   883
Asn Ser Phe Phe Asp Val Leu Leu Asp Arg Glu Arg Ser Ser Leu Ile
                250                 255                 260

gat cga tgg atc aga gaa gtt ctg gga cgc gat gag gct att gat ctg   931
Asp Arg Trp Ile Arg Glu Val Leu Gly Arg Asp Glu Ala Ile Asp Leu
            265                 270                 275

gat tca aaa tta agg aca ggg ctg tac cga att ttc cgg gat atg gag   979
Asp Ser Lys Leu Arg Thr Gly Leu Tyr Arg Ile Phe Arg Asp Met Glu
        280                 285                 290

gat gcc agc ttc gag gtc aac ggg gaa atg aca ggg ctg gct cga agt   1027
Asp Ala Ser Phe Glu Val Asn Gly Glu Met Thr Gly Leu Ala Arg Ser
    295                 300                 305

ttg cgt cac tat gtc act acc gag gag ttc gca gag agc cga cgc atg   1075
Leu Arg His Tyr Val Thr Thr Glu Glu Phe Ala Glu Ser Arg Arg Met
310                 315                 320                 325

att cag ttg ctt cgc gat acc cgc agt gcc gct gct aag gcc gcc gag   1123
Ile Gln Leu Leu Arg Asp Thr Arg Ser Ala Ala Ala Lys Ala Ala Glu
                330                 335                 340

gct ggt gaa gtg acc tca ctc aat cac atg gac aca cca ctc gtg cgc   1171
Ala Gly Glu Val Thr Ser Leu Asn His Met Asp Thr Pro Leu Val Arg
            345                 350                 355

att ggt atg gat gtt cgc tcg att gcg ggg ttg aaa ctg aag aac cca   1219
Ile Gly Met Asp Val Arg Ser Ile Ala Gly Leu Lys Leu Lys Asn Pro
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        360                 365                 370

ggt gaa gaa cgc gtc gaa gat ttg cct gag cca gtt gaa gaa caa gaa   1267
Gly Glu Glu Arg Val Glu Asp Leu Pro Glu Pro Val Glu Glu Gln Glu
    375                 380                 385

cta gac act gaa gtc ttg atg gaa caa att cgg gca agc gag att gat   1315
Leu Asp Thr Glu Val Leu Met Glu Gln Ile Arg Ala Ser Glu Ile Asp
390                 395                 400                 405

ttt gag gaa ttg gaa gag gct gtt tct tta gtt ctt gcc gag caa tcg   1363
Phe Glu Glu Leu Glu Glu Ala Val Ser Leu Val Leu Ala Glu Gln Ser
                410                 415                 420

cac gcc acg atc acc gag gta cta gaa cat ttc ccg gca acg caa ggt   1411
His Ala Thr Ile Thr Glu Val Leu Glu His Phe Pro Ala Thr Gln Gly
            425                 430                 435

ctc gcc agc att gtt gga ttg tta tac ctg gcg atg cgt gat ggt gtt   1459
Leu Ala Ser Ile Val Gly Leu Leu Tyr Leu Ala Met Arg Asp Gly Val
        440                 445                 450

ccc aca ggt cgc gcg caa ata gtg gag tgg gaa agt gat gat gcc aca   1507
Pro Thr Gly Arg Ala Gln Ile Val Glu Trp Glu Ser Asp Asp Ala Thr
    455                 460                 465

cac cgc cgg cgg att aca gga tgg cag ttc atc agg ggt tta aac agt   1555
His Arg Arg Arg Ile Thr Gly Trp Gln Phe Ile Arg Gly Leu Asn Ser
470                 475                 480                 485

gaa gat ttg gca gaa agc gag atg gat aaa tgaatgatca gctgtgggaa     1605
Glu Asp Leu Ala Glu Ser Glu Met Asp Lys
                490                 495

ggc                                                              1608


<210> 1670
<211> 495
<212> PRT
<213> Corynebacterium glutamicum

<400> 1670
Met Thr Val Val Ser His Ala Leu Gly Phe Lys Arg Phe Arg Gln Glu
  1               5                  10                  15

Ser Leu Glu Leu Ser Leu Leu Arg Ser Asp Asn Phe Pro Val Val Leu
             20                  25                  30

Ala Val Val Ala Gln Tyr Phe Pro Gln Gly Ala Ile Ala Lys Pro Ala
         35                  40                  45

Ser Glu Leu Tyr Gln Leu Leu Ser Asp Asp Phe Arg Val Leu Arg Glu
     50                  55                  60

Glu Gly Phe Glu Leu Pro Lys Ser Pro Ser Asp Tyr Val Ser Asp Trp
 65                  70                  75                  80

Val Lys Ser Arg Trp Phe Val Arg Arg Pro Gly Ser Ser Gln Thr Gly
                 85                  90                  95
```

```
Glu Thr Val Glu Pro Ser Glu Glu Leu Leu Ala Val Leu Asp Ser Val
            100                 105                 110

Gln Arg Trp Asp Asn Pro His Arg Ser Ile Ser Ala Ser Arg Ile Glu
        115                 120                 125

Ser Leu Thr Gln Ala Leu Gln Thr Leu Ala Leu Glu Ser Asp Pro Ser
    130                 135                 140

Thr Ala Lys Arg Leu Ala Glu Leu Glu Arg Glu Arg Asp Arg Ile Glu
145                 150                 155                 160

Arg Gln Ile Glu Ala Val His Ala Gly Glu Phe Glu Val Leu Thr Thr
                165                 170                 175

Val Gln Ile Gly Asp Arg Val Ala Asp Ile Leu Asp Leu Ala Ala Ser
            180                 185                 190

Ile Pro Ala Asp Phe Ala Arg Val Arg His Glu Leu Ser Asp Leu Asn
        195                 200                 205

Arg Lys Leu Arg Arg Gln Leu Leu Asp Pro Glu Asp Ser Arg Gly Asp
    210                 215                 220

Val Leu Glu Glu Ile Phe Arg Gly Val Asp Leu Ile Gly Asp Ser Asp
225                 230                 235                 240

Ala Gly Arg Ser Phe Asn Ser Phe Phe Asp Val Leu Leu Asp Arg Glu
                245                 250                 255

Arg Ser Ser Leu Ile Asp Arg Trp Ile Arg Glu Val Leu Gly Arg Asp
            260                 265                 270

Glu Ala Ile Asp Leu Asp Ser Lys Leu Arg Thr Gly Leu Tyr Arg Ile
        275                 280                 285

Phe Arg Asp Met Glu Asp Ala Ser Phe Glu Val Asn Gly Glu Met Thr
    290                 295                 300

Gly Leu Ala Arg Ser Leu Arg His Tyr Val Thr Thr Glu Glu Phe Ala
305                 310                 315                 320

Glu Ser Arg Arg Met Ile Gln Leu Leu Arg Asp Thr Arg Ser Ala Ala
                325                 330                 335

Ala Lys Ala Ala Glu Ala Gly Glu Val Thr Ser Leu Asn His Met Asp
            340                 345                 350

Thr Pro Leu Val Arg Ile Gly Met Asp Val Arg Ser Ile Ala Gly Leu
        355                 360                 365

Lys Leu Lys Asn Pro Gly Glu Glu Arg Val Glu Asp Leu Pro Glu Pro
    370                 375                 380

Val Glu Glu Gln Glu Leu Asp Thr Glu Val Leu Met Glu Gln Ile Arg
385                 390                 395                 400

Ala Ser Glu Ile Asp Phe Glu Glu Leu Glu Glu Ala Val Ser Leu Val
                405                 410                 415

Leu Ala Glu Gln Ser His Ala Thr Ile Thr Glu Val Leu Glu His Phe
```

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            420                 425                 430

Pro Ala Thr Gln Gly Leu Ala Ser Ile Val Gly Leu Leu Tyr Leu Ala
        435                 440                 445

Met Arg Asp Gly Val Pro Thr Gly Arg Ala Gln Ile Val Glu Trp Glu
    450                 455                 460

Ser Asp Asp Ala Thr His Arg Arg Arg Ile Thr Gly Trp Gln Phe Ile
465                 470                 475                 480

Arg Gly Leu Asn Ser Glu Asp Leu Ala Glu Ser Glu Met Asp Lys
                485                 490                 495


<210> 1671
<211> 846
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(823)
<223> RXA00248

<400> 1671
tccggcgata ccctcgcagc tggcttggtt ggccaccgcc tacgcaataa ctggtcgatc 60

tagaccagtg tcttaggcaa gaccccattt aggacacctc atg att ccc ctg att   115
                                            Met Ile Pro Leu Ile
                                              1               5

acg ctt tcc cac ggt tcc cgc aaa aag tcc gca gct gca ggc att act   163
Thr Leu Ser His Gly Ser Arg Lys Lys Ser Ala Ala Ala Gly Ile Thr
                10                  15                  20

gcg ctg act cat gag gcc gga cga atg ctg gaa aca cca gcc gtg gaa   211
Ala Leu Thr His Glu Ala Gly Arg Met Leu Glu Thr Pro Ala Val Glu
            25                  30                  35

gcg cat tta gag ctt gct gaa cct tcc ctt gat cag gtt gtg gca acg   259
Ala His Leu Glu Leu Ala Glu Pro Ser Leu Asp Gln Val Val Ala Thr
        40                  45                  50

ctc agt gcg gaa ggt gta acc agg gca gcg ttg gtt cct ttg ctg ttt   307
Leu Ser Ala Glu Gly Val Thr Arg Ala Ala Leu Val Pro Leu Leu Phe
    55                  60                  65

agc aat gcg tat cac gca aag att gac gtt cct gag gca gta aaa gat   355
Ser Asn Ala Tyr His Ala Lys Ile Asp Val Pro Glu Ala Val Lys Asp
70                  75                  80                  85

gct tca gaa aag tat ggt gtg gaa ctt ctc gtg ggt ccg cat ttg ggc   403
Ala Ser Glu Lys Tyr Gly Val Glu Leu Leu Val Gly Pro His Leu Gly
                90                  95                  100

act ggc tcc gat gta gcc agc gtg ctt gcg cag cgg ttg agt gcg gac   451
Thr Gly Ser Asp Val Ala Ser Val Leu Ala Gln Arg Leu Ser Ala Asp
            105                 110                 115

gcc ccc aca gat gcc cat gtg att ttg tat tcc gtt ggc agc tca cac   499
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Ala Pro Thr Asp Ala His Val Ile Leu Tyr Ser Val Gly Ser Ser His
        120                 125                 130

gtg tcc gcc aat gaa tca gtc atc gat ctt gcc cac acc att gct ctc   547
Val Ser Ala Asn Glu Ser Val Ile Asp Leu Ala His Thr Ile Ala Leu
    135                 140                 145

ctc act ggc ttt tcg gtt gag gtg gtg ccc gct acc ggt ggg cca ggt   595
Leu Thr Gly Phe Ser Val Glu Val Val Pro Ala Thr Gly Gly Pro Gly
150                 155                 160                 165

gcc ggc ggc gcc gga gta ata gag gtg gcc tcg aaa cac aag gcc gtc   643
Ala Gly Gly Ala Gly Val Ile Glu Val Ala Ser Lys His Lys Ala Val
                170                 175                 180

cac atc ctg ccg ctg ttt gtt acg gaa ggt ttg ctg ctg gat cgg gct   691
His Ile Leu Pro Leu Phe Val Thr Glu Gly Leu Leu Leu Asp Arg Ala
            185                 190                 195

att gat caa tcc gcc aac atc gca gct gcc acc ggc aca aac ttc acc   739
Ile Asp Gln Ser Ala Asn Ile Ala Ala Ala Thr Gly Thr Asn Phe Thr
        200                 205                 210

tat tcc gaa ccc cta act act gac ctc gca cca ctt gtt gca gcc cgt   787
Tyr Ser Glu Pro Leu Thr Thr Asp Leu Ala Pro Leu Val Ala Ala Arg
    215                 220                 225

tac cac gct gca ttg agc gca ctg ctg gca cat atc taagaccgct        833
Tyr His Ala Ala Leu Ser Ala Leu Leu Ala His Ile
230                 235                 240

aaggaaatca gct                                                   846


<210> 1672
<211> 241
<212> PRT
<213> Corynebacterium glutamicum

<400> 1672
Met Ile Pro Leu Ile Thr Leu Ser His Gly Ser Arg Lys Lys Ser Ala
  1               5                  10                  15

Ala Ala Gly Ile Thr Ala Leu Thr His Glu Ala Gly Arg Met Leu Glu
             20                  25                  30

Thr Pro Ala Val Glu Ala His Leu Glu Leu Ala Glu Pro Ser Leu Asp
         35                  40                  45

Gln Val Val Ala Thr Leu Ser Ala Glu Gly Val Thr Arg Ala Ala Leu
     50                  55                  60

Val Pro Leu Leu Phe Ser Asn Ala Tyr His Ala Lys Ile Asp Val Pro
 65                  70                  75                  80

Glu Ala Val Lys Asp Ala Ser Glu Lys Tyr Gly Val Glu Leu Leu Val
                 85                  90                  95

Gly Pro His Leu Gly Thr Gly Ser Asp Val Ala Ser Val Leu Ala Gln
            100                 105                 110
```

```
Arg Leu Ser Ala Asp Ala Pro Thr Asp Ala His Val Ile Leu Tyr Ser
        115                 120                 125

Val Gly Ser Ser His Val Ser Ala Asn Glu Ser Val Ile Asp Leu Ala
    130                 135                 140

His Thr Ile Ala Leu Leu Thr Gly Phe Ser Val Glu Val Val Pro Ala
145                 150                 155                 160

Thr Gly Gly Pro Gly Ala Gly Gly Ala Gly Val Ile Glu Val Ala Ser
                165                 170                 175

Lys His Lys Ala Val His Ile Leu Pro Leu Phe Val Thr Glu Gly Leu
            180                 185                 190

Leu Leu Asp Arg Ala Ile Asp Gln Ser Ala Asn Ile Ala Ala Ala Thr
        195                 200                 205

Gly Thr Asn Phe Thr Tyr Ser Glu Pro Leu Thr Thr Asp Leu Ala Pro
    210                 215                 220

Leu Val Ala Ala Arg Tyr His Ala Ala Leu Ser Ala Leu Leu Ala His
225                 230                 235                 240

Ile
```

<210> 1673
<211> 239
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(216)
<223> RXA00250

<400> 1673

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gct ttg ggt gct gcg ttg ggt cag ttc gat ttc gtc cgc aac aat att   48
Ala Leu Gly Ala Ala Leu Gly Gln Phe Asp Phe Val Arg Asn Asn Ile
  1               5                  10                  15

gat ctg att ttc ttg ctg atc gtg ttc att tcg gtg gtt cct ggt ttg   96
Asp Leu Ile Phe Leu Leu Ile Val Phe Ile Ser Val Val Pro Gly Leu
             20                  25                  30

gtc ggc atg gcc cgc aag ctg gct gac ggc cac aag caa gcc aac acc   144
Val Gly Met Ala Arg Lys Leu Ala Asp Gly His Lys Gln Ala Asn Thr
         35                  40                  45

gag cca caa gaa aac ccc gca gtc cag aca gcc cca gta aaa acc cag   192
Glu Pro Gln Glu Asn Pro Ala Val Gln Thr Ala Pro Val Lys Thr Gln
     50                  55                  60

gaa gcc cag gaa gcc ccc cag aac taatctttcc ggtccgccag ttc        239
Glu Ala Gln Glu Ala Pro Gln Asn
 65                  70
```

<210> 1674

<211> 72
<212> PRT
<213> Corynebacterium glutamicum

<400> 1674
Ala Leu Gly Ala Ala Leu Gly Gln Phe Asp Phe Val Arg Asn Asn Ile
1 5 10 15

Asp Leu Ile Phe Leu Leu Ile Val Phe Ile Ser Val Val Pro Gly Leu
20 25 30

Val Gly Met Ala Arg Lys Leu Ala Asp Gly His Lys Gln Ala Asn Thr
35 40 45

Glu Pro Gln Glu Asn Pro Ala Val Gln Thr Ala Pro Val Lys Thr Gln
50 55 60

Glu Ala Gln Glu Ala Pro Gln Asn
65 70

<210> 1675
<211> 366
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(343)
<223> RXA00252

<400> 1675
gcagcatggg ggtgttggtg gggccggggc tgacagtgct gacgcggatg ccgttgttgg 60

cttcttcttt gcggaaggcg tcggcgagtc cgcggagggc gtg ttt gct ggc ggc 115
Val Phe Ala Gly Gly
1 5

gta gat ggt gtt gcc ggg gtg tgg tcc gtt gcc ggc gcc gga gtt gat 163
Val Asp Gly Val Ala Gly Val Trp Ser Val Ala Gly Ala Gly Val Asp
10 15 20

gta gat gac gca gcc gga tgc cgc gcg gag ggc ggg caa gag ttg gcg 211
Val Asp Asp Ala Ala Gly Cys Arg Ala Glu Gly Gly Gln Glu Leu Ala
25 30 35

act caa ctc ggc cgg gac aat gac gtt gag atc aag gtg tgc gtg cca 259
Thr Gln Leu Gly Arg Asp Asn Asp Val Glu Ile Lys Val Cys Val Pro
40 45 50

ttc ggc cac act gcc ggc ttc gat ggt cgt gtc acg cgc cac cgc cgc 307
Phe Gly His Thr Ala Gly Phe Asp Gly Arg Val Thr Arg His Arg Arg
55 60 65

ggc gtg cac cag cgt atc cac gtg gtc gag gtt ttt tagcttgtcg 353
Gly Val His Gln Arg Ile His Val Val Glu Val Phe
70 75 80

acgcctccct ctt 366

<210> 1676
<211> 81
<212> PRT
<213> Corynebacterium glutamicum

<400> 1676
Val Phe Ala Gly Gly Val Asp Gly Val Ala Gly Val Trp Ser Val Ala
1 5 10 15

Gly Ala Gly Val Asp Val Asp Asp Ala Ala Gly Cys Arg Ala Glu Gly
20 25 30

Gly Gln Glu Leu Ala Thr Gln Leu Gly Arg Asp Asn Asp Val Glu Ile
35 40 45

Lys Val Cys Val Pro Phe Gly His Thr Ala Gly Phe Asp Gly Arg Val
50 55 60

Thr Arg His Arg Arg Gly Val His Gln Arg Ile His Val Val Glu Val
65 70 75 80

Phe

<210> 1677
<211> 579
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> RXA00257

<400> 1677
catcatcaat ggcgatgaaa cgggtgcgct cagtacttgt gtatccatgg ctaatatcgg 60

gctacttcat actctgttgt aaacaaagga agtttctatc atg aaa atc aag aaa 115
Met Lys Ile Lys Lys
1 5

ttc agc atc aca gcg cta gcc tca gtt cta atg ctc acg ggt tgc gcg 163
Phe Ser Ile Thr Ala Leu Ala Ser Val Leu Met Leu Thr Gly Cys Ala
10 15 20

acc aat cac agc tca cct ctg tac agt tat ctg aat gcg tca aca tca 211
Thr Asn His Ser Ser Pro Leu Tyr Ser Tyr Leu Asn Ala Ser Thr Ser
25 30 35

acc act gtt gaa caa gta cgt ctc agc gat ctt tac ggt gag cag tgg 259
Thr Thr Val Glu Gln Val Arg Leu Ser Asp Leu Tyr Gly Glu Gln Trp
40 45 50

acc gag ttc gct ctt gtc tgc ccc tac acc aca aaa gac gag gta aaa 307
Thr Glu Phe Ala Leu Val Cys Pro Tyr Thr Thr Lys Asp Glu Val Lys
55 60 65

gaa gag ctt ggt ata aaa ata aac acc tac ctc acc gat tcg acc gat 355
Glu Glu Leu Gly Ile Lys Ile Asn Thr Tyr Leu Thr Asp Ser Thr Asp
70 75 80 85

```
gac agt agt aac gat att gtg ctc agg gat aaa gac ggt tca tat gat   403
Asp Ser Ser Asn Asp Ile Val Leu Arg Asp Lys Asp Gly Ser Tyr Asp
                 90                  95                 100

tgg atc tat ttc aac aga ttc gac att gtg tac ctc tgc aac ggc tca   451
Trp Ile Tyr Phe Asn Arg Phe Asp Ile Val Tyr Leu Cys Asn Gly Ser
            105                 110                 115

gcg gaa aat cta aaa atc tac ccc att gat tca gtt cta gaa ttt gag   499
Ala Glu Asn Leu Lys Ile Tyr Pro Ile Asp Ser Val Leu Glu Phe Glu
        120                 125                 130

cat aga gac gac tac ggt acc tgg aaa ctg agc gct atc aca gag ccg   547
His Arg Asp Asp Tyr Gly Thr Trp Lys Leu Ser Ala Ile Thr Glu Pro
    135                 140                 145

ggt aat caa taataacgcg gacacttaag tac                            579
Gly Asn Gln
150
```

<210> 1678
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 1678

```
Met Lys Ile Lys Lys Phe Ser Ile Thr Ala Leu Ala Ser Val Leu Met
  1               5                  10                  15

Leu Thr Gly Cys Ala Thr Asn His Ser Ser Pro Leu Tyr Ser Tyr Leu
             20                  25                  30

Asn Ala Ser Thr Ser Thr Thr Val Glu Gln Val Arg Leu Ser Asp Leu
         35                  40                  45

Tyr Gly Glu Gln Trp Thr Glu Phe Ala Leu Val Cys Pro Tyr Thr Thr
     50                  55                  60

Lys Asp Glu Val Lys Glu Glu Leu Gly Ile Lys Ile Asn Thr Tyr Leu
 65                  70                  75                  80

Thr Asp Ser Thr Asp Asp Ser Ser Asn Asp Ile Val Leu Arg Asp Lys
                 85                  90                  95

Asp Gly Ser Tyr Asp Trp Ile Tyr Phe Asn Arg Phe Asp Ile Val Tyr
            100                 105                 110

Leu Cys Asn Gly Ser Ala Glu Asn Leu Lys Ile Tyr Pro Ile Asp Ser
        115                 120                 125

Val Leu Glu Phe Glu His Arg Asp Asp Tyr Gly Thr Trp Lys Leu Ser
    130                 135                 140

Ala Ile Thr Glu Pro Gly Asn Gln
145                 150
```

<210> 1679
<211> 795

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(772)
<223> RXA00258

<400> 1679
taattaatat aattaatgta gtttattaac ctattatgca atgacatttt ttaataatta 60

```
accacgtcac aacattctct cagatcacag aggttcgctc atg cgc cac acc acg   115
                                            Met Arg His Thr Thr
                                              1               5

tca gcc aca tca act aca tct att att aag cgt gct atg acc att agt   163
Ser Ala Thr Ser Thr Thr Ser Ile Ile Lys Arg Ala Met Thr Ile Ser
                 10                  15                  20

gcc gct gtt ctt att gcc agc gct gtt ggt ctc aca acc agc gca agt   211
Ala Ala Val Leu Ile Ala Ser Ala Val Gly Leu Thr Thr Ser Ala Ser
             25                  30                  35

tcg ctc aat act ctc agc gct aca tca cct gaa tca ccc gat cag gca   259
Ser Leu Asn Thr Leu Ser Ala Thr Ser Pro Glu Ser Pro Asp Gln Ala
         40                  45                  50

gcc act gtg tca cag gct gaa tca gat agt gaa tta gat gac ggc atg   307
Ala Thr Val Ser Gln Ala Glu Ser Asp Ser Glu Leu Asp Asp Gly Met
     55                  60                  65

aaa aag ctt gca acc aag atc ctt aat cgc gct gac aac gct gaa aat   355
Lys Lys Leu Ala Thr Lys Ile Leu Asn Arg Ala Asp Asn Ala Glu Asn
 70                  75                  80                  85

aat gat gac acc ggc aaa aac ctc aac aat gat gat aag aag ctc aac   403
Asn Asp Asp Thr Gly Lys Asn Leu Asn Asn Asp Asp Lys Lys Leu Asn
                 90                  95                 100

acg aag cag ccg cag cgc cct gct gaa aaa gtt gcc cag gcg atc gag   451
Thr Lys Gln Pro Gln Arg Pro Ala Glu Lys Val Ala Gln Ala Ile Glu
            105                 110                 115

cta agc ctt gat acc acc acg aat gca gaa aag cct gat aaa agt ttt   499
Leu Ser Leu Asp Thr Thr Thr Asn Ala Glu Lys Pro Asp Lys Ser Phe
        120                 125                 130

cac cat gaa aaa ccc gta aac gcc tat gtc aca agt gtc agc tac aac   547
His His Glu Lys Pro Val Asn Ala Tyr Val Thr Ser Val Ser Tyr Asn
    135                 140                 145

aaa agc aat gac acc tgg act atc aaa cca tca gac agc gcg gtg aat   595
Lys Ser Asn Asp Thr Trp Thr Ile Lys Pro Ser Asp Ser Ala Val Asn
150                 155                 160                 165

aca ccg acc aat gat gct gag cgc atc agc aat atc atc caa gaa gct   643
Thr Pro Thr Asn Asp Ala Glu Arg Ile Ser Asn Ile Ile Gln Glu Ala
                170                 175                 180

cgc gac ctc ggt ctc agc gac gat gaa tcc ttg acg caa cag atc gca   691
Arg Asp Leu Gly Leu Ser Asp Asp Glu Ser Leu Thr Gln Gln Ile Ala
```

```
            185                 190                 195

ttt cac gct cat gct gct aat tat tta gtc acc gaa tgg gta ctt cgc   739
Phe His Ala His Ala Ala Asn Tyr Leu Val Thr Glu Trp Val Leu Arg
        200                 205                 210

ggc tat cag ctt gct aac ccg aag gtg ctt cca tgagaaaaca acgacgcatg 792
Gly Tyr Gln Leu Ala Asn Pro Lys Val Leu Pro
    215                 220

atg                                                               795


<210> 1680
<211> 224
<212> PRT
<213> Corynebacterium glutamicum

<400> 1680
Met Arg His Thr Thr Ser Ala Thr Ser Thr Thr Ser Ile Ile Lys Arg
  1               5                  10                  15

Ala Met Thr Ile Ser Ala Ala Val Leu Ile Ala Ser Ala Val Gly Leu
             20                  25                  30

Thr Thr Ser Ala Ser Ser Leu Asn Thr Leu Ser Ala Thr Ser Pro Glu
         35                  40                  45

Ser Pro Asp Gln Ala Ala Thr Val Ser Gln Ala Glu Ser Asp Ser Glu
     50                  55                  60

Leu Asp Asp Gly Met Lys Lys Leu Ala Thr Lys Ile Leu Asn Arg Ala
 65                  70                  75                  80

Asp Asn Ala Glu Asn Asn Asp Asp Thr Gly Lys Asn Leu Asn Asn Asp
                 85                  90                  95

Asp Lys Lys Leu Asn Thr Lys Gln Pro Gln Arg Pro Ala Glu Lys Val
            100                 105                 110

Ala Gln Ala Ile Glu Leu Ser Leu Asp Thr Thr Thr Asn Ala Glu Lys
        115                 120                 125

Pro Asp Lys Ser Phe His His Glu Lys Pro Val Asn Ala Tyr Val Thr
    130                 135                 140

Ser Val Ser Tyr Asn Lys Ser Asn Asp Thr Trp Thr Ile Lys Pro Ser
145                 150                 155                 160

Asp Ser Ala Val Asn Thr Pro Thr Asn Asp Ala Glu Arg Ile Ser Asn
                165                 170                 175

Ile Ile Gln Glu Ala Arg Asp Leu Gly Leu Ser Asp Asp Glu Ser Leu
            180                 185                 190

Thr Gln Gln Ile Ala Phe His Ala His Ala Ala Asn Tyr Leu Val Thr
        195                 200                 205

Glu Trp Val Leu Arg Gly Tyr Gln Leu Ala Asn Pro Lys Val Leu Pro
    210                 215                 220
```

<210> 1681
<211> 1299
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1276)
<223> RXA00260

<400> 1681
gcaacagcgg cttgcagatc agaaggcgcg agaggcgcga cagctgctag atattgaacg 60

tcagcaggtg attgcagatc gctatgggcc gttggtgaat atg cat agc gac gct 115
Met His Ser Asp Ala
1 5

gtg cta gcg ggt gct tca ata aga gca aaa ata ggt gct ctc gca act 163
Val Leu Ala Gly Ala Ser Ile Arg Ala Lys Ile Gly Ala Leu Ala Thr
10 15 20

att tac ggt gct caa aac tta gag aat gtc att cac tca gtt agt ttt 211
Ile Tyr Gly Ala Gln Asn Leu Glu Asn Val Ile His Ser Val Ser Phe
25 30 35

act gac aga cgt att tct ccc gat gga caa ctg tcg aaa gaa tta ttt 259
Thr Asp Arg Arg Ile Ser Pro Asp Gly Gln Leu Ser Lys Glu Leu Phe
40 45 50

cgc gaa gct tgg agc gca aac ctt ctt atc cct gat cca tct tct gat 307
Arg Glu Ala Trp Ser Ala Asn Leu Leu Ile Pro Asp Pro Ser Ser Asp
55 60 65

gtg gaa gcg ttt gcg tgg agc gaa aag aat tcc act gag cta gcg gga 355
Val Glu Ala Phe Ala Trp Ser Glu Lys Asn Ser Thr Glu Leu Ala Gly
70 75 80 85

ggc ata ttc gtt gag aaa atg cta ttt act gtc ccg gac aca ggc cgc 403
Gly Ile Phe Val Glu Lys Met Leu Phe Thr Val Pro Asp Thr Gly Arg
90 95 100

tcc aat aac cgt gtc cag agc ttc tca gaa gaa ctt cgt aac cac att 451
Ser Asn Asn Arg Val Gln Ser Phe Ser Glu Glu Leu Arg Asn His Ile
105 110 115

tct ttg aaa gat atg tat tct aca caa cgt gaa gag cta tta gac ctt 499
Ser Leu Lys Asp Met Tyr Ser Thr Gln Arg Glu Glu Leu Leu Asp Leu
120 125 130

gcc tac gag ctc atg gtg ggg gaa gca gta cgt ttt gct aac ttc cgc 547
Ala Tyr Glu Leu Met Val Gly Glu Ala Val Arg Phe Ala Asn Phe Arg
135 140 145

ctt tat gat cag aat ctc cca cca ctt act gaa gca aat ata gac aaa 595
Leu Tyr Asp Gln Asn Leu Pro Pro Leu Thr Glu Ala Asn Ile Asp Lys
150 155 160 165

```
ttg aga gcc cat cta cgt gag gcc gca gct agt gcg tca cta gga gtg   643
Leu Arg Ala His Leu Arg Glu Ala Ala Ala Ser Ala Ser Leu Gly Val
                170                 175                 180

tta tat cta atg gtg tgg cga tct gta aaa gac gca gct gca gcg cac   691
Leu Tyr Leu Met Val Trp Arg Ser Val Lys Asp Ala Ala Ala Ala His
            185                 190                 195

act aaa cat aca aga atg agc aaa gaa aat gcg aca acg cat agt gtt   739
Thr Lys His Thr Arg Met Ser Lys Glu Asn Ala Thr Thr His Ser Val
        200                 205                 210

aca aaa gtt tct atc ttt gtt gac caa tta tta agc gga aca ttc cct   787
Thr Lys Val Ser Ile Phe Val Asp Gln Leu Leu Ser Gly Thr Phe Pro
    215                 220                 225

tgt tca aag cct ttt cac gaa tct tca caa gtc cca ctg agt gaa gcc   835
Cys Ser Lys Pro Phe His Glu Ser Ser Gln Val Pro Leu Ser Glu Ala
230                 235                 240                 245

acc aag ata gtt ttt aat ttg att atg gag tca ccg ccg atg gaa act   883
Thr Lys Ile Val Phe Asn Leu Ile Met Glu Ser Pro Pro Met Glu Thr
                250                 255                 260

gag ccg agt gtg ctg cga aat tcc ctc caa gaa cac tcg gat tgg gag   931
Glu Pro Ser Val Leu Arg Asn Ser Leu Gln Glu His Ser Asp Trp Glu
            265                 270                 275

cta ttg caa cag tgt gat gag aag att cct gat cgg gag ttt ctg atg   979
Leu Leu Gln Gln Cys Asp Glu Lys Ile Pro Asp Arg Glu Phe Leu Met
        280                 285                 290

gag tgg tta tat caa gaa cag acg tgg act gca gag caa ttt ttt gat   1027
Glu Trp Leu Tyr Gln Glu Gln Thr Trp Thr Ala Glu Gln Phe Phe Asp
    295                 300                 305

gct cta gct atg gtt tct tct agc gag ttt cgt ata tgt gca cct gga   1075
Ala Leu Ala Met Val Ser Ser Ser Glu Phe Arg Ile Cys Ala Pro Gly
310                 315                 320                 325

tgt gcg cat caa gta agt gca gac atc gct aca caa gtc tta gaa ttc   1123
Cys Ala His Gln Val Ser Ala Asp Ile Ala Thr Gln Val Leu Glu Phe
                330                 335                 340

cac gat cga gtg tct ttc cat gac gat cgt aaa agc gcc atg ctt gct   1171
His Asp Arg Val Ser Phe His Asp Asp Arg Lys Ser Ala Met Leu Ala
            345                 350                 355

gct gaa gca act att att ggt aac aaa att ggt tca caa gca cgg gcc   1219
Ala Glu Ala Thr Ile Ile Gly Asn Lys Ile Gly Ser Gln Ala Arg Ala
        360                 365                 370

gga gac ttt gtt tta ggt gaa gta atc acc aag ctg cag aac ata cct   1267
Gly Asp Phe Val Leu Gly Glu Val Ile Thr Lys Leu Gln Asn Ile Pro
    375                 380                 385

ggt gag gta taacttctgc gtcgtccaat tag                            1299
Gly Glu Val
390
```

<210> 1682
<211> 392
<212> PRT
<213> Corynebacterium glutamicum

<400> 1682
Met His Ser Asp Ala Val Leu Ala Gly Ala Ser Ile Arg Ala Lys Ile
1 5 10 15

Gly Ala Leu Ala Thr Ile Tyr Gly Ala Gln Asn Leu Glu Asn Val Ile
20 25 30

His Ser Val Ser Phe Thr Asp Arg Arg Ile Ser Pro Asp Gly Gln Leu
35 40 45

Ser Lys Glu Leu Phe Arg Glu Ala Trp Ser Ala Asn Leu Leu Ile Pro
50 55 60

Asp Pro Ser Ser Asp Val Glu Ala Phe Ala Trp Ser Glu Lys Asn Ser
65 70 75 80

Thr Glu Leu Ala Gly Gly Ile Phe Val Glu Lys Met Leu Phe Thr Val
85 90 95

Pro Asp Thr Gly Arg Ser Asn Asn Arg Val Gln Ser Phe Ser Glu Glu
100 105 110

Leu Arg Asn His Ile Ser Leu Lys Asp Met Tyr Ser Thr Gln Arg Glu
115 120 125

Glu Leu Leu Asp Leu Ala Tyr Glu Leu Met Val Gly Glu Ala Val Arg
130 135 140

Phe Ala Asn Phe Arg Leu Tyr Asp Gln Asn Leu Pro Pro Leu Thr Glu
145 150 155 160

Ala Asn Ile Asp Lys Leu Arg Ala His Leu Arg Glu Ala Ala Ala Ser
165 170 175

Ala Ser Leu Gly Val Leu Tyr Leu Met Val Trp Arg Ser Val Lys Asp
180 185 190

Ala Ala Ala Ala His Thr Lys His Thr Arg Met Ser Lys Glu Asn Ala
195 200 205

Thr Thr His Ser Val Thr Lys Val Ser Ile Phe Val Asp Gln Leu Leu
210 215 220

Ser Gly Thr Phe Pro Cys Ser Lys Pro Phe His Glu Ser Ser Gln Val
225 230 235 240

Pro Leu Ser Glu Ala Thr Lys Ile Val Phe Asn Leu Ile Met Glu Ser
245 250 255

Pro Pro Met Glu Thr Glu Pro Ser Val Leu Arg Asn Ser Leu Gln Glu
260 265 270

His Ser Asp Trp Glu Leu Leu Gln Gln Cys Asp Glu Lys Ile Pro Asp
275 280 285

Arg Glu Phe Leu Met Glu Trp Leu Tyr Gln Glu Gln Thr Trp Thr Ala

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    290                 295                 300

Glu Gln Phe Phe Asp Ala Leu Ala Met Val Ser Ser Ser Glu Phe Arg
305                 310                 315                 320

Ile Cys Ala Pro Gly Cys Ala His Gln Val Ser Ala Asp Ile Ala Thr
                325                 330                 335

Gln Val Leu Glu Phe His Asp Arg Val Ser Phe His Asp Asp Arg Lys
            340                 345                 350

Ser Ala Met Leu Ala Ala Glu Ala Thr Ile Ile Gly Asn Lys Ile Gly
        355                 360                 365

Ser Gln Ala Arg Ala Gly Asp Phe Val Leu Gly Glu Val Ile Thr Lys
    370                 375                 380

Leu Gln Asn Ile Pro Gly Glu Val
385                 390


<210> 1683
<211> 1236
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1213)
<223> RXA00273

<400> 1683
tcggtcttgg tggcggctcc gtcattagtt ccagtaagta gttttttcac tccctgtttt 60

gagtttttttt ctcaccttta tatagataag gaatattcac atg tct ttg aag ctt   115
                                            Met Ser Leu Lys Leu
                                              1               5

aat tct cgt cgt ctt gca tcc att gct gtc gct gtt gca gtc ggt gtc   163
Asn Ser Arg Arg Leu Ala Ser Ile Ala Val Ala Val Ala Val Gly Val
                10                  15                  20

tct ggt gtt gct gct gtt ggt gcg gca cca gct acg gct cag cag gta   211
Ser Gly Val Ala Ala Val Gly Ala Ala Pro Ala Thr Ala Gln Gln Val
            25                  30                  35

ggt gct ggt acc ccg att cac gtt gtc aac ctt gat cgc acc gtt gtt   259
Gly Ala Gly Thr Pro Ile His Val Val Asn Leu Asp Arg Thr Val Val
        40                  45                  50

gat cca gtg act ggt gac atc acc ttc cac ttc acc gac ggc act ttt   307
Asp Pro Val Thr Gly Asp Ile Thr Phe His Phe Thr Asp Gly Thr Phe
    55                  60                  65

gtc acc ctc aag gcg ggt gtt gat ggc aag gat ggt acc gat ggc caa   355
Val Thr Leu Lys Ala Gly Val Asp Gly Lys Asp Gly Thr Asp Gly Gln
70                  75                  80                  85

gat ggt gtg atc ggc aag gac gca acc att gtt gat gtc gct acg gag   403
Asp Gly Val Ile Gly Lys Asp Ala Thr Ile Val Asp Val Ala Thr Glu
                90                  95                  100
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tcc aat ggt gat gtc aag ctc acc ttc tct gat ggc acc gtc gtc acc   451
Ser Asn Gly Asp Val Lys Leu Thr Phe Ser Asp Gly Thr Val Val Thr
            105                 110                 115

att cct gca gct aag gac ggt gtg gat ggt gaa gat ggc aag gat ggc   499
Ile Pro Ala Ala Lys Asp Gly Val Asp Gly Glu Asp Gly Lys Asp Gly
        120                 125                 130

gag gac gct act gtg gtg tct act gcg act gac gcc aac ggc aat atc   547
Glu Asp Ala Thr Val Val Ser Thr Ala Thr Asp Ala Asn Gly Asn Ile
    135                 140                 145

gtc att acg ttc tct gat ggc tct gtg ctt gtt gtt gct aac ggt aag   595
Val Ile Thr Phe Ser Asp Gly Ser Val Leu Val Val Ala Asn Gly Lys
150                 155                 160                 165

gac ggc aac gat ggc tca gac ggc cag gat ggt gct gat ggt gaa aat   643
Asp Gly Asn Asp Gly Ser Asp Gly Gln Asp Gly Ala Asp Gly Glu Asn
                170                 175                 180

ggc aag gat ggt gag aac ggc gct aac gcg acc att gtc gat cag att   691
Gly Lys Asp Gly Glu Asn Gly Ala Asn Ala Thr Ile Val Asp Gln Ile
            185                 190                 195

gcc aat gac gat ggt tcc att acc att gtg ttc tcc gat ggt tct gag   739
Ala Asn Asp Asp Gly Ser Ile Thr Ile Val Phe Ser Asp Gly Ser Glu
        200                 205                 210

gtc act atc cca gcg cca gct aag ggt gcc acc gat gag ctg gca cag   787
Val Thr Ile Pro Ala Pro Ala Lys Gly Ala Thr Asp Glu Leu Ala Gln
    215                 220                 225

tgt ctg ctg aac ccg aag atg ttg ctg ctg gca gca att cct gct gca   835
Cys Leu Leu Asn Pro Lys Met Leu Leu Leu Ala Ala Ile Pro Ala Ala
230                 235                 240                 245

ggt gct att gct aac gct gtg gca ccg gcg atc cca cgt gtt gtt gaa   883
Gly Ala Ile Ala Asn Ala Val Ala Pro Ala Ile Pro Arg Val Val Glu
                250                 255                 260

gat gtg cgt gca cag ttc aat ctt cca agc ctc aac ccc cag ttt gat   931
Asp Val Arg Ala Gln Phe Asn Leu Pro Ser Leu Asn Pro Gln Phe Asp
            265                 270                 275

cag tgg ctc tac aac gcg acc aag gat att gat gca ggg ttg ttg atc   979
Gln Trp Leu Tyr Asn Ala Thr Lys Asp Ile Asp Ala Gly Leu Leu Ile
        280                 285                 290

tct ggt gct acc ggc ctt gct gtg ctg tcg gtg ctc gct gat gat ttc  1027
Ser Gly Ala Thr Gly Leu Ala Val Leu Ser Val Leu Ala Asp Asp Phe
    295                 300                 305

tgt ggc gac att gat gcc gat gac aac gca gat ggt gac gtg gcg gca  1075
Cys Gly Asp Ile Asp Ala Asp Asp Asn Ala Asp Gly Asp Val Ala Ala
310                 315                 320                 325

gaa aag cca act ggc tct tct ggg ctt gga tca tct gaa cag agt gaa  1123
Glu Lys Pro Thr Gly Ser Ser Gly Leu Gly Ser Ser Glu Gln Ser Glu
                330                 335                 340
```

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aag gtt gat ggt gac gac gat agt gtg atc gac act gaa act gat gca   1171
Lys Val Asp Gly Asp Asp Asp Ser Val Ile Asp Thr Glu Thr Asp Ala
            345                 350                 355

gat ctc gaa gta gaa gaa gac cct gag ctt gtt aac gca ggt           1213
Asp Leu Glu Val Glu Glu Asp Pro Glu Leu Val Asn Ala Gly
        360                 365                 370

taacgccagt gtaatgctgg att                                        1236
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<210> 1684
<211> 371
<212> PRT
<213> Corynebacterium glutamicum

<400> 1684

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Met Ser Leu Lys Leu Asn Ser Arg Arg Leu Ala Ser Ile Ala Val Ala
  1               5                  10                  15

Val Ala Val Gly Val Ser Gly Val Ala Ala Val Gly Ala Ala Pro Ala
             20                  25                  30

Thr Ala Gln Gln Val Gly Ala Gly Thr Pro Ile His Val Val Asn Leu
         35                  40                  45

Asp Arg Thr Val Val Asp Pro Val Thr Gly Asp Ile Thr Phe His Phe
     50                  55                  60

Thr Asp Gly Thr Phe Val Thr Leu Lys Ala Gly Val Asp Gly Lys Asp
 65                  70                  75                  80

Gly Thr Asp Gly Gln Asp Gly Val Ile Gly Lys Asp Ala Thr Ile Val
                 85                  90                  95

Asp Val Ala Thr Glu Ser Asn Gly Asp Val Lys Leu Thr Phe Ser Asp
            100                 105                 110

Gly Thr Val Val Thr Ile Pro Ala Ala Lys Asp Gly Val Asp Gly Glu
        115                 120                 125

Asp Gly Lys Asp Gly Glu Asp Ala Thr Val Val Ser Thr Ala Thr Asp
    130                 135                 140

Ala Asn Gly Asn Ile Val Ile Thr Phe Ser Asp Gly Ser Val Leu Val
145                 150                 155                 160

Val Ala Asn Gly Lys Asp Gly Asn Asp Gly Ser Asp Gly Gln Asp Gly
                165                 170                 175

Ala Asp Gly Glu Asn Gly Lys Asp Gly Glu Asn Gly Ala Asn Ala Thr
            180                 185                 190

Ile Val Asp Gln Ile Ala Asn Asp Asp Gly Ser Ile Thr Ile Val Phe
        195                 200                 205

Ser Asp Gly Ser Glu Val Thr Ile Pro Ala Pro Ala Lys Gly Ala Thr
    210                 215                 220

Asp Glu Leu Ala Gln Cys Leu Leu Asn Pro Lys Met Leu Leu Leu Ala
225                 230                 235                 240
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```
Ala Ile Pro Ala Ala Gly Ala Ile Ala Asn Ala Val Ala Pro Ala Ile
               245                 250                 255

Pro Arg Val Val Glu Asp Val Arg Ala Gln Phe Asn Leu Pro Ser Leu
            260                 265                 270

Asn Pro Gln Phe Asp Gln Trp Leu Tyr Asn Ala Thr Lys Asp Ile Asp
        275                 280                 285

Ala Gly Leu Leu Ile Ser Gly Ala Thr Gly Leu Ala Val Leu Ser Val
    290                 295                 300

Leu Ala Asp Asp Phe Cys Gly Asp Ile Asp Ala Asp Asp Asn Ala Asp
305                 310                 315                 320

Gly Asp Val Ala Ala Glu Lys Pro Thr Gly Ser Ser Gly Leu Gly Ser
               325                 330                 335

Ser Glu Gln Ser Glu Lys Val Asp Gly Asp Asp Asp Ser Val Ile Asp
            340                 345                 350

Thr Glu Thr Asp Ala Asp Leu Glu Val Glu Glu Asp Pro Glu Leu Val
        355                 360                 365

Asn Ala Gly
    370


<210> 1685
<211> 2733
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2710)
<223> RXA00274

<400> 1685
agtttaaaag tcattaatta ctttatggga ataataattt aagttttcat cttttaacta 60

gttacagcat gttattacct tttatgaaag gcgtttcacc ttg tct ctt aat ttg   115
                                              Leu Ser Leu Asn Leu
                                                1               5

aag aag aat tct gcg cgt tct att acc gcg ctg act gtt gct ggt ctg   163
Lys Lys Asn Ser Ala Arg Ser Ile Thr Ala Leu Thr Val Ala Gly Leu
                10                  15                  20

ggt ctg tct att gtt cct gcg gca tct gca cag gat gtt gcg gat gac   211
Gly Leu Ser Ile Val Pro Ala Ala Ser Ala Gln Asp Val Ala Asp Asp
            25                  30                  35

act acc aac tcc gat tcc acc cgt gat gcc att tgt gct gct gca ccg   259
Thr Thr Asn Ser Asp Ser Thr Arg Asp Ala Ile Cys Ala Ala Ala Pro
        40                  45                  50

ctt gtt gca ggc gca gca gtg ggt gtt ggt ctg ctg tct cag cag cca   307
Leu Val Ala Gly Ala Ala Val Gly Val Gly Leu Leu Ser Gln Gln Pro
    55                  60                  65
```

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gaa ttc cag cat atg gtg tcc cag att cag tct gac gca cag cgc att   355
Glu Phe Gln His Met Val Ser Gln Ile Gln Ser Asp Ala Gln Arg Ile
 70                  75                  80                  85

ggg cag gat ctc agc aat cag ttc aac aac tct ctt gaa tcg ctc aac   403
Gly Gln Asp Leu Ser Asn Gln Phe Asn Asn Ser Leu Glu Ser Leu Asn
                90                  95                 100

att ggc ctc ggt aac ggc gtg cac ggc cca cag cag aac gct gtg cag   451
Ile Gly Leu Gly Asn Gly Val His Gly Pro Gln Gln Asn Ala Val Gln
            105                 110                 115

ggt att gat ctc act gaa gca gca cga acc atg gct gga tgg aat gac   499
Gly Ile Asp Leu Thr Glu Ala Ala Arg Thr Met Ala Gly Trp Asn Asp
        120                 125                 130

ctg gcg gca cag gtg ggc cag act gca ggc cct gct atc ggc gct gtt   547
Leu Ala Ala Gln Val Gly Gln Thr Ala Gly Pro Ala Ile Gly Ala Val
    135                 140                 145

gct ggt act gcc ggc ctg atc gca ctg gtt gac tac tgc tgg ctg gaa   595
Ala Gly Thr Ala Gly Leu Ile Ala Leu Val Asp Tyr Cys Trp Leu Glu
150                 155                 160                 165

ggc ttc gac ttc gcg ggt ggc tcc agt ggc act gat ggt gaa aat ggt   643
Gly Phe Asp Phe Ala Gly Gly Ser Ser Gly Thr Asp Gly Glu Asn Gly
                170                 175                 180

gtt gat ggt caa gat ggt acc tcg atc acc att act gag att aag act   691
Val Asp Gly Gln Asp Gly Thr Ser Ile Thr Ile Thr Glu Ile Lys Thr
            185                 190                 195

gat gat gac ggc aat acc att gtt gtc ttt tcc gat ggt tct gaa atc   739
Asp Asp Asp Gly Asn Thr Ile Val Val Phe Ser Asp Gly Ser Glu Ile
        200                 205                 210

acc atc acc aat ggt aaa gac ggc gct gct atc acc att gtt aat act   787
Thr Ile Thr Asn Gly Lys Asp Gly Ala Ala Ile Thr Ile Val Asn Thr
    215                 220                 225

tac cgc gac gat gaa ggt aat act gtt gtt gag ttc tct gac ggt tcc   835
Tyr Arg Asp Asp Glu Gly Asn Thr Val Val Glu Phe Ser Asp Gly Ser
230                 235                 240                 245

acc att gtt atc gac aag ggt gaa gac ggt aaa gat gga gaa gac ggc   883
Thr Ile Val Ile Asp Lys Gly Glu Asp Gly Lys Asp Gly Glu Asp Gly
                250                 255                 260

aag gac ggc gaa gac ggt aag gac ctt acc gta act gat acc tac atc   931
Lys Asp Gly Glu Asp Gly Lys Asp Leu Thr Val Thr Asp Thr Tyr Ile
            265                 270                 275

aac gat gat gga gac acc gtt gtt gag ctt tcc gat ggt tcc acg atc   979
Asn Asp Asp Gly Asp Thr Val Val Glu Leu Ser Asp Gly Ser Thr Ile
        280                 285                 290

att gta aag aag ggt acc gat ggt aag gac ggt gct gac ggc tct gac  1027
Ile Val Lys Lys Gly Thr Asp Gly Lys Asp Gly Ala Asp Gly Ser Asp
    295                 300                 305
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ggt gct gat gga gtc agc atc act gtg gag aac tct tat gtt gat gcg   1075
Gly Ala Asp Gly Val Ser Ile Thr Val Glu Asn Ser Tyr Val Asp Ala
310                 315                 320                 325

gac ggc aac act gtt gtc gaa ttc tcc gat ggc tcc aat gtg acc atc   1123
Asp Gly Asn Thr Val Val Glu Phe Ser Asp Gly Ser Asn Val Thr Ile
                330                 335                 340

aac aag ggt gag aag ggc gac aag ggt gac gct ggc gcc gat ggc gaa   1171
Asn Lys Gly Glu Lys Gly Asp Lys Gly Asp Ala Gly Ala Asp Gly Glu
            345                 350                 355

gac ggc gca gat ggt gaa tca att act gtt gtt aac acc agc aac gat   1219
Asp Gly Ala Asp Gly Glu Ser Ile Thr Val Val Asn Thr Ser Asn Asp
        360                 365                 370

gct gaa ggc aac act ctt gtt gag ctc tcc gat ggc act gtt att acc   1267
Ala Glu Gly Asn Thr Leu Val Glu Leu Ser Asp Gly Thr Val Ile Thr
    375                 380                 385

att aat aag ggt gat aag ggt gac gct ggc gcc gat ggt gaa gat gga   1315
Ile Asn Lys Gly Asp Lys Gly Asp Ala Gly Ala Asp Gly Glu Asp Gly
390                 395                 400                 405

agt aat ggc gca gat ggc gag tcc att acg gtc atc gaa acc cgt ttc   1363
Ser Asn Gly Ala Asp Gly Glu Ser Ile Thr Val Ile Glu Thr Arg Phe
                410                 415                 420

gat gcg gac ggc aac act gtt gtg gtg ttc tcg aac ggc act gaa atc   1411
Asp Ala Asp Gly Asn Thr Val Val Val Phe Ser Asn Gly Thr Glu Ile
            425                 430                 435

acc atc aac aag ggt gag aag ggc gac aag gga gat acc ggc gaa gac   1459
Thr Ile Asn Lys Gly Glu Lys Gly Asp Lys Gly Asp Thr Gly Glu Asp
        440                 445                 450

ggt aag gac gga ctg acc ccg tac atc ggc cca gat ggt aac tgg tgg   1507
Gly Lys Asp Gly Leu Thr Pro Tyr Ile Gly Pro Asp Gly Asn Trp Trp
    455                 460                 465

atc ggt gag aac aac acc tgt act gct gca cgt ggc aat gac ggt aaa   1555
Ile Gly Glu Asn Asn Thr Cys Thr Ala Ala Arg Gly Asn Asp Gly Lys
470                 475                 480                 485

gac ggt gac acc cca cgc atc ggt gat aat ggt aat tgg tgg atc ggc   1603
Asp Gly Asp Thr Pro Arg Ile Gly Asp Asn Gly Asn Trp Trp Ile Gly
                490                 495                 500

atc gtt gat acc ggc gtt cct gct cgt ggt cag gat ggc gcc aac gga   1651
Ile Val Asp Thr Gly Val Pro Ala Arg Gly Gln Asp Gly Ala Asn Gly
            505                 510                 515

gcc gat ggt gct aac acc gtt gag atc att aat ggc tac tgg tac atc   1699
Ala Asp Gly Ala Asn Thr Val Glu Ile Ile Asn Gly Tyr Trp Tyr Ile
        520                 525                 530

aat ggt gaa aat acc ggt gtc aag gca gtt ggt gaa aat ggc acc aac   1747
Asn Gly Glu Asn Thr Gly Val Lys Ala Val Gly Glu Asn Gly Thr Asn
    535                 540                 545

gga gcc gat gga caa gac ggt gaa aat gga acc aac ggt gct aac acc   1795
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Gly Ala Asp Gly Gln Asp Gly Glu Asn Gly Thr Asn Gly Ala Asn Thr
550                 555                 560                 565

gtt gag atc att aat ggc tac tgg tac atc aat ggt gaa aat acc ggt   1843
Val Glu Ile Ile Asn Gly Tyr Trp Tyr Ile Asn Gly Glu Asn Thr Gly
                570                 575                 580

gtc aag gcg cag ggt cca aag ggc gat aag ggt gac act ggt gac acg   1891
Val Lys Ala Gln Gly Pro Lys Gly Asp Lys Gly Asp Thr Gly Asp Thr
            585                 590                 595

ggc gct ccg ggc gag ggt tcc ggt aat gtg gac att gag atc cga gaa   1939
Gly Ala Pro Gly Glu Gly Ser Gly Asn Val Asp Ile Glu Ile Arg Glu
        600                 605                 610

tcg agt tat cca ggt ggt ggc cag gcc acc atc atc att ctt gat caa   1987
Ser Ser Tyr Pro Gly Gly Gly Gln Ala Thr Ile Ile Ile Leu Asp Gln
    615                 620                 625

ttt gaa tat gaa atc ccg cac act gtt att ggt gac aac ggt aac tgg   2035
Phe Glu Tyr Glu Ile Pro His Thr Val Ile Gly Asp Asn Gly Asn Trp
630                 635                 640                 645

tac atc ggt gaa aag gat act ggt atc cca gct cag ggt ggc act gga   2083
Tyr Ile Gly Glu Lys Asp Thr Gly Ile Pro Ala Gln Gly Gly Thr Gly
                650                 655                 660

aca cct ggt gag gat ggc ctc aca cca cac att ggc gac aac ggt aac   2131
Thr Pro Gly Glu Asp Gly Leu Thr Pro His Ile Gly Asp Asn Gly Asn
            665                 670                 675

tgg tgg atc ggt gat acc gat aca ggt gtc tct gca agc ccg acc ccc   2179
Trp Trp Ile Gly Asp Thr Asp Thr Gly Val Ser Ala Ser Pro Thr Pro
        680                 685                 690

gtt ggt gag gcg gta gcg ggt gtc act gat gtg gtc ttc aac act agt   2227
Val Gly Glu Ala Val Ala Gly Val Thr Asp Val Val Phe Asn Thr Ser
    695                 700                 705

gat gaa ccc aag acc att act gca acg atc aat ggt gaa gaa tat gat   2275
Asp Glu Pro Lys Thr Ile Thr Ala Thr Ile Asn Gly Glu Glu Tyr Asp
710                 715                 720                 725

tac acc ctt cca cca cat agt gct gtt gtg ttc tac gct aca ggt tca   2323
Tyr Thr Leu Pro Pro His Ser Ala Val Val Phe Tyr Ala Thr Gly Ser
                730                 735                 740

cca atg gca tat tct cta ccg aat gca tcg ggc ctc act gtt ata ggt   2371
Pro Met Ala Tyr Ser Leu Pro Asn Ala Ser Gly Leu Thr Val Ile Gly
            745                 750                 755

act gaa gag act cct ggt ttc acc act att cga ttc agt gac cat tcc   2419
Thr Glu Glu Thr Pro Gly Phe Thr Thr Ile Arg Phe Ser Asp His Ser
        760                 765                 770

act gtg acc att cca cat gga cga gat ggc acc aac ggt act aac gaa   2467
Thr Val Thr Ile Pro His Gly Arg Asp Gly Thr Asn Gly Thr Asn Glu
    775                 780                 785

ctg acg gta agg atg gtc tca ccc cgc aca tcg gtg aga acg gaa act   2515
Leu Thr Val Arg Met Val Ser Pro Arg Thr Ser Val Arg Thr Glu Thr
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790                 795                 800                 805

ggt gga tcg gcg aaa agg aca ctg gta ttt cga caa cct ttg gcg gtg   2563
Gly Gly Ser Ala Lys Arg Thr Leu Val Phe Arg Gln Pro Leu Ala Val
                810                 815                 820

gcg gca acc ctg gta ccg gca atg act gca tca cgg tcc cag gtg atg   2611
Ala Ala Thr Leu Val Pro Ala Met Thr Ala Ser Arg Ser Gln Val Met
            825                 830                 835

atc ttg gat tcc cag atg atg ctg agg ccg gtg cag aga ccg gtg cag   2659
Ile Leu Asp Ser Gln Met Met Leu Arg Pro Val Gln Arg Pro Val Gln
        840                 845                 850

atg ccg aag gta cta ttg act aaa ggt cat aga gca acg acc atg act   2707
Met Pro Lys Val Leu Leu Thr Lys Gly His Arg Ala Thr Thr Met Thr
    855                 860                 865

gat taaagtcgga acacaacccc tag                                    2733
Asp
870
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<210> 1686
<211> 870
<212> PRT
<213> Corynebacterium glutamicum

<400> 1686

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Leu Ser Leu Asn Leu Lys Lys Asn Ser Ala Arg Ser Ile Thr Ala Leu
  1               5                  10                  15

Thr Val Ala Gly Leu Gly Leu Ser Ile Val Pro Ala Ala Ser Ala Gln
             20                  25                  30

Asp Val Ala Asp Asp Thr Thr Asn Ser Asp Ser Thr Arg Asp Ala Ile
         35                  40                  45

Cys Ala Ala Ala Pro Leu Val Ala Gly Ala Ala Val Gly Val Gly Leu
     50                  55                  60

Leu Ser Gln Gln Pro Glu Phe Gln His Met Val Ser Gln Ile Gln Ser
 65                  70                  75                  80

Asp Ala Gln Arg Ile Gly Gln Asp Leu Ser Asn Gln Phe Asn Asn Ser
                 85                  90                  95

Leu Glu Ser Leu Asn Ile Gly Leu Gly Asn Gly Val His Gly Pro Gln
            100                 105                 110

Gln Asn Ala Val Gln Gly Ile Asp Leu Thr Glu Ala Ala Arg Thr Met
        115                 120                 125

Ala Gly Trp Asn Asp Leu Ala Ala Gln Val Gly Gln Thr Ala Gly Pro
    130                 135                 140

Ala Ile Gly Ala Val Ala Gly Thr Ala Gly Leu Ile Ala Leu Val Asp
145                 150                 155                 160

Tyr Cys Trp Leu Glu Gly Phe Asp Phe Ala Gly Gly Ser Ser Gly Thr
                165                 170                 175
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Asp Gly Glu Asn Gly Val Asp Gly Gln Asp Gly Thr Ser Ile Thr Ile
            180                 185                 190

Thr Glu Ile Lys Thr Asp Asp Asp Gly Asn Thr Ile Val Val Phe Ser
        195                 200                 205

Asp Gly Ser Glu Ile Thr Ile Thr Asn Gly Lys Asp Gly Ala Ala Ile
    210                 215                 220

Thr Ile Val Asn Thr Tyr Arg Asp Asp Glu Gly Asn Thr Val Val Glu
225                 230                 235                 240

Phe Ser Asp Gly Ser Thr Ile Val Ile Asp Lys Gly Glu Asp Gly Lys
                245                 250                 255

Asp Gly Glu Asp Gly Lys Asp Gly Glu Asp Gly Lys Asp Leu Thr Val
            260                 265                 270

Thr Asp Thr Tyr Ile Asn Asp Asp Gly Asp Thr Val Val Glu Leu Ser
        275                 280                 285

Asp Gly Ser Thr Ile Ile Val Lys Lys Gly Thr Asp Gly Lys Asp Gly
    290                 295                 300

Ala Asp Gly Ser Asp Gly Ala Asp Gly Val Ser Ile Thr Val Glu Asn
305                 310                 315                 320

Ser Tyr Val Asp Ala Asp Gly Asn Thr Val Val Glu Phe Ser Asp Gly
                325                 330                 335

Ser Asn Val Thr Ile Asn Lys Gly Glu Lys Gly Asp Lys Gly Asp Ala
            340                 345                 350

Gly Ala Asp Gly Glu Asp Gly Ala Asp Gly Glu Ser Ile Thr Val Val
        355                 360                 365

Asn Thr Ser Asn Asp Ala Glu Gly Asn Thr Leu Val Glu Leu Ser Asp
    370                 375                 380

Gly Thr Val Ile Thr Ile Asn Lys Gly Asp Lys Gly Asp Ala Gly Ala
385                 390                 395                 400

Asp Gly Glu Asp Gly Ser Asn Gly Ala Asp Gly Glu Ser Ile Thr Val
                405                 410                 415

Ile Glu Thr Arg Phe Asp Ala Asp Gly Asn Thr Val Val Val Phe Ser
            420                 425                 430

Asn Gly Thr Glu Ile Thr Ile Asn Lys Gly Glu Lys Gly Asp Lys Gly
        435                 440                 445

Asp Thr Gly Glu Asp Gly Lys Asp Gly Leu Thr Pro Tyr Ile Gly Pro
    450                 455                 460

Asp Gly Asn Trp Trp Ile Gly Glu Asn Asn Thr Cys Thr Ala Ala Arg
465                 470                 475                 480

Gly Asn Asp Gly Lys Asp Gly Asp Thr Pro Arg Ile Gly Asp Asn Gly
                485                 490                 495
```

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Asn Trp Trp Ile Gly Ile Val Asp Thr Gly Val Pro Ala Arg Gly Gln
            500                 505                 510

Asp Gly Ala Asn Gly Ala Asp Gly Ala Asn Thr Val Glu Ile Ile Asn
        515                 520                 525

Gly Tyr Trp Tyr Ile Asn Gly Glu Asn Thr Gly Val Lys Ala Val Gly
    530                 535                 540

Glu Asn Gly Thr Asn Gly Ala Asp Gly Gln Asp Gly Glu Asn Gly Thr
545                 550                 555                 560

Asn Gly Ala Asn Thr Val Glu Ile Ile Asn Gly Tyr Trp Tyr Ile Asn
                565                 570                 575

Gly Glu Asn Thr Gly Val Lys Ala Gln Gly Pro Lys Gly Asp Lys Gly
            580                 585                 590

Asp Thr Gly Asp Thr Gly Ala Pro Gly Glu Gly Ser Gly Asn Val Asp
        595                 600                 605

Ile Glu Ile Arg Glu Ser Ser Tyr Pro Gly Gly Gly Gln Ala Thr Ile
    610                 615                 620

Ile Ile Leu Asp Gln Phe Glu Tyr Glu Ile Pro His Thr Val Ile Gly
625                 630                 635                 640

Asp Asn Gly Asn Trp Tyr Ile Gly Glu Lys Asp Thr Gly Ile Pro Ala
                645                 650                 655

Gln Gly Gly Thr Gly Thr Pro Gly Glu Asp Gly Leu Thr Pro His Ile
            660                 665                 670

Gly Asp Asn Gly Asn Trp Trp Ile Gly Asp Thr Asp Thr Gly Val Ser
        675                 680                 685

Ala Ser Pro Thr Pro Val Gly Glu Ala Val Ala Gly Val Thr Asp Val
    690                 695                 700

Val Phe Asn Thr Ser Asp Glu Pro Lys Thr Ile Thr Ala Thr Ile Asn
705                 710                 715                 720

Gly Glu Glu Tyr Asp Tyr Thr Leu Pro Pro His Ser Ala Val Val Phe
                725                 730                 735

Tyr Ala Thr Gly Ser Pro Met Ala Tyr Ser Leu Pro Asn Ala Ser Gly
            740                 745                 750

Leu Thr Val Ile Gly Thr Glu Glu Thr Pro Gly Phe Thr Thr Ile Arg
        755                 760                 765

Phe Ser Asp His Ser Thr Val Thr Ile Pro His Gly Arg Asp Gly Thr
    770                 775                 780

Asn Gly Thr Asn Glu Leu Thr Val Arg Met Val Ser Pro Arg Thr Ser
785                 790                 795                 800

Val Arg Thr Glu Thr Gly Gly Ser Ala Lys Arg Thr Leu Val Phe Arg
                805                 810                 815

Gln Pro Leu Ala Val Ala Ala Thr Leu Val Pro Ala Met Thr Ala Ser
```

```
            820                 825                 830

Arg Ser Gln Val Met Ile Leu Asp Ser Gln Met Met Leu Arg Pro Val
        835                 840                 845

Gln Arg Pro Val Gln Met Pro Lys Val Leu Leu Thr Lys Gly His Arg
    850                 855                 860

Ala Thr Thr Met Thr Asp
865                 870


<210> 1687
<211> 582
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(559)
<223> RXA00275

<400> 1687
ctgacgcaga cgttgcacag ctcgcaaccg ctattgacga acagaaccgc cccacaaaga 60

gctgttccct acggcagatc gcaaggaact attcgcctgg ttg gat aag cgt cgc   115
                                              Leu Asp Lys Arg Arg
                                                1               5

cca gaa tta agc gac gat ttc atc aaa gct ttt gat gat ttc ctt cat   163
Pro Glu Leu Ser Asp Asp Phe Ile Lys Ala Phe Asp Asp Phe Leu His
                10                  15                  20

tct ttt gcg tgc ctg gac aaa aca acg atc acc cta ttg gcg caa tca   211
Ser Phe Ala Cys Leu Asp Lys Thr Thr Ile Thr Leu Leu Ala Gln Ser
            25                  30                  35

ccg gtg cgc aca tcc act ggc tat aca ggt act ttt atc ggc atc ccc   259
Pro Val Arg Thr Ser Thr Gly Tyr Thr Gly Thr Phe Ile Gly Ile Pro
        40                  45                  50

aat aat gaa cca ctg tcc gaa gag ccc acc ccc acc att tac att gtg   307
Asn Asn Glu Pro Leu Ser Glu Glu Pro Thr Pro Thr Ile Tyr Ile Val
    55                  60                  65

cac gat aat cac aca ggg ata atc cac agt tac ccc gca cga atg att   355
His Asp Asn His Thr Gly Ile Ile His Ser Tyr Pro Ala Arg Met Ile
70                  75                  80                  85

aat ctt aaa tct gag ctc ggt tcc gct gag atg att cac gag gca atc   403
Asn Leu Lys Ser Glu Leu Gly Ser Ala Glu Met Ile His Glu Ala Ile
                90                  95                  100

tgg ggg tca ccc cat caa cag cag tta atc tca tgg tat gag act tac   451
Trp Gly Ser Pro His Gln Gln Gln Leu Ile Ser Trp Tyr Glu Thr Tyr
            105                 110                 115

tac acc aac atc tac tat ggt ttt aac cca ccc act gaa cca cat aag   499
Tyr Thr Asn Ile Tyr Tyr Gly Phe Asn Pro Pro Thr Glu Pro His Lys
        120                 125                 130
```

```
agt ctt gag att ttt gct caa gac ttc tgt ctg acc cca cca gag aaa   547
Ser Leu Glu Ile Phe Ala Gln Asp Phe Cys Leu Thr Pro Pro Glu Lys
    135                 140                 145

cct cct ttt ttc taaggcaagg cccgtggcac aca                         582
Pro Pro Phe Phe
150
```

<210> 1688
<211> 153
<212> PRT
<213> Corynebacterium glutamicum

<400> 1688

```
Leu Asp Lys Arg Arg Pro Glu Leu Ser Asp Asp Phe Ile Lys Ala Phe
  1               5                  10                  15

Asp Asp Phe Leu His Ser Phe Ala Cys Leu Asp Lys Thr Thr Ile Thr
             20                  25                  30

Leu Leu Ala Gln Ser Pro Val Arg Thr Ser Thr Gly Tyr Thr Gly Thr
         35                  40                  45

Phe Ile Gly Ile Pro Asn Asn Glu Pro Leu Ser Glu Glu Pro Thr Pro
     50                  55                  60

Thr Ile Tyr Ile Val His Asp Asn His Thr Gly Ile Ile His Ser Tyr
 65                  70                  75                  80

Pro Ala Arg Met Ile Asn Leu Lys Ser Glu Leu Gly Ser Ala Glu Met
                 85                  90                  95

Ile His Glu Ala Ile Trp Gly Ser Pro His Gln Gln Gln Leu Ile Ser
            100                 105                 110

Trp Tyr Glu Thr Tyr Tyr Thr Asn Ile Tyr Tyr Gly Phe Asn Pro Pro
        115                 120                 125

Thr Glu Pro His Lys Ser Leu Glu Ile Phe Ala Gln Asp Phe Cys Leu
    130                 135                 140

Thr Pro Pro Glu Lys Pro Pro Phe Phe
145                 150
```

<210> 1689
<211> 465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(442)
<223> RXA00276

<400> 1689

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ggcacactac cctatgacta caccgcaacc cagcaaacct gcgccatggt cgcttgccta 60

taagtatcaa gccatcagca atgatgattt tgacaaccat atg gat gac ctc agc   115
                                            Met Asp Asp Leu Ser
```

```
                                                    1               5

agt cgc caa gac cat gaa gcc tac ggc acg tac aac ccc gat aac ggt   163
Ser Arg Gln Asp His Glu Ala Tyr Gly Thr Tyr Asn Pro Asp Asn Gly
                10                  15                  20

gtc atg ccc gat cat gtc atc gtg cct tca ccc tat gaa cca tat gat   211
Val Met Pro Asp His Val Ile Val Pro Ser Pro Tyr Glu Pro Tyr Asp
            25                  30                  35

gat gct gcg ccg att gat cct ttc gac tac gac gaa gat ctt ctc gat   259
Asp Ala Ala Pro Ile Asp Pro Phe Asp Tyr Asp Glu Asp Leu Leu Asp
        40                  45                  50

gag att aaa gaa gag cgc gct gca cat gcg gtt gac gca caa gta aca   307
Glu Ile Lys Glu Glu Arg Ala Ala His Ala Val Asp Ala Gln Val Thr
    55                  60                  65

gaa aca act aaa gct gac gca gac gtt gca cag ctc gca acc gct att   355
Glu Thr Thr Lys Ala Asp Ala Asp Val Ala Gln Leu Ala Thr Ala Ile
70                  75                  80                  85

gac gaa cag aac cgc ccc aca aag agc tgt tcc cta cgg cag atc gca   403
Asp Glu Gln Asn Arg Pro Thr Lys Ser Cys Ser Leu Arg Gln Ile Ala
                90                  95                  100

agg aac tat tcg cct ggt tgg ata agc gtc gcc cag aat taagcgacga    452
Arg Asn Tyr Ser Pro Gly Trp Ile Ser Val Ala Gln Asn
            105                 110

tttcatcaaa gct                                                   465


<210> 1690
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 1690
Met Asp Asp Leu Ser Ser Arg Gln Asp His Glu Ala Tyr Gly Thr Tyr
  1               5                  10                  15

Asn Pro Asp Asn Gly Val Met Pro Asp His Val Ile Val Pro Ser Pro
            20                  25                  30

Tyr Glu Pro Tyr Asp Asp Ala Ala Pro Ile Asp Pro Phe Asp Tyr Asp
        35                  40                  45

Glu Asp Leu Leu Asp Glu Ile Lys Glu Glu Arg Ala Ala His Ala Val
    50                  55                  60

Asp Ala Gln Val Thr Glu Thr Thr Lys Ala Asp Ala Asp Val Ala Gln
65                  70                  75                  80

Leu Ala Thr Ala Ile Asp Glu Gln Asn Arg Pro Thr Lys Ser Cys Ser
                85                  90                  95

Leu Arg Gln Ile Ala Arg Asn Tyr Ser Pro Gly Trp Ile Ser Val Ala
            100                 105                 110

Gln Asn
```

<210> 1691
<211> 1509
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1486)
<223> RXA00279

<400> 1691
tggggagcat tcagaggtgc ctaatcctct ggatgattct gcggtgcaaa attcagcccc 60

acattcagcc ccacattcag ctcggacccg gttggagttt ttg gat acc gat gac 115
Leu Asp Thr Asp Asp
1 5

tcg cct gat cat tgg ctt gat ccg tta acg gag aag gat act tct aag 163
Ser Pro Asp His Trp Leu Asp Pro Leu Thr Glu Lys Asp Thr Ser Lys
10 15 20

cgc act ctc gtt aat tcg att gtt cag gaa act ttc ggc cag cct att 211
Arg Thr Leu Val Asn Ser Ile Val Gln Glu Thr Phe Gly Gln Pro Ile
25 30 35

ttt gtt gcc cgc aag att tgg gct ttc gtc aat acg tcg ccg ggc cgg 259
Phe Val Ala Arg Lys Ile Trp Ala Phe Val Asn Thr Ser Pro Gly Arg
40 45 50

atg acg ttg atg acg att atc att tcg atc gcc att ttt gct gct ggt 307
Met Thr Leu Met Thr Ile Ile Ile Ser Ile Ala Ile Phe Ala Ala Gly
55 60 65

tac gcc atg tcg gtg tct tcg gat act agg cag tcc aat ttg gat gat 355
Tyr Ala Met Ser Val Ser Ser Asp Thr Arg Gln Ser Asn Leu Asp Asp
70 75 80 85

ttg atc act aat gcg gag cct gtt tcc tat aac gcg cat gtg ctg tat 403
Leu Ile Thr Asn Ala Glu Pro Val Ser Tyr Asn Ala His Val Leu Tyr
90 95 100

aca tca ttg tcg gtt gct gat acc act gct acc act ggt ttt gtt cag 451
Thr Ser Leu Ser Val Ala Asp Thr Thr Ala Thr Thr Gly Phe Val Gln
105 110 115

gct ggt gtg gag ggc ccg gtg aat cgg gtg aag tat cac act gct att 499
Ala Gly Val Glu Gly Pro Val Asn Arg Val Lys Tyr His Thr Ala Ile
120 125 130

gat cgt gct gcg gtt gct gct act cat act gcg gcg tct gcg gat agt 547
Asp Arg Ala Ala Val Ala Ala Thr His Thr Ala Ala Ser Ala Asp Ser
135 140 145

agt aat gag cat ttg atg gag ttg gtg ctg gag att cag cgt cag ttg 595
Ser Asn Glu His Leu Met Glu Leu Val Leu Glu Ile Gln Arg Gln Leu
150 155 160 165

ccg gtg tat acg ggg ttg gtg gaa act gct cgg act aat aac cgt gcg 643

```
Pro Val Tyr Thr Gly Leu Val Glu Thr Ala Arg Thr Asn Asn Arg Ala
                170                 175                 180

ggt aat ccc gtg ggt gtg gcc tat atg tct gag gcc agc gcg atg atg   691
Gly Asn Pro Val Gly Val Ala Tyr Met Ser Glu Ala Ser Ala Met Met
            185                 190                 195

cgt aat gaa att ttg ccg atg gcg tct gag ctt tac aac ctg acg agt   739
Arg Asn Glu Ile Leu Pro Met Ala Ser Glu Leu Tyr Asn Leu Thr Ser
        200                 205                 210

cgt gcg gtg tct gat cag cag cgt tcg gtg acg ggt ccg cag tgg ttt   787
Arg Ala Val Ser Asp Gln Gln Arg Ser Val Thr Gly Pro Gln Trp Phe
    215                 220                 225

ccg ctg tct gga ttg ctt gcg gct ctt gcc atg ttg att gtt gcg cag   835
Pro Leu Ser Gly Leu Leu Ala Ala Leu Ala Met Leu Ile Val Ala Gln
230                 235                 240                 245

tgg tgg ttg atg cgg att acg cgc agg cgc atc aac aag ggg ttt gcc   883
Trp Trp Leu Met Arg Ile Thr Arg Arg Arg Ile Asn Lys Gly Phe Ala
                250                 255                 260

ctg gcc acg gtg atg atg atg acg gca acg tta tgg gtg tca gct gca   931
Leu Ala Thr Val Met Met Met Thr Ala Thr Leu Trp Val Ser Ala Ala
            265                 270                 275

aac tgg gcg acg tgg cag gct ggc acg aag ggt ttt gag gaa gcg tcg   979
Asn Trp Ala Thr Trp Gln Ala Gly Thr Lys Gly Phe Glu Glu Ala Ser
        280                 285                 290

ggg ccg ttg aat tcc atg act acg gct cgt att tat gcg cag cag acc   1027
Gly Pro Leu Asn Ser Met Thr Thr Ala Arg Ile Tyr Ala Gln Gln Thr
    295                 300                 305

cgc acg acg gag acg ttg tcg ttg gtg cgt agg cag tcg att cag ggc   1075
Arg Thr Thr Glu Thr Leu Ser Leu Val Arg Arg Gln Ser Ile Gln Gly
310                 315                 320                 325

agt ggc act ggt ttt acc gca acg att aat cag att aag cgt gcg ctg   1123
Ser Gly Thr Gly Phe Thr Ala Thr Ile Asn Gln Ile Lys Arg Ala Leu
                330                 335                 340

gat gag tat gaa acc act gcg cag tca cag act ccg gag cat cag cag   1171
Asp Glu Tyr Glu Thr Thr Ala Gln Ser Gln Thr Pro Glu His Gln Gln
            345                 350                 355

ttg att acg gcg att cgt aat gcg att gct gca tgg act gcc gat cac   1219
Leu Ile Thr Ala Ile Arg Asn Ala Ile Ala Ala Trp Thr Ala Asp His
        360                 365                 370

gat gag ttc acg gtg ttg ttg gcg tct ggt gat tac aac ggt gcg gtc   1267
Asp Glu Phe Thr Val Leu Leu Ala Ser Gly Asp Tyr Asn Gly Ala Val
    375                 380                 385

aat gcg gtg ctc aac aaa gat gag gag ggc cag acc agc ttt gat gag   1315
Asn Ala Val Leu Asn Lys Asp Glu Glu Gly Gln Thr Ser Phe Asp Glu
390                 395                 400                 405

ctc gat act gcg ctg gct gag ctg atc gcg gat tct cgc agc tcc atg   1363
Leu Asp Thr Ala Leu Ala Glu Leu Ile Ala Asp Ser Arg Ser Ser Met
```

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                410                 415                 420

cgt tcc tat atc cag tcg ggc ctg cag gcc acg gag ttg gtg tcc gtc   1411
Arg Ser Tyr Ile Gln Ser Gly Leu Gln Ala Thr Glu Leu Val Ser Val
            425                 430                 435

atg gtg atg att ctg tct gtc gtt tct gtg ttg gct ttg tgg gtc ggc   1459
Met Val Met Ile Leu Ser Val Val Ser Val Leu Ala Leu Trp Val Gly
        440                 445                 450

atc cgc ccc cgt ttg cag gag tac tta taaatgcacg cttttcgacg         1506
Ile Arg Pro Arg Leu Gln Glu Tyr Leu
    455                 460

ccc                                                               1509


<210> 1692
<211> 462
<212> PRT
<213> Corynebacterium glutamicum

<400> 1692
Leu Asp Thr Asp Asp Ser Pro Asp His Trp Leu Asp Pro Leu Thr Glu
  1               5                  10                  15

Lys Asp Thr Ser Lys Arg Thr Leu Val Asn Ser Ile Val Gln Glu Thr
             20                  25                  30

Phe Gly Gln Pro Ile Phe Val Ala Arg Lys Ile Trp Ala Phe Val Asn
         35                  40                  45

Thr Ser Pro Gly Arg Met Thr Leu Met Thr Ile Ile Ile Ser Ile Ala
     50                  55                  60

Ile Phe Ala Ala Gly Tyr Ala Met Ser Val Ser Ser Asp Thr Arg Gln
 65                  70                  75                  80

Ser Asn Leu Asp Asp Leu Ile Thr Asn Ala Glu Pro Val Ser Tyr Asn
                 85                  90                  95

Ala His Val Leu Tyr Thr Ser Leu Ser Val Ala Asp Thr Thr Ala Thr
            100                 105                 110

Thr Gly Phe Val Gln Ala Gly Val Glu Gly Pro Val Asn Arg Val Lys
        115                 120                 125

Tyr His Thr Ala Ile Asp Arg Ala Ala Val Ala Ala Thr His Thr Ala
    130                 135                 140

Ala Ser Ala Asp Ser Ser Asn Glu His Leu Met Glu Leu Val Leu Glu
145                 150                 155                 160

Ile Gln Arg Gln Leu Pro Val Tyr Thr Gly Leu Val Glu Thr Ala Arg
                165                 170                 175

Thr Asn Asn Arg Ala Gly Asn Pro Val Gly Val Ala Tyr Met Ser Glu
            180                 185                 190

Ala Ser Ala Met Met Arg Asn Glu Ile Leu Pro Met Ala Ser Glu Leu
        195                 200                 205
```

```
Tyr Asn Leu Thr Ser Arg Ala Val Ser Asp Gln Gln Arg Ser Val Thr
    210                 215                 220

Gly Pro Gln Trp Phe Pro Leu Ser Gly Leu Leu Ala Ala Leu Ala Met
225                 230                 235                 240

Leu Ile Val Ala Gln Trp Trp Leu Met Arg Ile Thr Arg Arg Arg Ile
                245                 250                 255

Asn Lys Gly Phe Ala Leu Ala Thr Val Met Met Met Thr Ala Thr Leu
            260                 265                 270

Trp Val Ser Ala Ala Asn Trp Ala Thr Trp Gln Ala Gly Thr Lys Gly
        275                 280                 285

Phe Glu Glu Ala Ser Gly Pro Leu Asn Ser Met Thr Thr Ala Arg Ile
    290                 295                 300

Tyr Ala Gln Gln Thr Arg Thr Thr Glu Thr Leu Ser Leu Val Arg Arg
305                 310                 315                 320

Gln Ser Ile Gln Gly Ser Gly Thr Gly Phe Thr Ala Thr Ile Asn Gln
                325                 330                 335

Ile Lys Arg Ala Leu Asp Glu Tyr Glu Thr Thr Ala Gln Ser Gln Thr
            340                 345                 350

Pro Glu His Gln Gln Leu Ile Thr Ala Ile Arg Asn Ala Ile Ala Ala
        355                 360                 365

Trp Thr Ala Asp His Asp Glu Phe Thr Val Leu Leu Ala Ser Gly Asp
    370                 375                 380

Tyr Asn Gly Ala Val Asn Ala Val Leu Asn Lys Asp Glu Glu Gly Gln
385                 390                 395                 400

Thr Ser Phe Asp Glu Leu Asp Thr Ala Leu Ala Glu Leu Ile Ala Asp
                405                 410                 415

Ser Arg Ser Ser Met Arg Ser Tyr Ile Gln Ser Gly Leu Gln Ala Thr
            420                 425                 430

Glu Leu Val Ser Val Met Val Met Ile Leu Ser Val Val Ser Val Leu
        435                 440                 445

Ala Leu Trp Val Gly Ile Arg Pro Arg Leu Gln Glu Tyr Leu
    450                 455                 460
```

<210> 1693
<211> 789
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(789)
<223> RXA00282

<400> 1693

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atg agc cgc gac gac cag acg aac aac aac ggt gag ggc gac gac aca   48
Met Ser Arg Asp Asp Gln Thr Asn Asn Asn Gly Glu Gly Asp Asp Thr
  1               5                  10                  15

tcg cgc gag cag tcc tgg gat caa tcc tgg cag aac cta aat aag gat   96
Ser Arg Glu Gln Ser Trp Asp Gln Ser Trp Gln Asn Leu Asn Lys Asp
            20                  25                  30

tcc cag tac ggt ccg acc tcg cat ccg gag gac gcg ccg gga gga ttc  144
Ser Gln Tyr Gly Pro Thr Ser His Pro Glu Asp Ala Pro Gly Gly Phe
         35                  40                  45

cag gga aac ggc cag ggt aac agc cgg ggc aac gct cag ggc aat ggt  192
Gln Gly Asn Gly Gln Gly Asn Ser Arg Gly Asn Ala Gln Gly Asn Gly
     50                  55                  60

cag ggc aat ggt cag ggc ttt ggc ccg ggt aat gct tcg gga tat gga  240
Gln Gly Asn Gly Gln Gly Phe Gly Pro Gly Asn Ala Ser Gly Tyr Gly
 65                  70                  75                  80

ggc tac ggt cag cca tac ccg cag act ccg tac cag aat tcc tac caa  288
Gly Tyr Gly Gln Pro Tyr Pro Gln Thr Pro Tyr Gln Asn Ser Tyr Gln
                85                  90                  95

ggt tat ggc gct act tca ccg cag aac gac gtg gcg ctg gaa gcg agc  336
Gly Tyr Gly Ala Thr Ser Pro Gln Asn Asp Val Ala Leu Glu Ala Ser
            100                 105                 110

aac ggc aaa gtc gac atc atg cgg gcg att cgc ttc gga ttc aaa gcc  384
Asn Gly Lys Val Asp Ile Met Arg Ala Ile Arg Phe Gly Phe Lys Ala
        115                 120                 125

acg ttt gcc aat cca gca gtg tgg att ttg ggc acc gtc ggt ctt ggc  432
Thr Phe Ala Asn Pro Ala Val Trp Ile Leu Gly Thr Val Gly Leu Gly
    130                 135                 140

ctt gcg ttc atg att gtg agt ggg ttg ctt ggc tac tta tca ttt ttg  480
Leu Ala Phe Met Ile Val Ser Gly Leu Leu Gly Tyr Leu Ser Phe Leu
145                 150                 155                 160

atc gac cct aat gcg ggc acg acg act tct ggt ttt tcg gtt tcc gag  528
Ile Asp Pro Asn Ala Gly Thr Thr Thr Ser Gly Phe Ser Val Ser Glu
                165                 170                 175

acc ctg ttg aac gta gct atc gga atc atc acc ttc gca ata acc att  576
Thr Leu Leu Asn Val Ala Ile Gly Ile Ile Thr Phe Ala Ile Thr Ile
            180                 185                 190

tgc gtc atg cgc ggt gca ctg ctt tct gtt gat gga cac aaa gtt cgc  624
Cys Val Met Arg Gly Ala Leu Leu Ser Val Asp Gly His Lys Val Arg
        195                 200                 205

ttc ggt gat ttc ttt aaa ccc atc aat gtt ggt caa aca gtg att ctg  672
Phe Gly Asp Phe Phe Lys Pro Ile Asn Val Gly Gln Thr Val Ile Leu
    210                 215                 220

atg gtg ggg ctg ggt atc ttc ggc atc atc ctg ggc acc ttc acc act  720
Met Val Gly Leu Gly Ile Phe Gly Ile Ile Leu Gly Thr Phe Thr Thr
225                 230                 235                 240

ttt ctc act caa aat ctg gtg tcg ttt aat gac gct gcc ggt acc gtt  768
```

Phe Leu Thr Gln Asn Leu Val Ser Phe Asn Asp Ala Ala Gly Thr Val
245 250 255

gag gtc aat aac agc ggt tta 789
Glu Val Asn Asn Ser Gly Leu
260

<210> 1694
<211> 263
<212> PRT
<213> Corynebacterium glutamicum

<400> 1694
Met Ser Arg Asp Asp Gln Thr Asn Asn Asn Gly Glu Gly Asp Asp Thr
1 5 10 15

Ser Arg Glu Gln Ser Trp Asp Gln Ser Trp Gln Asn Leu Asn Lys Asp
20 25 30

Ser Gln Tyr Gly Pro Thr Ser His Pro Glu Asp Ala Pro Gly Gly Phe
35 40 45

Gln Gly Asn Gly Gln Gly Asn Ser Arg Gly Asn Ala Gln Gly Asn Gly
50 55 60

Gln Gly Asn Gly Gln Gly Phe Gly Pro Gly Asn Ala Ser Gly Tyr Gly
65 70 75 80

Gly Tyr Gly Gln Pro Tyr Pro Gln Thr Pro Tyr Gln Asn Ser Tyr Gln
85 90 95

Gly Tyr Gly Ala Thr Ser Pro Gln Asn Asp Val Ala Leu Glu Ala Ser
100 105 110

Asn Gly Lys Val Asp Ile Met Arg Ala Ile Arg Phe Gly Phe Lys Ala
115 120 125

Thr Phe Ala Asn Pro Ala Val Trp Ile Leu Gly Thr Val Gly Leu Gly
130 135 140

Leu Ala Phe Met Ile Val Ser Gly Leu Leu Gly Tyr Leu Ser Phe Leu
145 150 155 160

Ile Asp Pro Asn Ala Gly Thr Thr Thr Ser Gly Phe Ser Val Ser Glu
165 170 175

Thr Leu Leu Asn Val Ala Ile Gly Ile Ile Thr Phe Ala Ile Thr Ile
180 185 190

Cys Val Met Arg Gly Ala Leu Leu Ser Val Asp Gly His Lys Val Arg
195 200 205

Phe Gly Asp Phe Phe Lys Pro Ile Asn Val Gly Gln Thr Val Ile Leu
210 215 220

Met Val Gly Leu Gly Ile Phe Gly Ile Ile Leu Gly Thr Phe Thr Thr
225 230 235 240

Phe Leu Thr Gln Asn Leu Val Ser Phe Asn Asp Ala Ala Gly Thr Val
245 250 255

```
Glu Val Asn Asn Ser Gly Leu
            260


<210> 1695
<211> 536
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(513)
<223> RXA00285

<400> 1695
gga act gaa ttg ggc gca ttg tta ctg cgt gtc ctc aac agg gaa gaa   48
Gly Thr Glu Leu Gly Ala Leu Leu Leu Arg Val Leu Asn Arg Glu Glu
  1               5                  10                  15

atg atg gac aga ttc gca cgg gag ctg ggt ttt ttc gtc gac aag cag   96
Met Met Asp Arg Phe Ala Arg Glu Leu Gly Phe Phe Val Asp Lys Gln
             20                  25                  30

ctt gaa gag gtc gag cgc atc aac tgt cac cat aac tac acg gtc cag   144
Leu Glu Glu Val Glu Arg Ile Asn Cys His His Asn Tyr Thr Val Gln
         35                  40                  45

gag gag cac tac ggc gag acc att tgg ctc acc cgt aag ggt gcc gtg   192
Glu Glu His Tyr Gly Glu Thr Ile Trp Leu Thr Arg Lys Gly Ala Val
     50                  55                  60

ttg gcg gac gaa ggc acg ccg gcg ttg att ccg ggg tcg atg ggc acc   240
Leu Ala Asp Glu Gly Thr Pro Ala Leu Ile Pro Gly Ser Met Gly Thr
 65                  70                  75                  80

gcg tcg tac gtg ggc agt ggc aag ggc aac gcc gag gca ctg cgg tcg   288
Ala Ser Tyr Val Gly Ser Gly Lys Gly Asn Ala Glu Ala Leu Arg Ser
                 85                  90                  95

gcg ccg cat ggg gcg ggc cgg agg atg tac cgc aac cag gct aaa aag   336
Ala Pro His Gly Ala Gly Arg Arg Met Tyr Arg Asn Gln Ala Lys Lys
            100                 105                 110

cgc ttc tcg acg gcc gac ctg gat tct cgg atg gcg ggc atc gtc tac   384
Arg Phe Ser Thr Ala Asp Leu Asp Ser Arg Met Ala Gly Ile Val Tyr
        115                 120                 125

cgg ccc ggc aag gag tgg atc gat gaa att ccc gac gct tac aaa gac   432
Arg Pro Gly Lys Glu Trp Ile Asp Glu Ile Pro Asp Ala Tyr Lys Asp
    130                 135                 140

atc gat cag gtg atg gcc gat gct gcc gat ttg gtg aca att cgc cat   480
Ile Asp Gln Val Met Ala Asp Ala Ala Asp Leu Val Thr Ile Arg His
145                 150                 155                 160

aaa ttg cgc cag atc gtc aac gtg aaa ggc acc taaagcgcat tacggtaaag 533
Lys Leu Arg Gln Ile Val Asn Val Lys Gly Thr
                165                 170

tgc                                                               536
```

<210> 1696
<211> 171
<212> PRT
<213> Corynebacterium glutamicum

<400> 1696

```
Gly Thr Glu Leu Gly Ala Leu Leu Leu Arg Val Leu Asn Arg Glu Glu
  1               5                  10                  15

Met Met Asp Arg Phe Ala Arg Glu Leu Gly Phe Phe Val Asp Lys Gln
             20                  25                  30

Leu Glu Glu Val Glu Arg Ile Asn Cys His His Asn Tyr Thr Val Gln
         35                  40                  45

Glu Glu His Tyr Gly Glu Thr Ile Trp Leu Thr Arg Lys Gly Ala Val
     50                  55                  60

Leu Ala Asp Glu Gly Thr Pro Ala Leu Ile Pro Gly Ser Met Gly Thr
 65                  70                  75                  80

Ala Ser Tyr Val Gly Ser Gly Lys Gly Asn Ala Glu Ala Leu Arg Ser
                 85                  90                  95

Ala Pro His Gly Ala Gly Arg Arg Met Tyr Arg Asn Gln Ala Lys Lys
            100                 105                 110

Arg Phe Ser Thr Ala Asp Leu Asp Ser Arg Met Ala Gly Ile Val Tyr
        115                 120                 125

Arg Pro Gly Lys Glu Trp Ile Asp Glu Ile Pro Asp Ala Tyr Lys Asp
    130                 135                 140

Ile Asp Gln Val Met Ala Asp Ala Ala Asp Leu Val Thr Ile Arg His
145                 150                 155                 160

Lys Leu Arg Gln Ile Val Asn Val Lys Gly Thr
                165                 170
```

<210> 1697
<211> 687
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(664)
<223> RXA00286

<400> 1697

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ccataaattg cgccagatcg tcaacgtgaa aggcacctaa agcgcattac ggtaaagtgc 60

gagaggtatt ttgacgggtt tagattgagg gatgtggata gtg ctg aaa atc cca   115
                                              Val Leu Lys Ile Pro
                                                1               5

cgg ctg ctt cta cgc cgt gtg ctt ccg gta ctc atc acc ttg gcg ctc   163
Arg Leu Leu Leu Arg Arg Val Leu Pro Val Leu Ile Thr Leu Ala Leu
```

```
                10                  15                  20

ctg tgc gga ctg gtg ctt gcg tgg ttt atc tat cct gcg aag gct gag   211
Leu Cys Gly Leu Val Leu Ala Trp Phe Ile Tyr Pro Ala Lys Ala Glu
            25                  30                  35

ccc aaa aaa gat gat gta gtt ctg gtg ctg gcc ggt tcc agc gat ggt   259
Pro Lys Lys Asp Asp Val Val Leu Val Leu Ala Gly Ser Ser Asp Gly
        40                  45                  50

cga cac gaa tat ggt gcc gag ctt gtt gaa gaa ggc tac gcc agc aat   307
Arg His Glu Tyr Gly Ala Glu Leu Val Glu Glu Gly Tyr Ala Ser Asn
    55                  60                  65

tac gtc gtc tcc aac ccg agt ggc tcc aaa gac aaa gtg gga tat gcc   355
Tyr Val Val Ser Asn Pro Ser Gly Ser Lys Asp Lys Val Gly Tyr Ala
70                  75                  80                  85

cac tgc gca gga aag tca cgg cca aaa aat gcg gaa agt ttc tgc atg   403
His Cys Ala Gly Lys Ser Arg Pro Lys Asn Ala Glu Ser Phe Cys Met
                90                  95                  100

gat cct tac ccc gtg atc acc tcc ggc gaa gcc cgc acg ttt aac gag   451
Asp Pro Tyr Pro Val Ile Thr Ser Gly Glu Ala Arg Thr Phe Asn Glu
            105                 110                 115

ctt gcc aaa aag gaa ggc tgg gaa agc gta ttg gta gtg acc agc cgc   499
Leu Ala Lys Lys Glu Gly Trp Glu Ser Val Leu Val Val Thr Ser Arg
        120                 125                 130

acg cac acc caa cgc gtt cgc acc atg ttt gac cag tgc tat acc ggt   547
Thr His Thr Gln Arg Val Arg Thr Met Phe Asp Gln Cys Tyr Thr Gly
    135                 140                 145

gat tcc aca gtg ctc aac gtc aac agc cta gga cgt acc ggg ctt cac   595
Asp Ser Thr Val Leu Asn Val Asn Ser Leu Gly Arg Thr Gly Leu His
150                 155                 160                 165

aat gca gta ctc cac gag att ggc ggc ttc att aaa ttt tgg att acc   643
Asn Ala Val Leu His Glu Ile Gly Gly Phe Ile Lys Phe Trp Ile Thr
                170                 175                 180

gct ccg tgc gcg gac aca aac taaggacgtt ccagctccaa cag            687
Ala Pro Cys Ala Asp Thr Asn
            185
```

Application Filed with Electronic Sequence Listing

<210> 1698
<211> 188
<212> PRT
<213> Corynebacterium glutamicum

<400> 1698

```
Val Leu Lys Ile Pro Arg Leu Leu Leu Arg Arg Val Leu Pro Val Leu
  1               5                  10                  15

Ile Thr Leu Ala Leu Leu Cys Gly Leu Val Leu Ala Trp Phe Ile Tyr
            20                  25                  30

Pro Ala Lys Ala Glu Pro Lys Lys Asp Asp Val Val Leu Val Leu Ala
        35                  40                  45
```

```
Gly Ser Ser Asp Gly Arg His Glu Tyr Gly Ala Glu Leu Val Glu Glu
     50                  55                  60

Gly Tyr Ala Ser Asn Tyr Val Val Ser Asn Pro Ser Gly Ser Lys Asp
 65                  70                  75                  80

Lys Val Gly Tyr Ala His Cys Ala Gly Lys Ser Arg Pro Lys Asn Ala
                 85                  90                  95

Glu Ser Phe Cys Met Asp Pro Tyr Pro Val Ile Thr Ser Gly Glu Ala
            100                 105                 110

Arg Thr Phe Asn Glu Leu Ala Lys Lys Glu Gly Trp Glu Ser Val Leu
        115                 120                 125

Val Val Thr Ser Arg Thr His Thr Gln Arg Val Arg Thr Met Phe Asp
    130                 135                 140

Gln Cys Tyr Thr Gly Asp Ser Thr Val Leu Asn Val Asn Ser Leu Gly
145                 150                 155                 160

Arg Thr Gly Leu His Asn Ala Val Leu His Glu Ile Gly Gly Phe Ile
                165                 170                 175

Lys Phe Trp Ile Thr Ala Pro Cys Ala Asp Thr Asn
            180                 185
```

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<210> 1699
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(529)
<223> RXA00294

<400> 1699

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ttgttggtgt gaggttgggt tttgtcatcc tgaatgcttc atttctaccc tcgtgggtaa 60

agttggtgcc gaatcaacaa tctcttttgg aggaacttta atg agc att tcc aac   115
                                            Met Ser Ile Ser Asn
                                              1               5

gca atc ctg cgt ggt gtg tct ggc gct tat att ctg cag tcc ggc tac   163
Ala Ile Leu Arg Gly Val Ser Gly Ala Tyr Ile Leu Gln Ser Gly Tyr
                10                  15                  20

gga aaa ctt gga ttg cct aat gag gcc gct gct ggc att cag ggt cta   211
Gly Lys Leu Gly Leu Pro Asn Glu Ala Ala Ala Gly Ile Gln Gly Leu
            25                  30                  35

gct gca acg ggt atc cca gcg gtg gct gat atg gat tca gat act ttc   259
Ala Ala Thr Gly Ile Pro Ala Val Ala Asp Met Asp Ser Asp Thr Phe
        40                  45                  50

ggt aag ttt gtt gcc tac tcg gag ttg ggt atc ggt gga gct ttg ctt   307
Gly Lys Phe Val Ala Tyr Ser Glu Leu Gly Ile Gly Gly Ala Leu Leu
    55                  60                  65
```

```
gct cca ttt atc cct agc cgt ctt gca ggt ttg ggt ctt ggt gct ttc   355
Ala Pro Phe Ile Pro Ser Arg Leu Ala Gly Leu Gly Leu Gly Ala Phe
 70                  75                  80                  85

tct aca ggt ttg ttg gcc att tac ttc cgt aac cca gcg atg act caa   403
Ser Thr Gly Leu Leu Ala Ile Tyr Phe Arg Asn Pro Ala Met Thr Gln
                90                  95                 100

gac gac gga atc cgc cct tcc cag gat gga acc gga ttg tct aag gat   451
Asp Asp Gly Ile Arg Pro Ser Gln Asp Gly Thr Gly Leu Ser Lys Asp
            105                 110                 115

ctt ttc ctt gct gct att gcg ggt gct ttg gtg ttc gca cct gct aag   499
Leu Phe Leu Ala Ala Ile Ala Gly Ala Leu Val Phe Ala Pro Ala Lys
        120                 125                 130

aag cgt aag aag gcg aag aac aag tct aag taagcttgct tgaacggcgc     549
Lys Arg Lys Lys Ala Lys Asn Lys Ser Lys
    135                 140

ttg                                                               552
```

Sequence Listing.ST25.txt

<210> 1700
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 1700

```
Met Ser Ile Ser Asn Ala Ile Leu Arg Gly Val Ser Gly Ala Tyr Ile
  1               5                  10                  15

Leu Gln Ser Gly Tyr Gly Lys Leu Gly Leu Pro Asn Glu Ala Ala Ala
             20                  25                  30

Gly Ile Gln Gly Leu Ala Ala Thr Gly Ile Pro Ala Val Ala Asp Met
         35                  40                  45

Asp Ser Asp Thr Phe Gly Lys Phe Val Ala Tyr Ser Glu Leu Gly Ile
     50                  55                  60

Gly Gly Ala Leu Leu Ala Pro Phe Ile Pro Ser Arg Leu Ala Gly Leu
 65                  70                  75                  80

Gly Leu Gly Ala Phe Ser Thr Gly Leu Leu Ala Ile Tyr Phe Arg Asn
                 85                  90                  95

Pro Ala Met Thr Gln Asp Asp Gly Ile Arg Pro Ser Gln Asp Gly Thr
            100                 105                 110

Gly Leu Ser Lys Asp Leu Phe Leu Ala Ala Ile Ala Gly Ala Leu Val
        115                 120                 125

Phe Ala Pro Ala Lys Lys Arg Lys Lys Ala Lys Asn Lys Ser Lys
    130                 135                 140
```

<210> 1701
<211> 1035
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1012)
<223> RXA00297

<400> 1701
aacaaggcac cggaaaacaa gcaacgcacc ttgcagaggt ggtcttaagc atcttggagc 60

aaaacaacat ggcacaataa cgatcatgca acaggtgctc atg ggt ttc acg gtg 115
Met Gly Phe Thr Val
1 5

gtg ttc atc gtc atc gga ata ggt tgg att ctc ggt aga aga gac acc 163
Val Phe Ile Val Ile Gly Ile Gly Trp Ile Leu Gly Arg Arg Asp Thr
10 15 20

ttg ggc aca cat gcc cag aaa cct ttg agc ctg ttt gtc tat tac gtg 211
Leu Gly Thr His Ala Gln Lys Pro Leu Ser Leu Phe Val Tyr Tyr Val
25 30 35

gcc acc cca gcg ttg ttg ttt gat cgg gtc acc aag tca gat acc tcg 259
Ala Thr Pro Ala Leu Leu Phe Asp Arg Val Thr Lys Ser Asp Thr Ser
40 45 50

acg att ttc tct ctg aac ttc gtg gtc att gca ctc tct gcg ttg atc 307
Thr Ile Phe Ser Leu Asn Phe Val Val Ile Ala Leu Ser Ala Leu Ile
55 60 65

gta ggt ttc ctg ttt ttc cta ctc atg cgg ttc gtg atc aaa aga act 355
Val Gly Phe Leu Phe Phe Leu Leu Met Arg Phe Val Ile Lys Arg Thr
70 75 80 85

gcc gca gta tcg gtg atc ggc atg cta gct gcg tcc tac gcc aac gcc 403
Ala Ala Val Ser Val Ile Gly Met Leu Ala Ala Ser Tyr Ala Asn Ala
90 95 100

ggt aac ctg ggt atc cct ttg gca gcc tat att ttg gat gat ttc acc 451
Gly Asn Leu Gly Ile Pro Leu Ala Ala Tyr Ile Leu Asp Asp Phe Thr
105 110 115

gtg gtg att ccc gtg att ttg ttc cag gtg gcg ttc tac gca ccg atc 499
Val Val Ile Pro Val Ile Leu Phe Gln Val Ala Phe Tyr Ala Pro Ile
120 125 130

acc atg acc atc atg gag atg ctg acc aac aag aaa tcc acc aac ttg 547
Thr Met Thr Ile Met Glu Met Leu Thr Asn Lys Lys Ser Thr Asn Leu
135 140 145

gtg cgc aac ctc ctg gtc acg cca cta acc aac acc atg gtg ctc gca 595
Val Arg Asn Leu Leu Val Thr Pro Leu Thr Asn Thr Met Val Leu Ala
150 155 160 165

gcg att gcc ggt att gct gtg tct ttg act tcg atg agc gtg ccc gtg 643
Ala Ile Ala Gly Ile Ala Val Ser Leu Thr Ser Met Ser Val Pro Val
170 175 180

gtg att gct cag cca gtg gaa atg ttg gcg aat gct tca gtg cca ctg 691
Val Ile Ala Gln Pro Val Glu Met Leu Ala Asn Ala Ser Val Pro Leu
185 190 195

```
gct ttg gtg gtg ttc gga ctg tcc ttg tcc aag agc aag atc ctg gaa   739
Ala Leu Val Val Phe Gly Leu Ser Leu Ser Lys Ser Lys Ile Leu Glu
        200                 205                 210

aag ggg cag gta tcc agg cgc gat gtg ttt acg gcg gca ctg ttc aag   787
Lys Gly Gln Val Ser Arg Arg Asp Val Phe Thr Ala Ala Leu Phe Lys
    215                 220                 225

aat gtt ctg cac cca att gtt gcg gga ctt tta gcc tta gcc ttt ggt   835
Asn Val Leu His Pro Ile Val Ala Gly Leu Leu Ala Leu Ala Phe Gly
230                 235                 240                 245

atg gaa ggt act gcc ttg ttg tcg gcg gtg att ctc ggt gca ctg cca   883
Met Glu Gly Thr Ala Leu Leu Ser Ala Val Ile Leu Gly Ala Leu Pro
                250                 255                 260

aca gcg cag aat gtc tac acc tac gcg ttg cga ttt aga aca gct gaa   931
Thr Ala Gln Asn Val Tyr Thr Tyr Ala Leu Arg Phe Arg Thr Ala Glu
            265                 270                 275

tcg atg gcg aga gac aca ggg gtg gtc acc aca ctc att tcc ttc ccc   979
Ser Met Ala Arg Asp Thr Gly Val Val Thr Thr Leu Ile Ser Phe Pro
        280                 285                 290

gta ttg gtg gcg gtc tcc att atc ttt gga tct tagggttagc attagtggtc 1032
Val Leu Val Ala Val Ser Ile Ile Phe Gly Ser
    295                 300

atg                                                               1035


<210> 1702
<211> 304
<212> PRT
<213> Corynebacterium glutamicum

<400> 1702
Met Gly Phe Thr Val Val Phe Ile Val Ile Gly Ile Gly Trp Ile Leu
  1               5                  10                  15

Gly Arg Arg Asp Thr Leu Gly Thr His Ala Gln Lys Pro Leu Ser Leu
             20                  25                  30

Phe Val Tyr Tyr Val Ala Thr Pro Ala Leu Leu Phe Asp Arg Val Thr
         35                  40                  45

Lys Ser Asp Thr Ser Thr Ile Phe Ser Leu Asn Phe Val Val Ile Ala
     50                  55                  60

Leu Ser Ala Leu Ile Val Gly Phe Leu Phe Phe Leu Leu Met Arg Phe
 65                  70                  75                  80

Val Ile Lys Arg Thr Ala Ala Val Ser Val Ile Gly Met Leu Ala Ala
                 85                  90                  95

Ser Tyr Ala Asn Ala Gly Asn Leu Gly Ile Pro Leu Ala Ala Tyr Ile
            100                 105                 110

Leu Asp Asp Phe Thr Val Val Ile Pro Val Ile Leu Phe Gln Val Ala
        115                 120                 125
```

```
Phe Tyr Ala Pro Ile Thr Met Thr Ile Met Glu Met Leu Thr Asn Lys
    130                 135                 140

Lys Ser Thr Asn Leu Val Arg Asn Leu Leu Val Thr Pro Leu Thr Asn
145                 150                 155                 160

Thr Met Val Leu Ala Ala Ile Ala Gly Ile Ala Val Ser Leu Thr Ser
                165                 170                 175

Met Ser Val Pro Val Val Ile Ala Gln Pro Val Glu Met Leu Ala Asn
            180                 185                 190

Ala Ser Val Pro Leu Ala Leu Val Val Phe Gly Leu Ser Leu Ser Lys
        195                 200                 205

Ser Lys Ile Leu Glu Lys Gly Gln Val Ser Arg Arg Asp Val Phe Thr
    210                 215                 220

Ala Ala Leu Phe Lys Asn Val Leu His Pro Ile Val Ala Gly Leu Leu
225                 230                 235                 240

Ala Leu Ala Phe Gly Met Glu Gly Thr Ala Leu Leu Ser Ala Val Ile
                245                 250                 255

Leu Gly Ala Leu Pro Thr Ala Gln Asn Val Tyr Thr Tyr Ala Leu Arg
            260                 265                 270

Phe Arg Thr Ala Glu Ser Met Ala Arg Asp Thr Gly Val Val Thr Thr
        275                 280                 285

Leu Ile Ser Phe Pro Val Leu Val Ala Val Ser Ile Ile Phe Gly Ser
    290                 295                 300
```

20040224 = 20040224 = 20040224 = 20040224 = 20040224 = 20040224 = 20040224 = 20040224 = 20040224 = 20040224

<210> 1703
<211> 303
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(280)
<223> RXA00320

<400> 1703
aacagaccca ctctagccgt tgcgggttct tattgaggtc tatagtgggg tgctacacac 60

```
tacaaaccgt gatttgtttc gtgattggag ctgagcccac atg gct aaa gaa gat   115
                                               Met Ala Lys Glu Asp
                                                 1               5

ttg aag tgg ttc tac gat ctg gca acc ggc aag gtt ttt caa ggc aag   163
Leu Lys Trp Phe Tyr Asp Leu Ala Thr Gly Lys Val Phe Gln Gly Lys
                 10                  15                  20

gtt tcc ggc ttt gaa acc cgc atg ggc cca tat gac act gaa gag gaa   211
Val Ser Gly Phe Glu Thr Arg Met Gly Pro Tyr Asp Thr Glu Glu Glu
```

```
             25                  30                  35

gcc cat cac gcc atc tcc att gcg gca gcc cga acc aag gca gcc gaa   259
Ala His His Ala Ile Ser Ile Ala Ala Ala Arg Thr Lys Ala Ala Glu
         40                  45                  50

att tgg gac gac aag gaa gac taaaaaaaac tggggtcaca ctt             303
Ile Trp Asp Asp Lys Glu Asp
     55                  60
```

<210> 1704
<211> 60
<212> PRT
<213> Corynebacterium glutamicum

<400> 1704

```
Met Ala Lys Glu Asp Leu Lys Trp Phe Tyr Asp Leu Ala Thr Gly Lys
  1               5                  10                  15

Val Phe Gln Gly Lys Val Ser Gly Phe Glu Thr Arg Met Gly Pro Tyr
             20                  25                  30

Asp Thr Glu Glu Glu Ala His His Ala Ile Ser Ile Ala Ala Ala Arg
         35                  40                  45

Thr Lys Ala Ala Glu Ile Trp Asp Asp Lys Glu Asp
     50                  55                  60
```

<210> 1705
<211> 1938
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1915)
<223> RXA00321

<400> 1705

```
caaagacaac acaggttccc tatgaaaacg gggaacctgt ttcacctact ttttaatcac 60

gcttcacaat cacataagtc tttaaaggat ggatacaaca atg ggc cag cat cta   115
                                            Met Gly Gln His Leu
                                              1               5

gaa gtg gaa act aag ttt tcc gtc agt gaa tca act cag att cca caa   163
Glu Val Glu Thr Lys Phe Ser Val Ser Glu Ser Thr Gln Ile Pro Gln
                 10                  15                  20

ctt gag gct atc gca gaa gtc gac cac att gat cgc acc gaa atc cac   211
Leu Glu Ala Ile Ala Glu Val Asp His Ile Asp Arg Thr Glu Ile His
             25                  30                  35

caa cta agc gct gtt tac ttt gac acc gta gat ttg cgc ctc acc cgc   259
Gln Leu Ser Ala Val Tyr Phe Asp Thr Val Asp Leu Arg Leu Thr Arg
         40                  45                  50

gca aaa att acc ctc cgt cgc cgc acc ggt gga aac gat gcc ggc tgg   307
Ala Lys Ile Thr Leu Arg Arg Arg Thr Gly Gly Asn Asp Ala Gly Trp
```

```
     55                  60                  65

cac att aag ttc ccc gga acc atc ggt cgc cgt gaa gtc caa gcc cca   355
His Ile Lys Phe Pro Gly Thr Ile Gly Arg Arg Glu Val Gln Ala Pro
 70                  75                  80                  85

ctt gat ggc gaa ggc gca aca gaa acc ctc cct cca cgt gag ctc ttg   403
Leu Asp Gly Glu Gly Ala Thr Glu Thr Leu Pro Pro Arg Glu Leu Leu
                90                  95                 100

gga cac atc cga gcg ctg atc caa ggc cgt gag ctg acc cct atc gcc   451
Gly His Ile Arg Ala Leu Ile Gln Gly Arg Glu Leu Thr Pro Ile Ala
            105                 110                 115

cag gtg gat aat gaa cgc cac atg tct tac ctc gcg gat gag gac ggc   499
Gln Val Asp Asn Glu Arg His Met Ser Tyr Leu Ala Asp Glu Asp Gly
        120                 125                 130

gca gtc atc gca gaa ttc tgc gac gat cat gta tcc acc gtg tcc cac   547
Ala Val Ile Ala Glu Phe Cys Asp Asp His Val Ser Thr Val Ser His
    135                 140                 145

ctt cca ggt ggc gtg cgc aag cag tgg cgt gag tgg gaa ttc gaa ctc   595
Leu Pro Gly Gly Val Arg Lys Gln Trp Arg Glu Trp Glu Phe Glu Leu
150                 155                 160                 165

gct gat ggc acc ctc gcc gaa gaa gcc atc tca gta ctg ctg caa tct   643
Ala Asp Gly Thr Leu Ala Glu Glu Ala Ile Ser Val Leu Leu Gln Ser
                170                 175                 180

gca cag tca gtc ctg acc gca gct gga gct ttt gtc tcc aac agc cca   691
Ala Gln Ser Val Leu Thr Ala Ala Gly Ala Phe Val Ser Asn Ser Pro
            185                 190                 195

tcc aaa ctt gtt tcg gcg ctg gac gaa tca gtc aac cac gcg cca aag   739
Ser Lys Leu Val Ser Ala Leu Asp Glu Ser Val Asn His Ala Pro Lys
        200                 205                 210

cct cca cag atg gcg cag ctg gac aag aat gac cca gca cgt ggt gtt   787
Pro Pro Gln Met Ala Gln Leu Asp Lys Asn Asp Pro Ala Arg Gly Val
    215                 220                 225

ctt gca gca atc gca gcc aac gcc tca aag atc gcc gaa tac gat cct   835
Leu Ala Ala Ile Ala Ala Asn Ala Ser Lys Ile Ala Glu Tyr Asp Pro
230                 235                 240                 245

cga gta cgc gcc gat gaa tat gat tca gtc cac cag atg cgc gta gct   883
Arg Val Arg Ala Asp Glu Tyr Asp Ser Val His Gln Met Arg Val Ala
                250                 255                 260

acc cga gaa cta cgc agc cac ctc caa acc ttt gag ggc atc ctc ggc   931
Thr Arg Glu Leu Arg Ser His Leu Gln Thr Phe Glu Gly Ile Leu Gly
            265                 270                 275

ggc gaa gac tac ctc aac ctg gaa aag gaa ctg aag gtt ctc gcc aac   979
Gly Glu Asp Tyr Leu Asn Leu Glu Lys Glu Leu Lys Val Leu Ala Asn
        280                 285                 290

atc ttg ggt cgc gca cgc gat gct gaa gtt gtg gaa gag cgc ctc agc   1027
Ile Leu Gly Arg Ala Arg Asp Ala Glu Val Val Glu Glu Arg Leu Ser
    295                 300                 305
```

```
aac ctg att aac act gag gtt ggc gac tcc atc gag gag gag act aag   1075
Asn Leu Ile Asn Thr Glu Val Gly Asp Ser Ile Glu Glu Glu Thr Lys
310                 315                 320                 325

aag gaa ctg ctt gaa gat ctt ggt gca gaa tac cgt cgt gag cat gag   1123
Lys Glu Leu Leu Glu Asp Leu Gly Ala Glu Tyr Arg Arg Glu His Glu
                330                 335                 340

cga gta gtt cgt gcg ctg gat aat gat cgc tac act gat ctt ctt cag   1171
Arg Val Val Arg Ala Leu Asp Asn Asp Arg Tyr Thr Asp Leu Leu Gln
            345                 350                 355

gca ctg gaa aac ctc ctt gtt gat cca ccg ctg atc aca gaa gtc gaa   1219
Ala Leu Glu Asn Leu Leu Val Asp Pro Pro Leu Ile Thr Glu Val Glu
        360                 365                 370

gaa ccc gaa gct acc gaa gcc cct gag tcc gct gag act acc gag tcc   1267
Glu Pro Glu Ala Thr Glu Ala Pro Glu Ser Ala Glu Thr Thr Glu Ser
    375                 380                 385

act gac gtc tct gaa gca acc gaa gaa gca gac gca gaa gct gag tct   1315
Thr Asp Val Ser Glu Ala Thr Glu Glu Ala Asp Ala Glu Ala Glu Ser
390                 395                 400                 405

gtc gaa gaa gct act gag cag gaa gaa tca gca gac gcg cct gaa tct   1363
Val Glu Glu Ala Thr Glu Gln Glu Glu Ser Ala Asp Ala Pro Glu Ser
                410                 415                 420

gca gat ctg gac gct ctc gat gag gag tac tcc cct ggt tcc caa gcg   1411
Ala Asp Leu Asp Ala Leu Asp Glu Glu Tyr Ser Pro Gly Ser Gln Ala
            425                 430                 435

ccg gtg gag gag ccg aag gaa ccg aag aag gtt gat gct gct ctc gta   1459
Pro Val Glu Glu Pro Lys Glu Pro Lys Lys Val Asp Ala Ala Leu Val
        440                 445                 450

ctt cta gag cac ctt gat aag gcg cac gtg aag ctc gtc aag ctg gaa   1507
Leu Leu Glu His Leu Asp Lys Ala His Val Lys Leu Val Lys Leu Glu
    455                 460                 465

aag aag gct cgc tca cag tgg gat gat ctc agc att ccg atg ctg gag   1555
Lys Lys Ala Arg Ser Gln Trp Asp Asp Leu Ser Ile Pro Met Leu Glu
470                 475                 480                 485

cgg gaa gaa aac ttc cac aac ctg cgc aag gct gcc aag aag ctt cgc   1603
Arg Glu Glu Asn Phe His Asn Leu Arg Lys Ala Ala Lys Lys Leu Arg
                490                 495                 500

tac agt gca gag gca gtg ggc aaa gca acc acc gtt gag acg aag aaa   1651
Tyr Ser Ala Glu Ala Val Gly Lys Ala Thr Thr Val Glu Thr Lys Lys
            505                 510                 515

ctg tac aag gcg tgc agt ggt ttg cag tca gtt ctt ggc gat tac caa   1699
Leu Tyr Lys Ala Cys Ser Gly Leu Gln Ser Val Leu Gly Asp Tyr Gln
        520                 525                 530

gat gcc att act tcc cgt aat gag ctg ttg cgc cga gct cag gtt gcc   1747
Asp Ala Ile Thr Ser Arg Asn Glu Leu Leu Arg Arg Ala Gln Val Ala
    535                 540                 545
```

```
cgc cgc caa ggc cgg gat acc ttc gca tac gga atc ctc tac cag cac   1795
Arg Arg Gln Gly Arg Asp Thr Phe Ala Tyr Gly Ile Leu Tyr Gln His
550                 555                 560                 565

gaa caa acc ctg tcg agg gaa tac ctg act ggt tat tcc gat gcg ttc   1843
Glu Gln Thr Leu Ser Arg Glu Tyr Leu Thr Gly Tyr Ser Asp Ala Phe
                570                 575                 580

aag agc gta gaa aaa gcc tat gca aag ctg gct gaa gat acc gcc aag   1891
Lys Ser Val Glu Lys Ala Tyr Ala Lys Leu Ala Glu Asp Thr Ala Lys
            585                 590                 595

cgt tca aag aag aac aag cgt aag taaacgcagg caataaaaaa ctg         1938
Arg Ser Lys Lys Asn Lys Arg Lys
        600                 605
```

<210> 1706
<211> 605
<212> PRT
<213> Corynebacterium glutamicum

<400> 1706

```
Met Gly Gln His Leu Glu Val Glu Thr Lys Phe Ser Val Ser Glu Ser
  1               5                  10                  15

Thr Gln Ile Pro Gln Leu Glu Ala Ile Ala Glu Val Asp His Ile Asp
             20                  25                  30

Arg Thr Glu Ile His Gln Leu Ser Ala Val Tyr Phe Asp Thr Val Asp
         35                  40                  45

Leu Arg Leu Thr Arg Ala Lys Ile Thr Leu Arg Arg Arg Thr Gly Gly
     50                  55                  60

Asn Asp Ala Gly Trp His Ile Lys Phe Pro Gly Thr Ile Gly Arg Arg
 65                  70                  75                  80

Glu Val Gln Ala Pro Leu Asp Gly Glu Gly Ala Thr Glu Thr Leu Pro
                 85                  90                  95

Pro Arg Glu Leu Leu Gly His Ile Arg Ala Leu Ile Gln Gly Arg Glu
            100                 105                 110

Leu Thr Pro Ile Ala Gln Val Asp Asn Glu Arg His Met Ser Tyr Leu
        115                 120                 125

Ala Asp Glu Asp Gly Ala Val Ile Ala Glu Phe Cys Asp Asp His Val
    130                 135                 140

Ser Thr Val Ser His Leu Pro Gly Gly Val Arg Lys Gln Trp Arg Glu
145                 150                 155                 160

Trp Glu Phe Glu Leu Ala Asp Gly Thr Leu Ala Glu Glu Ala Ile Ser
                165                 170                 175

Val Leu Leu Gln Ser Ala Gln Ser Val Leu Thr Ala Ala Gly Ala Phe
            180                 185                 190

Val Ser Asn Ser Pro Ser Lys Leu Val Ser Ala Leu Asp Glu Ser Val
        195                 200                 205
```

```
Asn His Ala Pro Lys Pro Pro Gln Met Ala Gln Leu Asp Lys Asn Asp
    210                 215                 220

Pro Ala Arg Gly Val Leu Ala Ala Ile Ala Ala Asn Ala Ser Lys Ile
225                 230                 235                 240

Ala Glu Tyr Asp Pro Arg Val Arg Ala Asp Glu Tyr Asp Ser Val His
                245                 250                 255

Gln Met Arg Val Ala Thr Arg Glu Leu Arg Ser His Leu Gln Thr Phe
            260                 265                 270

Glu Gly Ile Leu Gly Gly Glu Asp Tyr Leu Asn Leu Glu Lys Glu Leu
        275                 280                 285

Lys Val Leu Ala Asn Ile Leu Gly Arg Ala Arg Asp Ala Glu Val Val
    290                 295                 300

Glu Glu Arg Leu Ser Asn Leu Ile Asn Thr Glu Val Gly Asp Ser Ile
305                 310                 315                 320

Glu Glu Glu Thr Lys Lys Glu Leu Leu Glu Asp Leu Gly Ala Glu Tyr
                325                 330                 335

Arg Arg Glu His Glu Arg Val Val Arg Ala Leu Asp Asn Asp Arg Tyr
            340                 345                 350

Thr Asp Leu Leu Gln Ala Leu Glu Asn Leu Leu Val Asp Pro Pro Leu
        355                 360                 365

Ile Thr Glu Val Glu Glu Pro Glu Ala Thr Glu Ala Pro Glu Ser Ala
    370                 375                 380

Glu Thr Thr Glu Ser Thr Asp Val Ser Glu Ala Thr Glu Glu Ala Asp
385                 390                 395                 400

Ala Glu Ala Glu Ser Val Glu Glu Ala Thr Glu Gln Glu Glu Ser Ala
                405                 410                 415

Asp Ala Pro Glu Ser Ala Asp Leu Asp Ala Leu Asp Glu Glu Tyr Ser
            420                 425                 430

Pro Gly Ser Gln Ala Pro Val Glu Glu Pro Lys Glu Pro Lys Lys Val
        435                 440                 445

Asp Ala Ala Leu Val Leu Leu Glu His Leu Asp Lys Ala His Val Lys
    450                 455                 460

Leu Val Lys Leu Glu Lys Lys Ala Arg Ser Gln Trp Asp Asp Leu Ser
465                 470                 475                 480

Ile Pro Met Leu Glu Arg Glu Glu Asn Phe His Asn Leu Arg Lys Ala
                485                 490                 495

Ala Lys Lys Leu Arg Tyr Ser Ala Glu Ala Val Gly Lys Ala Thr Thr
            500                 505                 510

Val Glu Thr Lys Lys Leu Tyr Lys Ala Cys Ser Gly Leu Gln Ser Val
        515                 520                 525
```

```
Leu Gly Asp Tyr Gln Asp Ala Ile Thr Ser Arg Asn Glu Leu Leu Arg
    530                 535                 540

Arg Ala Gln Val Ala Arg Arg Gln Gly Arg Asp Thr Phe Ala Tyr Gly
545                 550                 555                 560

Ile Leu Tyr Gln His Glu Gln Thr Leu Ser Arg Glu Tyr Leu Thr Gly
                565                 570                 575

Tyr Ser Asp Ala Phe Lys Ser Val Glu Lys Ala Tyr Ala Lys Leu Ala
            580                 585                 590

Glu Asp Thr Ala Lys Arg Ser Lys Lys Asn Lys Arg Lys
        595                 600                 605


<210> 1707
<211> 1227
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1204)
<223> RXA00322

<400> 1707
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gcaccgaaat tagaacactc ctacgaataa ggaaaccgca atg act ctc tcc cac   115
                                              Met Thr Leu Ser His
                                                1               5

ttc tcc gac aac gtc acc gac gca caa gac tct tac cgt cag att tta   163
Phe Ser Asp Asn Val Thr Asp Ala Gln Asp Ser Tyr Arg Gln Ile Leu
                10                  15                  20

gaa gaa agc atc atc agc cac cta ggt ttc tgt gcg ctt cgt ggg tgg   211
Glu Glu Ser Ile Ile Ser His Leu Gly Phe Cys Ala Leu Arg Gly Trp
            25                  30                  35

act ccc gcc gat ctc cgc cat gag ttt tcc gcc gat att gat cca ctc   259
Thr Pro Ala Asp Leu Arg His Glu Phe Ser Ala Asp Ile Asp Pro Leu
        40                  45                  50

ctg ttt cac gcg cta cct gag att gct tac tcc tgc tcc gat gag atg   307
Leu Phe His Ala Leu Pro Glu Ile Ala Tyr Ser Cys Ser Asp Glu Met
    55                  60                  65

tac aca ctg tgg gtg aac gga acg cgt gcc gcc gaa act agc cac ttg   355
Tyr Thr Leu Trp Val Asn Gly Thr Arg Ala Ala Glu Thr Ser His Leu
70                  75                  80                  85

ccg gtg atg acc ctg gag aag att ctc acc gag cta ccg aag cta agt   403
Pro Val Met Thr Leu Glu Lys Ile Leu Thr Glu Leu Pro Lys Leu Ser
                90                  95                  100

acc ttg cct gac tgg gca atg ctc gca gag ctc cac gcc tta gac aat   451
Thr Leu Pro Asp Trp Ala Met Leu Ala Glu Leu His Ala Leu Asp Asn
            105                 110                 115
```

```
caa gac acc agc cca atg acc ccg gca cag gcc aaa gcg cat cat cgt   499
Gln Asp Thr Ser Pro Met Thr Pro Ala Gln Ala Lys Ala His His Arg
        120                 125                 130

atc acc gca ctt ttg aaa aag gca gag tcc acc aac ttc gaa gaa gaa   547
Ile Thr Ala Leu Leu Lys Lys Ala Glu Ser Thr Asn Phe Glu Glu Glu
    135                 140                 145

gcc gaa gca ttg atc ctt aaa gca gag aca ctt cga cag cag tac cgg   595
Ala Glu Ala Leu Ile Leu Lys Ala Glu Thr Leu Arg Gln Gln Tyr Arg
150                 155                 160                 165

att gaa tca ctg ctg att aat tcc tat gac caa gat gtc caa gct cga   643
Ile Glu Ser Leu Leu Ile Asn Ser Tyr Asp Gln Asp Val Gln Ala Arg
                170                 175                 180

tct tct acg att cgt gca tct cgg gtg tat ctg gaa gct cca tgg atc   691
Ser Ser Thr Ile Arg Ala Ser Arg Val Tyr Leu Glu Ala Pro Trp Ile
            185                 190                 195

cga cac caa tac aaa ctg ctc aat gcc att gct cgg gtg cat tcc agc   739
Arg His Gln Tyr Lys Leu Leu Asn Ala Ile Ala Arg Val His Ser Ser
        200                 205                 210

gaa gcg ctg ctg atc acc aaa tct ggc atc tgc acc ctc ttc ggc gag   787
Glu Ala Leu Leu Ile Thr Lys Ser Gly Ile Cys Thr Leu Phe Gly Glu
    215                 220                 225

caa gat gac gta gcc cac att att gat ctg ttc aac agt ctt aat cga   835
Gln Asp Asp Val Ala His Ile Ile Asp Leu Phe Asn Ser Leu Asn Arg
230                 235                 240                 245

caa cgt gcc cac ttc atg aaa acg tca gca ggt gcc cga att gcc caa   883
Gln Arg Ala His Phe Met Lys Thr Ser Ala Gly Ala Arg Ile Ala Gln
                250                 255                 260

tta aat ggc gaa aca agc tca tat cgc cgt agt ttt atg atc tcc tac   931
Leu Asn Gly Glu Thr Ser Ser Tyr Arg Arg Ser Phe Met Ile Ser Tyr
            265                 270                 275

gcc agc caa atc tct aga ctt ctc atc tca gca aaa gag gat gca ttc   979
Ala Ser Gln Ile Ser Arg Leu Leu Ile Ser Ala Lys Glu Asp Ala Phe
        280                 285                 290

aac gaa cta gct ggt cag gca cca cta gct cac agc gcc atc gtt cct   1027
Asn Glu Leu Ala Gly Gln Ala Pro Leu Ala His Ser Ala Ile Val Pro
    295                 300                 305

gtc cta gag aac aga agt gtg agg tca aag gaa gca ctg aag gaa acc   1075
Val Leu Glu Asn Arg Ser Val Arg Ser Lys Glu Ala Leu Lys Glu Thr
310                 315                 320                 325

ttc ccg aat atg cgg aca atg acc ttc aaa tcg acc aac cga cga ggc   1123
Phe Pro Asn Met Arg Thr Met Thr Phe Lys Ser Thr Asn Arg Arg Gly
                330                 335                 340

att att gac gga ttt aat gct gcc aat gaa tcc cac ctt ggc ggg gaa   1171
Ile Ile Asp Gly Phe Asn Ala Ala Asn Glu Ser His Leu Gly Gly Glu
            345                 350                 355

tct gcc agc ttg gaa gac tca aca ttc atg ttc tagagcgggt gaaagcccca 1224
```

```
Ser Ala Ser Leu Glu Asp Ser Thr Phe Met Phe
        360                 365

ttt                                                                    1227


<210> 1708
<211> 368
<212> PRT
<213> Corynebacterium glutamicum

<400> 1708
Met Thr Leu Ser His Phe Ser Asp Asn Val Thr Asp Ala Gln Asp Ser
  1               5                  10                  15

Tyr Arg Gln Ile Leu Glu Glu Ser Ile Ile Ser His Leu Gly Phe Cys
             20                  25                  30

Ala Leu Arg Gly Trp Thr Pro Ala Asp Leu Arg His Glu Phe Ser Ala
         35                  40                  45

Asp Ile Asp Pro Leu Leu Phe His Ala Leu Pro Glu Ile Ala Tyr Ser
     50                  55                  60

Cys Ser Asp Glu Met Tyr Thr Leu Trp Val Asn Gly Thr Arg Ala Ala
 65                  70                  75                  80

Glu Thr Ser His Leu Pro Val Met Thr Leu Glu Lys Ile Leu Thr Glu
                 85                  90                  95

Leu Pro Lys Leu Ser Thr Leu Pro Asp Trp Ala Met Leu Ala Glu Leu
            100                 105                 110

His Ala Leu Asp Asn Gln Asp Thr Ser Pro Met Thr Pro Ala Gln Ala
        115                 120                 125

Lys Ala His His Arg Ile Thr Ala Leu Leu Lys Lys Ala Glu Ser Thr
    130                 135                 140

Asn Phe Glu Glu Glu Ala Glu Ala Leu Ile Leu Lys Ala Glu Thr Leu
145                 150                 155                 160

Arg Gln Gln Tyr Arg Ile Glu Ser Leu Leu Ile Asn Ser Tyr Asp Gln
                165                 170                 175

Asp Val Gln Ala Arg Ser Ser Thr Ile Arg Ala Ser Arg Val Tyr Leu
            180                 185                 190

Glu Ala Pro Trp Ile Arg His Gln Tyr Lys Leu Leu Asn Ala Ile Ala
        195                 200                 205

Arg Val His Ser Ser Glu Ala Leu Leu Ile Thr Lys Ser Gly Ile Cys
    210                 215                 220

Thr Leu Phe Gly Glu Gln Asp Asp Val Ala His Ile Ile Asp Leu Phe
225                 230                 235                 240

Asn Ser Leu Asn Arg Gln Arg Ala His Phe Met Lys Thr Ser Ala Gly
                245                 250                 255

Ala Arg Ile Ala Gln Leu Asn Gly Glu Thr Ser Ser Tyr Arg Arg Ser
```

```
            260                 265                 270

Phe Met Ile Ser Tyr Ala Ser Gln Ile Ser Arg Leu Leu Ile Ser Ala
        275                 280                 285

Lys Glu Asp Ala Phe Asn Glu Leu Ala Gly Gln Ala Pro Leu Ala His
    290                 295                 300

Ser Ala Ile Val Pro Val Leu Glu Asn Arg Ser Val Arg Ser Lys Glu
305                 310                 315                 320

Ala Leu Lys Glu Thr Phe Pro Asn Met Arg Thr Met Thr Phe Lys Ser
                325                 330                 335

Thr Asn Arg Arg Gly Ile Ile Asp Gly Phe Asn Ala Ala Asn Glu Ser
            340                 345                 350

His Leu Gly Gly Glu Ser Ala Ser Leu Glu Asp Ser Thr Phe Met Phe
        355                 360                 365
```

Test Copy - Not for Distribution

<210> 1709
<211> 768
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(745)
<223> RXA00325

<400> 1709

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accgcggttg cggccacgca ggctcacaaa ggacaccact atg aca agc att att   115
                                              Met Thr Ser Ile Ile
                                                1               5

gca agc aac agc gac cta tcg gag gcg ctg cgc acc cac act gcg cag   163
Ala Ser Asn Ser Asp Leu Ser Glu Ala Leu Arg Thr His Thr Ala Gln
                10                  15                  20

gcc cat gaa gag gcc gag cac tca acg ttt atg aat gat ctg ctc acc   211
Ala His Glu Glu Ala Glu His Ser Thr Phe Met Asn Asp Leu Leu Thr
            25                  30                  35

ggg aag ctc gat gcg cag gca ttt atc aag ttg cag gag caa tca tgg   259
Gly Lys Leu Asp Ala Gln Ala Phe Ile Lys Leu Gln Glu Gln Ser Trp
        40                  45                  50

ttg ttc tac acc gct ttg gaa gct gca gct cgt gca tgt gca gag gat   307
Leu Phe Tyr Thr Ala Leu Glu Ala Ala Ala Arg Ala Cys Ala Glu Asp
    55                  60                  65

tcc cgt gcg gct ggt ctg ctg gac cca cgc ctc gag cgc aag gaa acg   355
Ser Arg Ala Ala Gly Leu Leu Asp Pro Arg Leu Glu Arg Lys Glu Thr
70                  75                  80                  85
```

```
ttg gaa gct gat ctg gat aag ctg cac gaa aac acc acc tgg cgt gac   403
Leu Glu Ala Asp Leu Asp Lys Leu His Glu Asn Thr Thr Trp Arg Asp
                 90                  95                 100

aac gtc acg gcc act gca gcg aca gcg tct tat gtg gaa cgt ctt gaa   451
Asn Val Thr Ala Thr Ala Ala Thr Ala Ser Tyr Val Glu Arg Leu Glu
            105                 110                 115

agc atc gaa gcg gcc aag gat ttc cct cgt ttg gtt gct cat cac tat   499
Ser Ile Glu Ala Ala Lys Asp Phe Pro Arg Leu Val Ala His His Tyr
        120                 125                 130

gtc cgc tac ctg ggt gat ttg tcc ggt ggg cag gtt att gca cgt ctg   547
Val Arg Tyr Leu Gly Asp Leu Ser Gly Gly Gln Val Ile Ala Arg Leu
    135                 140                 145

gtg aac agg gaa tat gga gtt tcg gaa gag gcg ttg agc ttc tac tgc   595
Val Asn Arg Glu Tyr Gly Val Ser Glu Glu Ala Leu Ser Phe Tyr Cys
150                 155                 160                 165

ttt gaa gat ctt ggc aag ctc aaa ccg tac aag gat aat tac cgt gca   643
Phe Glu Asp Leu Gly Lys Leu Lys Pro Tyr Lys Asp Asn Tyr Arg Ala
                170                 175                 180

gag ctt gat gct ttg gaa tta aca gca gag gag cgt gct gcg ttg ctg   691
Glu Leu Asp Ala Leu Glu Leu Thr Ala Glu Glu Arg Ala Ala Leu Leu
            185                 190                 195

gat gaa gca tct gat gcg ttc agg ttt aat cag caa gtt ttt cag gct   739
Asp Glu Ala Ser Asp Ala Phe Arg Phe Asn Gln Gln Val Phe Gln Ala
        200                 205                 210

ctt gct taaccgaagg tgaagtcttg gcg                                768
Leu Ala
    215


<210> 1710
<211> 215
<212> PRT
<213> Corynebacterium glutamicum

<400> 1710
Met Thr Ser Ile Ile Ala Ser Asn Ser Asp Leu Ser Glu Ala Leu Arg
  1               5                  10                  15

Thr His Thr Ala Gln Ala His Glu Glu Ala Glu His Ser Thr Phe Met
             20                  25                  30

Asn Asp Leu Leu Thr Gly Lys Leu Asp Ala Gln Ala Phe Ile Lys Leu
         35                  40                  45

Gln Glu Gln Ser Trp Leu Phe Tyr Thr Ala Leu Glu Ala Ala Ala Arg
     50                  55                  60

Ala Cys Ala Glu Asp Ser Arg Ala Ala Gly Leu Leu Asp Pro Arg Leu
 65                  70                  75                  80

Glu Arg Lys Glu Thr Leu Glu Ala Asp Leu Asp Lys Leu His Glu Asn
                 85                  90                  95
```

```
Thr Thr Trp Arg Asp Asn Val Thr Ala Thr Ala Ala Thr Ala Ser Tyr
            100                 105                 110

Val Glu Arg Leu Glu Ser Ile Glu Ala Ala Lys Asp Phe Pro Arg Leu
        115                 120                 125

Val Ala His His Tyr Val Arg Tyr Leu Gly Asp Leu Ser Gly Gly Gln
    130                 135                 140

Val Ile Ala Arg Leu Val Asn Arg Glu Tyr Gly Val Ser Glu Glu Ala
145                 150                 155                 160

Leu Ser Phe Tyr Cys Phe Glu Asp Leu Gly Lys Leu Lys Pro Tyr Lys
                165                 170                 175

Asp Asn Tyr Arg Ala Glu Leu Asp Ala Leu Glu Leu Thr Ala Glu Glu
            180                 185                 190

Arg Ala Ala Leu Leu Asp Glu Ala Ser Asp Ala Phe Arg Phe Asn Gln
        195                 200                 205

Gln Val Phe Gln Ala Leu Ala
    210                 215


<210> 1711
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(580)
<223> RXA00326

<400> 1711
cctgatcttt gcccctaagt ggtttacggg ctggaaaatg gtacgtagtc tcgggtgtaa 60

agcacacttc ggtactcgac aggaagttag gaattccacc atg gca atc aag ctg   115
                                              Met Ala Ile Lys Leu
                                                1               5

tcc att gac cta tca gat gca aca ttc gca gaa ctt tcg gca gtc atc   163
Ser Ile Asp Leu Ser Asp Ala Thr Phe Ala Glu Leu Ser Ala Val Ile
                10                  15                  20

ggt tac gca cat cag ttg ggt gtt gat gcg gat gag aag ctc acc ttt   211
Gly Tyr Ala His Gln Leu Gly Val Asp Ala Asp Glu Lys Leu Thr Phe
            25                  30                  35

gaa ggt aca gtc ctt aac att gaa ttc gac ggc gac ctt cag ttt gat   259
Glu Gly Thr Val Leu Asn Ile Glu Phe Asp Gly Asp Leu Gln Phe Asp
        40                  45                  50

gat gtt ttt gat gcc ttt gat gag gcg gaa att gag ctc gac aac cct   307
Asp Val Phe Asp Ala Phe Asp Glu Ala Glu Ile Glu Leu Asp Asn Pro
    55                  60                  65

cgc gaa gac ggc ccc atc tac gca gat gat ctg atc gat gag gat gag   355
Arg Glu Asp Gly Pro Ile Tyr Ala Asp Asp Leu Ile Asp Glu Asp Glu
70                  75                  80                  85
```

```
gac tac cgc gca cag acc aag agc cag atc aac gac gag gtt atc aac   403
Asp Tyr Arg Ala Gln Thr Lys Ser Gln Ile Asn Asp Glu Val Ile Asn
                 90                  95                 100

gag atc cgc gat ggt att tca agc ttc gtt gat ggc atc gta aat ggc   451
Glu Ile Arg Asp Gly Ile Ser Ser Phe Val Asp Gly Ile Val Asn Gly
            105                 110                 115

ctt ggc cag ggt cgc cgc ggt gga cgt tac ggt gat ttc ggt ggg cca   499
Leu Gly Gln Gly Arg Arg Gly Gly Arg Tyr Gly Asp Phe Gly Gly Pro
        120                 125                 130

cgc ggc cct cgc ggt cca cgc aat gac ggt cca ttc ggc cca ttt gga   547
Arg Gly Pro Arg Gly Pro Arg Asn Asp Gly Pro Phe Gly Pro Phe Gly
    135                 140                 145

cca ttc ggt ccg gga tac cgc ggt ccg cgt ttc tagcggttac ggtcgggttt 600
Pro Phe Gly Pro Gly Tyr Arg Gly Pro Arg Phe
150                 155                 160

tag                                                               603


<210> 1712
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 1712
Met Ala Ile Lys Leu Ser Ile Asp Leu Ser Asp Ala Thr Phe Ala Glu
  1               5                  10                  15

Leu Ser Ala Val Ile Gly Tyr Ala His Gln Leu Gly Val Asp Ala Asp
             20                  25                  30

Glu Lys Leu Thr Phe Glu Gly Thr Val Leu Asn Ile Glu Phe Asp Gly
         35                  40                  45

Asp Leu Gln Phe Asp Asp Val Phe Asp Ala Phe Asp Glu Ala Glu Ile
     50                  55                  60

Glu Leu Asp Asn Pro Arg Glu Asp Gly Pro Ile Tyr Ala Asp Asp Leu
 65                  70                  75                  80

Ile Asp Glu Asp Glu Asp Tyr Arg Ala Gln Thr Lys Ser Gln Ile Asn
                 85                  90                  95

Asp Glu Val Ile Asn Glu Ile Arg Asp Gly Ile Ser Ser Phe Val Asp
            100                 105                 110

Gly Ile Val Asn Gly Leu Gly Gln Gly Arg Arg Gly Gly Arg Tyr Gly
        115                 120                 125

Asp Phe Gly Gly Pro Arg Gly Pro Arg Gly Pro Arg Asn Asp Gly Pro
    130                 135                 140

Phe Gly Pro Phe Gly Pro Phe Gly Pro Gly Tyr Arg Gly Pro Arg Phe
145                 150                 155                 160
```

<210> 1713
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(571)
<223> RXA00336

<400> 1713
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gcagtatccg ccctctacat gtttggattt gattgtaaca atg gca aag ccg aag 115
Met Ala Lys Pro Lys
1 5

aga agt tgg ctt gac gga ccc gaa att cca gct gat ttt gac gat cct 163
Arg Ser Trp Leu Asp Gly Pro Glu Ile Pro Ala Asp Phe Asp Asp Pro
10 15 20

gat gca ccc ggc agg tgg cct ggc gaa aag ttg ggg ctt cct caa gaa 211
Asp Ala Pro Gly Arg Trp Pro Gly Glu Lys Leu Gly Leu Pro Gln Glu
25 30 35

ggg gcc ggc tct ctg tcc tca gtg gct cgt cgt atc ggc ggg gtc tgc 259
Gly Ala Gly Ser Leu Ser Ser Val Ala Arg Arg Ile Gly Gly Val Cys
40 45 50

gtg gac tgg ggt gtt tcc tgg gtt att gct att gtg ctg tcc aat ttc 307
Val Asp Trp Gly Val Ser Trp Val Ile Ala Ile Val Leu Ser Asn Phe
55 60 65

acg gat gtg ctg ggc gat gta gcg aca tcc acg ctc att att ttc gtg 355
Thr Asp Val Leu Gly Asp Val Ala Thr Ser Thr Leu Ile Ile Phe Val
70 75 80 85

atc ctg ggt tgg ctt acc ggt tgg atc ttt gct cgc acc cca ggt cat 403
Ile Leu Gly Trp Leu Thr Gly Trp Ile Phe Ala Arg Thr Pro Gly His
90 95 100

gcc gtg ttt ggc atg ggc ctt gcg cgt gtg gat gca gag gaa cgt gtg 451
Ala Val Phe Gly Met Gly Leu Ala Arg Val Asp Ala Glu Glu Arg Val
105 110 115

ggc tgg tgg cgt gcg ctg gtt cgc cca ctg ctg acg atc ttg att ctg 499
Gly Trp Trp Arg Ala Leu Val Arg Pro Leu Leu Thr Ile Leu Ile Leu
120 125 130

cct gcc gtg atg gtg gat gct gac ggc cgt ggg ctc cac gac aag gca 547
Pro Ala Val Met Val Asp Ala Asp Gly Arg Gly Leu His Asp Lys Ala
135 140 145

acg gga act gca gtt atc cgc ggg taatttgtct tgagtgaaat tta 594
Thr Gly Thr Ala Val Ile Arg Gly
150 155

<210> 1714
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 1714
Met Ala Lys Pro Lys Arg Ser Trp Leu Asp Gly Pro Glu Ile Pro Ala
1 5 10 15

Asp Phe Asp Asp Pro Asp Ala Pro Gly Arg Trp Pro Gly Glu Lys Leu
20 25 30

Gly Leu Pro Gln Glu Gly Ala Gly Ser Leu Ser Ser Val Ala Arg Arg
35 40 45

Ile Gly Gly Val Cys Val Asp Trp Gly Val Ser Trp Val Ile Ala Ile
50 55 60

Val Leu Ser Asn Phe Thr Asp Val Leu Gly Asp Val Ala Thr Ser Thr
65 70 75 80

Leu Ile Ile Phe Val Ile Leu Gly Trp Leu Thr Gly Trp Ile Phe Ala
85 90 95

Arg Thr Pro Gly His Ala Val Phe Gly Met Gly Leu Ala Arg Val Asp
100 105 110

Ala Glu Glu Arg Val Gly Trp Trp Arg Ala Leu Val Arg Pro Leu Leu
115 120 125

Thr Ile Leu Ile Leu Pro Ala Val Met Val Asp Ala Asp Gly Arg Gly
130 135 140

Leu His Asp Lys Ala Thr Gly Thr Ala Val Ile Arg Gly
145 150 155

<210> 1715
<211> 525
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(525)
<223> RXA00337

<400> 1715
gat gtg gag gga ggc gtc gaa aag cat tct tta agc act gcg gac att 48
Asp Val Glu Gly Gly Val Glu Lys His Ser Leu Ser Thr Ala Asp Ile
1 5 10 15

gca gct cgc gca cac gcc cat atg aaa tcc cat gat gtt ttg ggg cgg 96
Ala Ala Arg Ala His Ala His Met Lys Ser His Asp Val Leu Gly Arg
20 25 30

cag act acg ccg cct cag ccg gag ggc ggc gtt gct gcc cgg ttg ggc 144
Gln Thr Thr Pro Pro Gln Pro Glu Gly Gly Val Ala Ala Arg Leu Gly
35 40 45

ggg att gcg tgg aca atg atc cat aag caa atg ctt tcg cgt gac aca 192

```
Gly Ile Ala Trp Thr Met Ile His Lys Gln Met Leu Ser Arg Asp Thr
     50                  55                  60

aaa ggc ctg gat atc acc gtg ttg agc acc att cct gag ggg gtg ggg   240
Lys Gly Leu Asp Ile Thr Val Leu Ser Thr Ile Pro Glu Gly Val Gly
 65                  70                  75                  80

ctg ggt gaa aat tcc gcc atg gat gtg gcg ctc gca ttg gcg ctg tat   288
Leu Gly Glu Asn Ser Ala Met Asp Val Ala Leu Ala Leu Ala Leu Tyr
                85                  90                  95

cgg gaa aat att gag gaa gcc ccc acg aag gcg cgc att gcg gac att   336
Arg Glu Asn Ile Glu Glu Ala Pro Thr Lys Ala Arg Ile Ala Asp Ile
            100                 105                 110

tgt tcg cag tcc gca ttc atg ttc agt gag act tca gtg ttg cgt gcg   384
Cys Ser Gln Ser Ala Phe Met Phe Ser Glu Thr Ser Val Leu Arg Ala
        115                 120                 125

cgg cac acc gag gcg ttg cgg ggt gaa act gga cac att tcg gtg gtt   432
Arg His Thr Glu Ala Leu Arg Gly Glu Thr Gly His Ile Ser Val Val
    130                 135                 140

gat tac gcc gat ggt tcg gtc act cag gcg cca cat ccg gtg agt cgt   480
Asp Tyr Ala Asp Gly Ser Val Thr Gln Ala Pro His Pro Val Ser Arg
145                 150                 155                 160

tcc gct ggt ttg tcg gca ttt gtt gct gct gcg caa act gaa act        525
Ser Ala Gly Leu Ser Ala Phe Val Ala Ala Ala Gln Thr Glu Thr
                165                 170                 175
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<210> 1716
<211> 175
<212> PRT
<213> Corynebacterium glutamicum

<400> 1716

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Asp Val Glu Gly Gly Val Glu Lys His Ser Leu Ser Thr Ala Asp Ile
  1               5                  10                  15

Ala Ala Arg Ala His Ala His Met Lys Ser His Asp Val Leu Gly Arg
             20                  25                  30

Gln Thr Thr Pro Pro Gln Pro Glu Gly Gly Val Ala Ala Arg Leu Gly
         35                  40                  45

Gly Ile Ala Trp Thr Met Ile His Lys Gln Met Leu Ser Arg Asp Thr
     50                  55                  60

Lys Gly Leu Asp Ile Thr Val Leu Ser Thr Ile Pro Glu Gly Val Gly
 65                  70                  75                  80

Leu Gly Glu Asn Ser Ala Met Asp Val Ala Leu Ala Leu Ala Leu Tyr
                85                  90                  95

Arg Glu Asn Ile Glu Glu Ala Pro Thr Lys Ala Arg Ile Ala Asp Ile
            100                 105                 110

Cys Ser Gln Ser Ala Phe Met Phe Ser Glu Thr Ser Val Leu Arg Ala
        115                 120                 125
```

```
Arg His Thr Glu Ala Leu Arg Gly Glu Thr Gly His Ile Ser Val Val
    130                 135                 140

Asp Tyr Ala Asp Gly Ser Val Thr Gln Ala Pro His Pro Val Ser Arg
145                 150                 155                 160

Ser Ala Gly Leu Ser Ala Phe Val Ala Ala Ala Gln Thr Glu Thr
                165                 170                 175


<210> 1717
<211> 840
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(817)
<223> RXA00339

<400> 1717
acaggttgaa gttgatgtga tttcgatccg cacagacccc tggaccatgt ctgcgcgagc 60

agtgaactaa attcttgaga actaaaaaag gagaacttca atg aag ctg gac cca   115
                                            Met Lys Leu Asp Pro
                                              1               5

tct ctg cac aaa acc ctg ctg cag ctc gcc acc acc ctg cgc acc caa   163
Ser Leu His Lys Thr Leu Leu Gln Leu Ala Thr Thr Leu Arg Thr Gln
                10                  15                  20

aac gcc aac tcc gca ccg aag acc acc ccg gag cag gaa gct gta gac   211
Asn Ala Asn Ser Ala Pro Lys Thr Thr Pro Glu Gln Glu Ala Val Asp
            25                  30                  35

aag gct gtc gct gaa ctt tcc cgc aac cgc gac gct gca tcc gct gga   259
Lys Ala Val Ala Glu Leu Ser Arg Asn Arg Asp Ala Ala Ser Ala Gly
        40                  45                  50

caa atg gct gtc gat gac atg gaa aac gaa atc ctg cgc att cag tcc   307
Gln Met Ala Val Asp Asp Met Glu Asn Glu Ile Leu Arg Ile Gln Ser
    55                  60                  65

gac gaa cgc aaa ctg cgc cgc cgc aag aaa gac ggc cag gac gca ctc   355
Asp Glu Arg Lys Leu Arg Arg Arg Lys Lys Asp Gly Gln Asp Ala Leu
70                  75                  80                  85

ggt gca gaa act gac gaa gag cgt cgc cgc gac ctc aac cac gac gtc   403
Gly Ala Glu Thr Asp Glu Glu Arg Arg Arg Asp Leu Asn His Asp Val
                90                  95                  100

tac act gcg aag tcc cgc atc gct gac ctc atg agc gaa ctg caa gaa   451
Tyr Thr Ala Lys Ser Arg Ile Ala Asp Leu Met Ser Glu Leu Gln Glu
            105                 110                 115

gct cac aat gaa atc cat gcg ctg cgc aac aac cgc gac ctc gca cag   499
Ala His Asn Glu Ile His Ala Leu Arg Asn Asn Arg Asp Leu Ala Gln
        120                 125                 130

tct cgc gtc aaa gac acc gaa cgc aaa gtt gcc gac gcc cgc gca gcc   547
```

```
Ser Arg Val Lys Asp Thr Glu Arg Lys Val Ala Asp Ala Arg Ala Ala
    135                 140                 145

gca gaa gcc gcc gca gca gca acc cca gaa ggt gaa gac cca gca gta   595
Ala Glu Ala Ala Ala Ala Ala Thr Pro Glu Gly Glu Asp Pro Ala Val
150                 155                 160                 165

gtc atc gca cac ctg gaa gag aaa ctt ccc tcc gaa gca ctg gca gaa   643
Val Ile Ala His Leu Glu Glu Lys Leu Pro Ser Glu Ala Leu Ala Glu
                170                 175                 180

ttc cat gca caa cgc ctc gaa aac ggc gta ggc gca gca ctc ttc aac   691
Phe His Ala Gln Arg Leu Glu Asn Gly Val Gly Ala Ala Leu Phe Asn
            185                 190                 195

ggc cgc tcc tgc agc gga tgc gcc atg gtt ctc cct gca acc ggt atc   739
Gly Arg Ser Cys Ser Gly Cys Ala Met Val Leu Pro Ala Thr Gly Ile
        200                 205                 210

tcc gac atc cgc aac acc ccc aaa gat gag gtt cca cag tgc cca gaa   787
Ser Asp Ile Arg Asn Thr Pro Lys Asp Glu Val Pro Gln Cys Pro Glu
    215                 220                 225

tgt ggc tct tac ctc atc act gac atc tct tagaaagacc acccagtgaa     837
Cys Gly Ser Tyr Leu Ile Thr Asp Ile Ser
230                 235

att                                                               840
```

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<210> 1718
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

<400> 1718

```
Met Lys Leu Asp Pro Ser Leu His Lys Thr Leu Leu Gln Leu Ala Thr
  1               5                  10                  15

Thr Leu Arg Thr Gln Asn Ala Asn Ser Ala Pro Lys Thr Thr Pro Glu
             20                  25                  30

Gln Glu Ala Val Asp Lys Ala Val Ala Glu Leu Ser Arg Asn Arg Asp
         35                  40                  45

Ala Ala Ser Ala Gly Gln Met Ala Val Asp Asp Met Glu Asn Glu Ile
     50                  55                  60

Leu Arg Ile Gln Ser Asp Glu Arg Lys Leu Arg Arg Arg Lys Lys Asp
 65                  70                  75                  80

Gly Gln Asp Ala Leu Gly Ala Glu Thr Asp Glu Glu Arg Arg Arg Asp
                 85                  90                  95

Leu Asn His Asp Val Tyr Thr Ala Lys Ser Arg Ile Ala Asp Leu Met
            100                 105                 110

Ser Glu Leu Gln Glu Ala His Asn Glu Ile His Ala Leu Arg Asn Asn
        115                 120                 125

Arg Asp Leu Ala Gln Ser Arg Val Lys Asp Thr Glu Arg Lys Val Ala
```

```
    130                 135                 140

Asp Ala Arg Ala Ala Ala Glu Ala Ala Ala Ala Ala Thr Pro Glu Gly
145                 150                 155                 160

Glu Asp Pro Ala Val Val Ile Ala His Leu Glu Glu Lys Leu Pro Ser
                165                 170                 175

Glu Ala Leu Ala Glu Phe His Ala Gln Arg Leu Glu Asn Gly Val Gly
            180                 185                 190

Ala Ala Leu Phe Asn Gly Arg Ser Cys Ser Gly Cys Ala Met Val Leu
        195                 200                 205

Pro Ala Thr Gly Ile Ser Asp Ile Arg Asn Thr Pro Lys Asp Glu Val
    210                 215                 220

Pro Gln Cys Pro Glu Cys Gly Ser Tyr Leu Ile Thr Asp Ile Ser
225                 230                 235


<210> 1719
<211> 1082
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1059)
<223> RXA00349

<400> 1719
gag aaa atc ctg gac gag ttg gag caa tcc cct gcg tct tat ggt ttc   48
Glu Lys Ile Leu Asp Glu Leu Glu Gln Ser Pro Ala Ser Tyr Gly Phe
  1               5                  10                  15

cct gtt gcg ttg ctt ggc tgg cca atg atg ggt ggt gct gtt gct gtg   96
Pro Val Ala Leu Leu Gly Trp Pro Met Met Gly Gly Ala Val Ala Val
             20                  25                  30

ctg ttg ggt ggt gga tgc cag gtt tcc cta att gct ttt att acc gcg   144
Leu Leu Gly Gly Gly Cys Gln Val Ser Leu Ile Ala Phe Ile Thr Ala
         35                  40                  45

ttc acg atc att gcc acg acg tca ttt ttg gga aag aag ggt ttg cct   192
Phe Thr Ile Ile Ala Thr Thr Ser Phe Leu Gly Lys Lys Gly Leu Pro
     50                  55                  60

act ttc ttc caa aat gtt gtt ggt ggt ttt att gcc acg ctg cct gca   240
Thr Phe Phe Gln Asn Val Val Gly Gly Phe Ile Ala Thr Leu Pro Ala
 65                  70                  75                  80

tcg att gct tat tct ttg gcg ttg caa ttt ggt ctt gag atc aaa ccg   288
Ser Ile Ala Tyr Ser Leu Ala Leu Gln Phe Gly Leu Glu Ile Lys Pro
                 85                  90                  95

agc cag atc atc gca tct gga att gtt gtg ctg ttg gca ggt ttg aca   336
Ser Gln Ile Ile Ala Ser Gly Ile Val Val Leu Leu Ala Gly Leu Thr
            100                 105                 110

ctc gtg caa tct ctg cag gac ggc atc acg ggc gct ccg gtg aca gca   384
```

```
Leu Val Gln Ser Leu Gln Asp Gly Ile Thr Gly Ala Pro Val Thr Ala
        115                 120                 125

agt gca cga ttt ttc gaa aca ctc ctg ttt acc ggc ggc att gtt gct   432
Ser Ala Arg Phe Phe Glu Thr Leu Leu Phe Thr Gly Gly Ile Val Ala
    130                 135                 140

ggc gtg ggt ttg ggc att cag ctt tct gaa atc ttg cat gtc atg ttg   480
Gly Val Gly Leu Gly Ile Gln Leu Ser Glu Ile Leu His Val Met Leu
145                 150                 155                 160

cct gcc atg gag tcc gct gca gca cct aat tat tcg tct aca ttc gcc   528
Pro Ala Met Glu Ser Ala Ala Ala Pro Asn Tyr Ser Ser Thr Phe Ala
                165                 170                 175

cgc att atc gct ggt ggc gtc acc gca gcg gcc ttc gca gtg ggt tgt   576
Arg Ile Ile Ala Gly Gly Val Thr Ala Ala Ala Phe Ala Val Gly Cys
            180                 185                 190

tac gcg gag tgg tcc tcg gtg att att gcg ggg ctt act gcg ctg atg   624
Tyr Ala Glu Trp Ser Ser Val Ile Ile Ala Gly Leu Thr Ala Leu Met
        195                 200                 205

ggt tct gcg ttt tat tac ctc ttc gtt gtt tat tta ggc ccc gtc tct   672
Gly Ser Ala Phe Tyr Tyr Leu Phe Val Val Tyr Leu Gly Pro Val Ser
    210                 215                 220

gcc gct gcg att gct gca aca gca gtt ggt ttc act ggt ggt ttg ctt   720
Ala Ala Ala Ile Ala Ala Thr Ala Val Gly Phe Thr Gly Gly Leu Leu
225                 230                 235                 240

gcc cgt cga ttc ttg att cca ccg ttg att gtg gcg att gcc ggc atc   768
Ala Arg Arg Phe Leu Ile Pro Pro Leu Ile Val Ala Ile Ala Gly Ile
                245                 250                 255

aca cca atg ctt cca ggt cta gca att tac cgc gga atg tac gcc acc   816
Thr Pro Met Leu Pro Gly Leu Ala Ile Tyr Arg Gly Met Tyr Ala Thr
            260                 265                 270

ctg aat gat caa aca ctc atg ggt ttc acc aac att gcg gtt gct tta   864
Leu Asn Asp Gln Thr Leu Met Gly Phe Thr Asn Ile Ala Val Ala Leu
        275                 280                 285

gcc act gct tca tca ctt gcc gct ggc gtg gtt ttg ggt gag tgg att   912
Ala Thr Ala Ser Ser Leu Ala Ala Gly Val Val Leu Gly Glu Trp Ile
    290                 295                 300

gcc cgc agg cta cgt cgt cca cca cgc ttc aac cca tac cgt gca ttt   960
Ala Arg Arg Leu Arg Arg Pro Pro Arg Phe Asn Pro Tyr Arg Ala Phe
305                 310                 315                 320

acc aag gcg aat gag ttc tcc ttc cag gag gaa gct gag cag aat cag   1008
Thr Lys Ala Asn Glu Phe Ser Phe Gln Glu Glu Ala Glu Gln Asn Gln
                325                 330                 335

cgc cgg cag aga aaa cgt cca aag act aat cag aga ttc ggt aat aaa   1056
Arg Arg Gln Arg Lys Arg Pro Lys Thr Asn Gln Arg Phe Gly Asn Lys
            340                 345                 350

agg taaaaatcaa cctgcttagg cgt                                    1082
Arg
```

<210> 1720
<211> 353
<212> PRT
<213> Corynebacterium glutamicum

<400> 1720

```
Glu Lys Ile Leu Asp Glu Leu Glu Gln Ser Pro Ala Ser Tyr Gly Phe
  1               5                  10                  15

Pro Val Ala Leu Leu Gly Trp Pro Met Met Gly Gly Ala Val Ala Val
             20                  25                  30

Leu Leu Gly Gly Gly Cys Gln Val Ser Leu Ile Ala Phe Ile Thr Ala
         35                  40                  45

Phe Thr Ile Ile Ala Thr Thr Ser Phe Leu Gly Lys Lys Gly Leu Pro
     50                  55                  60

Thr Phe Phe Gln Asn Val Val Gly Gly Phe Ile Ala Thr Leu Pro Ala
 65                  70                  75                  80

Ser Ile Ala Tyr Ser Leu Ala Leu Gln Phe Gly Leu Glu Ile Lys Pro
                 85                  90                  95

Ser Gln Ile Ile Ala Ser Gly Ile Val Val Leu Leu Ala Gly Leu Thr
            100                 105                 110

Leu Val Gln Ser Leu Gln Asp Gly Ile Thr Gly Ala Pro Val Thr Ala
        115                 120                 125

Ser Ala Arg Phe Phe Glu Thr Leu Leu Phe Thr Gly Gly Ile Val Ala
    130                 135                 140

Gly Val Gly Leu Gly Ile Gln Leu Ser Glu Ile Leu His Val Met Leu
145                 150                 155                 160

Pro Ala Met Glu Ser Ala Ala Ala Pro Asn Tyr Ser Ser Thr Phe Ala
                165                 170                 175

Arg Ile Ile Ala Gly Gly Val Thr Ala Ala Ala Phe Ala Val Gly Cys
            180                 185                 190

Tyr Ala Glu Trp Ser Ser Val Ile Ile Ala Gly Leu Thr Ala Leu Met
        195                 200                 205

Gly Ser Ala Phe Tyr Tyr Leu Phe Val Val Tyr Leu Gly Pro Val Ser
    210                 215                 220

Ala Ala Ala Ile Ala Ala Thr Ala Val Gly Phe Thr Gly Gly Leu Leu
225                 230                 235                 240

Ala Arg Arg Phe Leu Ile Pro Pro Leu Ile Val Ala Ile Ala Gly Ile
                245                 250                 255

Thr Pro Met Leu Pro Gly Leu Ala Ile Tyr Arg Gly Met Tyr Ala Thr
            260                 265                 270

Leu Asn Asp Gln Thr Leu Met Gly Phe Thr Asn Ile Ala Val Ala Leu
```

```
        275                 280                 285

Ala Thr Ala Ser Ser Leu Ala Ala Gly Val Val Leu Gly Glu Trp Ile
    290                 295                 300

Ala Arg Arg Leu Arg Arg Pro Pro Arg Phe Asn Pro Tyr Arg Ala Phe
305                 310                 315                 320

Thr Lys Ala Asn Glu Phe Ser Phe Gln Glu Glu Ala Glu Gln Asn Gln
                325                 330                 335

Arg Arg Gln Arg Lys Arg Pro Lys Thr Asn Gln Arg Phe Gly Asn Lys
            340                 345                 350

Arg
```

<210> 1721
<211> 149
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(126)
<223> RXA00355

<400> 1721

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atc gct ttc ggt cgc gca gct cac cgc atg aag cag cag ggc caa agc   48
Ile Ala Phe Gly Arg Ala Ala His Arg Met Lys Gln Gln Gly Gln Ser
  1               5                  10                  15

gga gct ttc acc gtc ctc gaa gtt gct cca tac ctg ctc tcc cca gag   96
Gly Ala Phe Thr Val Leu Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu
             20                  25                  30

aac ttg gac gat ctg atc gca cgc gac gtc taatttagct cgaggggcaa     146
Asn Leu Asp Asp Leu Ile Ala Arg Asp Val
         35                  40

gga                                                               149
```

<210> 1722
<211> 42
<212> PRT
<213> Corynebacterium glutamicum

<400> 1722

```
Ile Ala Phe Gly Arg Ala Ala His Arg Met Lys Gln Gln Gly Gln Ser
  1               5                  10                  15

Gly Ala Phe Thr Val Leu Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu
             20                  25                  30

Asn Leu Asp Asp Leu Ile Ala Arg Asp Val
         35                  40
```

<210> 1723

<211> 624
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(601)
<223> RXA00375

<400> 1723
cagcctgtca aaatgctcac cgactacgca ccagaagacg ctaaacggta agtactgaag 60

aatttttaaa gacgacggag atttcaccac aatgccaagc atg ttc cca tca ccc 115
Met Phe Pro Ser Pro
1 5

gca act ggc gga gat gac atc aac cga cgc ccc ctg aat gaa cca aac 163
Ala Thr Gly Gly Asp Asp Ile Asn Arg Arg Pro Leu Asn Glu Pro Asn
10 15 20

gca gat gca acc acc atc ccc act gca cta aaa gtg gtg ttc tgg atg 211
Ala Asp Ala Thr Thr Ile Pro Thr Ala Leu Lys Val Val Phe Trp Met
25 30 35

ctg ttt gcc act gca gcg ttc atg att ttt aca ggc ctg gtg atg tac 259
Leu Phe Ala Thr Ala Ala Phe Met Ile Phe Thr Gly Leu Val Met Tyr
40 45 50

acc gcc gga tac acg gga cct gat gat gtg gat gag agc tac aaa gcc 307
Thr Ala Gly Tyr Thr Gly Pro Asp Asp Val Asp Glu Ser Tyr Lys Ala
55 60 65

gtt gtg gtg aac aac cag gag ttc atc ggt ggc atc aat gcc ttt gct 355
Val Val Val Asn Asn Gln Glu Phe Ile Gly Gly Ile Asn Ala Phe Ala
70 75 80 85

ggc gtc gtg att gct gca ctt act tca caa ctg cca aag ggc ggc aag 403
Gly Val Val Ile Ala Ala Leu Thr Ser Gln Leu Pro Lys Gly Gly Lys
90 95 100

aat ccg cgc cgt ctt ttg ttg gcc atc atg ttg ttg gta ttg ctg aca 451
Asn Pro Arg Arg Leu Leu Leu Ala Ile Met Leu Leu Val Leu Leu Thr
105 110 115

gat ctg ttg tct ttt gcc acc cgc gct gga ggc ttc gca ctc gca atc 499
Asp Leu Leu Ser Phe Ala Thr Arg Ala Gly Gly Phe Ala Leu Ala Ile
120 125 130

atc gca gtc ttg ttg gct ttg gaa gca ctc ttg atg ttc cgc cca gca 547
Ile Ala Val Leu Leu Ala Leu Glu Ala Leu Leu Met Phe Arg Pro Ala
135 140 145

gtc aat gat cac att gac cga aat cat atg gct cgt gta atg aat cgc 595
Val Asn Asp His Ile Asp Arg Asn His Met Ala Arg Val Met Asn Arg
150 155 160 165

gag aag tagaacggtt cgaccgtact ttt 624
Glu Lys

<210> 1724
<211> 167
<212> PRT
<213> Corynebacterium glutamicum

<400> 1724

```
Met Phe Pro Ser Pro Ala Thr Gly Gly Asp Asp Ile Asn Arg Arg Pro
  1               5                  10                  15

Leu Asn Glu Pro Asn Ala Asp Ala Thr Thr Ile Pro Thr Ala Leu Lys
             20                  25                  30

Val Val Phe Trp Met Leu Phe Ala Thr Ala Ala Phe Met Ile Phe Thr
         35                  40                  45

Gly Leu Val Met Tyr Thr Ala Gly Tyr Thr Gly Pro Asp Asp Val Asp
     50                  55                  60

Glu Ser Tyr Lys Ala Val Val Val Asn Asn Gln Glu Phe Ile Gly Gly
 65                  70                  75                  80

Ile Asn Ala Phe Ala Gly Val Val Ile Ala Ala Leu Thr Ser Gln Leu
                 85                  90                  95

Pro Lys Gly Gly Lys Asn Pro Arg Arg Leu Leu Leu Ala Ile Met Leu
            100                 105                 110

Leu Val Leu Leu Thr Asp Leu Leu Ser Phe Ala Thr Arg Ala Gly Gly
        115                 120                 125

Phe Ala Leu Ala Ile Ile Ala Val Leu Leu Ala Leu Glu Ala Leu Leu
    130                 135                 140

Met Phe Arg Pro Ala Val Asn Asp His Ile Asp Arg Asn His Met Ala
145                 150                 155                 160

Arg Val Met Asn Arg Glu Lys
                165
```

<210> 1725
<211> 744
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(721)
<223> RXA00380

<400> 1725

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caggcaatgc gacctcgcct cagtgacatc cttggtgttc caagacgatc aaattgtcgg 60

cgtgcattac aacgaaccag ctcaggagat ttgatcactc gtg cgt ttg acc aaa   115
                                          Val Arg Leu Thr Lys
                                            1               5

cta gca gca aca atc ggc tgc gtg aca ctc agc gga ctt gcg cta gta   163
Leu Ala Ala Thr Ile Gly Cys Val Thr Leu Ser Gly Leu Ala Leu Val
                10                  15                  20
```

```
gcc tgc agc agt gac agt acc gct ggt act gac gct gtt gct gtc ggc   211
Ala Cys Ser Ser Asp Ser Thr Ala Gly Thr Asp Ala Val Ala Val Gly
            25                  30                  35

gga acc ttc caa ttc cac tcc ccg gat gga aag atg gaa att ttc tac   259
Gly Thr Phe Gln Phe His Ser Pro Asp Gly Lys Met Glu Ile Phe Tyr
        40                  45                  50

gac gag gct gac cgt caa caa ctc ccc gac att ggt gga gat tcc ctc   307
Asp Glu Ala Asp Arg Gln Gln Leu Pro Asp Ile Gly Gly Asp Ser Leu
    55                  60                  65

atg gaa gag ggc aca cag atc aac ctg tct gat ttc gaa aac caa gtt   355
Met Glu Glu Gly Thr Gln Ile Asn Leu Ser Asp Phe Glu Asn Gln Val
70                  75                  80                  85

gtc atc ctc aat gcg tgg ggg cag tgg tgt gca ccg tgc cgc tcc gaa   403
Val Ile Leu Asn Ala Trp Gly Gln Trp Cys Ala Pro Cys Arg Ser Glu
                90                  95                  100

tcc gat gat ctc cag att atc cat gag gaa ctc caa gct gcc gga aac   451
Ser Asp Asp Leu Gln Ile Ile His Glu Glu Leu Gln Ala Ala Gly Asn
            105                 110                 115

ggc gac acc cct ggt ggc acc gtg ttg ggt atc aat gtg cgt gat tac   499
Gly Asp Thr Pro Gly Gly Thr Val Leu Gly Ile Asn Val Arg Asp Tyr
        120                 125                 130

tcc cgc gac atc gcc caa gac ttt gtc acc gac aac ggc ctt gat tac   547
Ser Arg Asp Ile Ala Gln Asp Phe Val Thr Asp Asn Gly Leu Asp Tyr
    135                 140                 145

cca agc att tac gat cca cca ttt atg aca gca gca tcc ctc ggt ggt   595
Pro Ser Ile Tyr Asp Pro Pro Phe Met Thr Ala Ala Ser Leu Gly Gly
150                 155                 160                 165

gtt ccc gca tcg gtg atc cca acc acc atc gtg ctg gat aaa cag cac   643
Val Pro Ala Ser Val Ile Pro Thr Thr Ile Val Leu Asp Lys Gln His
                170                 175                 180

cgc ccc gca gca gtg ttc ttg cgc gaa gtc acc tcc aaa gat gtg ttg   691
Arg Pro Ala Ala Val Phe Leu Arg Glu Val Thr Ser Lys Asp Val Leu
            185                 190                 195

gat gtt gcg ttg cca ttg gta gat gag gcc taaatgtctg agattgtggt     741
Asp Val Ala Leu Pro Leu Val Asp Glu Ala
        200                 205

agc                                                               744
```

<210> 1726
<211> 207
<212> PRT
<213> Corynebacterium glutamicum

<400> 1726

```
Val Arg Leu Thr Lys Leu Ala Ala Thr Ile Gly Cys Val Thr Leu Ser
  1               5                  10                  15

Gly Leu Ala Leu Val Ala Cys Ser Ser Asp Ser Thr Ala Gly Thr Asp
```

```
            20                  25                  30

Ala Val Ala Val Gly Gly Thr Phe Gln Phe His Ser Pro Asp Gly Lys
        35                  40                  45

Met Glu Ile Phe Tyr Asp Glu Ala Asp Arg Gln Gln Leu Pro Asp Ile
    50                  55                  60

Gly Gly Asp Ser Leu Met Glu Glu Gly Thr Gln Ile Asn Leu Ser Asp
65                  70                  75                  80

Phe Glu Asn Gln Val Val Ile Leu Asn Ala Trp Gly Gln Trp Cys Ala
                85                  90                  95

Pro Cys Arg Ser Glu Ser Asp Asp Leu Gln Ile Ile His Glu Glu Leu
            100                 105                 110

Gln Ala Ala Gly Asn Gly Asp Thr Pro Gly Gly Thr Val Leu Gly Ile
        115                 120                 125

Asn Val Arg Asp Tyr Ser Arg Asp Ile Ala Gln Asp Phe Val Thr Asp
    130                 135                 140

Asn Gly Leu Asp Tyr Pro Ser Ile Tyr Asp Pro Pro Phe Met Thr Ala
145                 150                 155                 160

Ala Ser Leu Gly Gly Val Pro Ala Ser Val Ile Pro Thr Thr Ile Val
                165                 170                 175

Leu Asp Lys Gln His Arg Pro Ala Ala Val Phe Leu Arg Glu Val Thr
            180                 185                 190

Ser Lys Asp Val Leu Asp Val Ala Leu Pro Leu Val Asp Glu Ala
        195                 200                 205


<210> 1727
<211> 836
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(813)
<223> RXA00387

<400> 1727
caa aac gac cca gaa acc tgg gaa gac tac gaa ctt cgc gtc aac cac   48
Gln Asn Asp Pro Glu Thr Trp Glu Asp Tyr Glu Leu Arg Val Asn His
  1               5                  10                  15

cca ctg cgc atc gaa ggc gac cgc gtc tac ctt cag ggc cac ggc ttc   96
Pro Leu Arg Ile Glu Gly Asp Arg Val Tyr Leu Gln Gly His Gly Phe
             20                  25                  30

gcc cca aca ttc acc gtg acc tgg cca aat ggc gag acc cgc acc cag   144
Ala Pro Thr Phe Thr Val Thr Trp Pro Asn Gly Glu Thr Arg Thr Gln
         35                  40                  45

acc gtg cag tgg cgc cca gac gac ccg acc ttc ttc ctg tcc tca ggc   192
Thr Val Gln Trp Arg Pro Asp Asp Pro Thr Phe Phe Leu Ser Ser Gly
```

```
     50                  55                  60

gtg gtc cgt ttc gat cca ccc gcc ggc atg tac cca gac ctt tac gag   240
Val Val Arg Phe Asp Pro Pro Ala Gly Met Tyr Pro Asp Leu Tyr Glu
 65                  70                  75                  80

cgc cgc caa aac cag ttg gcc atc cag gga ctt ttc gca ccg acc gcg   288
Arg Arg Gln Asn Gln Leu Ala Ile Gln Gly Leu Phe Ala Pro Thr Ala
                85                  90                  95

gaa tgg gaa ggc gac aac aac gaa ctg ctg acc tcc tcc tac ccg gcg   336
Glu Trp Glu Gly Asp Asn Asn Glu Leu Leu Thr Ser Ser Tyr Pro Ala
            100                 105                 110

atg cgt gac cca gcc gtg gcg atc gat att tac cgc ggc gac aat ggc   384
Met Arg Asp Pro Ala Val Ala Ile Asp Ile Tyr Arg Gly Asp Asn Gly
        115                 120                 125

ctc gat acc ggc atc gga cag tca ttg ttc agc ctg gac tct agt ctc   432
Leu Asp Thr Gly Ile Gly Gln Ser Leu Phe Ser Leu Asp Ser Ser Leu
    130                 135                 140

atg cac agc ggc gtg ctg caa aaa att gag cgc gtc aac ctc caa atc   480
Met His Ser Gly Val Leu Gln Lys Ile Glu Arg Val Asn Leu Gln Ile
145                 150                 155                 160

ggc gac acc gtc acc ctg gat gat ggc acc acc gtc tcc ttc gac ggc   528
Gly Asp Thr Val Thr Leu Asp Asp Gly Thr Thr Val Ser Phe Asp Gly
                165                 170                 175

gcg tca gaa ttt gcc aac tac cag atc agc cgc gac ccc aca caa aac   576
Ala Ser Glu Phe Ala Asn Tyr Gln Ile Ser Arg Asp Pro Thr Gln Asn
            180                 185                 190

tgg gtg ctg gtc acc acc gtg att tcg ctg gtc tcc ctg gtt gga tcc   624
Trp Val Leu Val Thr Thr Val Ile Ser Leu Val Ser Leu Val Gly Ser
        195                 200                 205

ctg atg atc cga cgc cgc cgc att tgg gtg cgt ttc tat cca caa gaa   672
Leu Met Ile Arg Arg Arg Arg Ile Trp Val Arg Phe Tyr Pro Gln Glu
    210                 215                 220

aac gga acc acc cgc gtg gaa acc ggc gga ctt gcc cgc acc gac cgc   720
Asn Gly Thr Thr Arg Val Glu Thr Gly Gly Leu Ala Arg Thr Asp Arg
225                 230                 235                 240

gca ggc tgg ggt ggc gaa tac gag aaa ttc cac cgc gaa ctg ctg ggt   768
Ala Gly Trp Gly Gly Glu Tyr Glu Lys Phe His Arg Glu Leu Leu Gly
                245                 250                 255

ctg aag gag gaa gat gaa gac gaa gag tac ttc gac cac gac gac       813
Leu Lys Glu Glu Asp Glu Asp Glu Glu Tyr Phe Asp His Asp Asp
            260                 265                 270

taacaccgca atttaaaggc ttt                                        836
```

<210> 1728
<211> 271
<212> PRT
<213> Corynebacterium glutamicum

<400> 1728

```
Gln Asn Asp Pro Glu Thr Trp Glu Asp Tyr Glu Leu Arg Val Asn His
 1               5                  10                  15

Pro Leu Arg Ile Glu Gly Asp Arg Val Tyr Leu Gln Gly His Gly Phe
            20                  25                  30

Ala Pro Thr Phe Thr Val Thr Trp Pro Asn Gly Glu Thr Arg Thr Gln
        35                  40                  45

Thr Val Gln Trp Arg Pro Asp Asp Pro Thr Phe Phe Leu Ser Ser Gly
    50                  55                  60

Val Val Arg Phe Asp Pro Pro Ala Gly Met Tyr Pro Asp Leu Tyr Glu
65                  70                  75                  80

Arg Arg Gln Asn Gln Leu Ala Ile Gln Gly Leu Phe Ala Pro Thr Ala
                85                  90                  95

Glu Trp Glu Gly Asp Asn Asn Glu Leu Leu Thr Ser Ser Tyr Pro Ala
            100                 105                 110

Met Arg Asp Pro Ala Val Ala Ile Asp Ile Tyr Arg Gly Asp Asn Gly
        115                 120                 125

Leu Asp Thr Gly Ile Gly Gln Ser Leu Phe Ser Leu Asp Ser Ser Leu
    130                 135                 140

Met His Ser Gly Val Leu Gln Lys Ile Glu Arg Val Asn Leu Gln Ile
145                 150                 155                 160

Gly Asp Thr Val Thr Leu Asp Asp Gly Thr Thr Val Ser Phe Asp Gly
                165                 170                 175

Ala Ser Glu Phe Ala Asn Tyr Gln Ile Ser Arg Asp Pro Thr Gln Asn
            180                 185                 190

Trp Val Leu Val Thr Thr Val Ile Ser Leu Val Ser Leu Val Gly Ser
        195                 200                 205

Leu Met Ile Arg Arg Arg Arg Ile Trp Val Arg Phe Tyr Pro Gln Glu
    210                 215                 220

Asn Gly Thr Thr Arg Val Glu Thr Gly Gly Leu Ala Arg Thr Asp Arg
225                 230                 235                 240

Ala Gly Trp Gly Gly Glu Tyr Glu Lys Phe His Arg Glu Leu Leu Gly
                245                 250                 255

Leu Lys Glu Glu Asp Glu Asp Glu Glu Tyr Phe Asp His Asp Asp
            260                 265                 270
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<210> 1729
<211> 987
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(964)
<223> RXA00392

<400> 1729
tgcttgaaat acgttcggca ggctatgggg gagtgtgaaa cgctattgtg aaatgaatag 60

ataggttcca tagtcgatcg aggaggagtc gcagaagttt atg tgg gtt ggt tat 115
Met Trp Val Gly Tyr
1 5

gcg gtt cga cag atc gcc agt gtt ttt ctt act ctt ttg cgc atg ctg 163
Ala Val Arg Gln Ile Ala Ser Val Phe Leu Thr Leu Leu Arg Met Leu
10 15 20

cca cta gca gcg cga aat cga gtt gcc agg gga cgc atc ccg gaa acc 211
Pro Leu Ala Ala Arg Asn Arg Val Ala Arg Gly Arg Ile Pro Glu Thr
25 30 35

ggc gat gtg gtg atc tca ttg acc acc cat ggg aag cga att aac tac 259
Gly Asp Val Val Ile Ser Leu Thr Thr His Gly Lys Arg Ile Asn Tyr
40 45 50

gtt cac ttc acc atc gaa tcg atc gca cgc ggc cat gtg aaa gca cca 307
Val His Phe Thr Ile Glu Ser Ile Ala Arg Gly His Val Lys Ala Pro
55 60 65

att gtg ctg tgg ttg gac aaa cca gac ttt gat gcg ccg tgg cct gcc 355
Ile Val Leu Trp Leu Asp Lys Pro Asp Phe Asp Ala Pro Trp Pro Ala
70 75 80 85

acc att aag cga ctt gtc gcc cgc ggt ctg caa gta cgg tgc agc gac 403
Thr Ile Lys Arg Leu Val Ala Arg Gly Leu Gln Val Arg Cys Ser Asp
90 95 100

ggc ttc tac ggc ccc cac acc aaa tac tgg aac caa ttc cga gaa atc 451
Gly Phe Tyr Gly Pro His Thr Lys Tyr Trp Asn Gln Phe Arg Glu Ile
105 110 115

cac ggc acc ggc gtg cgt gtc gcc acc gtc gac gat gac atg atc tac 499
His Gly Thr Gly Val Arg Val Ala Thr Val Asp Asp Asp Met Ile Tyr
120 125 130

ccc gag tgg ttc ctg cag cgc ttg ctt ttt att ggc gac ctg cgc atg 547
Pro Glu Trp Phe Leu Gln Arg Leu Leu Phe Ile Gly Asp Leu Arg Met
135 140 145

gat gcg gtt gtc gcc tac cgg gcg cac aga att gag ctt cgc gac gac 595
Asp Ala Val Val Ala Tyr Arg Ala His Arg Ile Glu Leu Arg Asp Asp
150 155 160 165

cga atg ctc ccg tac gtt aaa tgg agt gcc gca gac acc tca aaa gcg 643
Arg Met Leu Pro Tyr Val Lys Trp Ser Ala Ala Asp Thr Ser Lys Ala
170 175 180

tca ttc ctg cac ttt gcc acg gga gtg tca ggc gtt ttg tac ccc gtg 691
Ser Phe Leu His Phe Ala Thr Gly Val Ser Gly Val Leu Tyr Pro Val
185 190 195

acc ttc att gat tat gtg gtc tcc cag ggc gat gta ttc ctt gag aac 739
Thr Phe Ile Asp Tyr Val Val Ser Gln Gly Asp Val Phe Leu Glu Asn
200 205 210

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tgc aag cgc gcc gat gac gta tgg ctg cat gcc tgc gca ctg cgc tct   787
Cys Lys Arg Ala Asp Asp Val Trp Leu His Ala Cys Ala Leu Arg Ser
    215                 220                 225

gat cac cct att cgc cag gtc tac gct cag ccc cga cac ttc gct gtc   835
Asp His Pro Ile Arg Gln Val Tyr Ala Gln Pro Arg His Phe Ala Val
230                 235                 240                 245

gtg ccc acc acc caa gtg gga gca cta gtt gtt ggc aac acc ctc atg   883
Val Pro Thr Thr Gln Val Gly Ala Leu Val Val Gly Asn Thr Leu Met
                250                 255                 260

ggt gga aat gat gag cag atc gcc aaa gtg tac acc gat gaa gat gtg   931
Gly Gly Asn Asp Glu Gln Ile Ala Lys Val Tyr Thr Asp Glu Asp Val
            265                 270                 275

gca aaa cta gtt gca gcc agc aag aat gaa gac taaaacagct tcgcgatagc 984
Ala Lys Leu Val Ala Ala Ser Lys Asn Glu Asp
        280                 285

acg                                                               987
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<210> 1730
<211> 288
<212> PRT
<213> Corynebacterium glutamicum

<400> 1730

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Met Trp Val Gly Tyr Ala Val Arg Gln Ile Ala Ser Val Phe Leu Thr
  1               5                  10                  15

Leu Leu Arg Met Leu Pro Leu Ala Ala Arg Asn Arg Val Ala Arg Gly
             20                  25                  30

Arg Ile Pro Glu Thr Gly Asp Val Val Ile Ser Leu Thr Thr His Gly
         35                  40                  45

Lys Arg Ile Asn Tyr Val His Phe Thr Ile Glu Ser Ile Ala Arg Gly
     50                  55                  60

His Val Lys Ala Pro Ile Val Leu Trp Leu Asp Lys Pro Asp Phe Asp
 65                  70                  75                  80

Ala Pro Trp Pro Ala Thr Ile Lys Arg Leu Val Ala Arg Gly Leu Gln
                 85                  90                  95

Val Arg Cys Ser Asp Gly Phe Tyr Gly Pro His Thr Lys Tyr Trp Asn
            100                 105                 110

Gln Phe Arg Glu Ile His Gly Thr Gly Val Arg Val Ala Thr Val Asp
        115                 120                 125

Asp Asp Met Ile Tyr Pro Glu Trp Phe Leu Gln Arg Leu Leu Phe Ile
    130                 135                 140

Gly Asp Leu Arg Met Asp Ala Val Val Ala Tyr Arg Ala His Arg Ile
145                 150                 155                 160

Glu Leu Arg Asp Asp Arg Met Leu Pro Tyr Val Lys Trp Ser Ala Ala
```

```
                165                 170                 175

Asp Thr Ser Lys Ala Ser Phe Leu His Phe Ala Thr Gly Val Ser Gly
            180                 185                 190

Val Leu Tyr Pro Val Thr Phe Ile Asp Tyr Val Val Ser Gln Gly Asp
        195                 200                 205

Val Phe Leu Glu Asn Cys Lys Arg Ala Asp Asp Val Trp Leu His Ala
    210                 215                 220

Cys Ala Leu Arg Ser Asp His Pro Ile Arg Gln Val Tyr Ala Gln Pro
225                 230                 235                 240

Arg His Phe Ala Val Val Pro Thr Thr Gln Val Gly Ala Leu Val Val
                245                 250                 255

Gly Asn Thr Leu Met Gly Gly Asn Asp Glu Gln Ile Ala Lys Val Tyr
            260                 265                 270

Thr Asp Glu Asp Val Ala Lys Leu Val Ala Ala Ser Lys Asn Glu Asp
        275                 280                 285
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20100297849

<210> 1731
<211> 456
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(433)
<223> RXA00394

<400> 1731

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acccacttga acctctcctt aaatatttgc ttcaacctcc cacaatacgg aactttgagg 60

cattcttggg tatcggtatg tattgagtag ggttgaatat gtg agt gag tcc aat   115
                                            Val Ser Glu Ser Asn
                                              1               5

acc ccc aat ctc cag aca cac caa gcg ccg gaa tta aac ccg gaa cta   163
Thr Pro Asn Leu Gln Thr His Gln Ala Pro Glu Leu Asn Pro Glu Leu
                10                  15                  20

caa aaa gct gcc cgg aaa aac gtg ctg att tac ggt ctg gca cgt ttg   211
Gln Lys Ala Ala Arg Lys Asn Val Leu Ile Tyr Gly Leu Ala Arg Leu
            25                  30                  35

ctt ctg ttc gtc gtg ctg acc ttg att att cat agc ctg gct ctg ctg   259
Leu Leu Phe Val Val Leu Thr Leu Ile Ile His Ser Leu Ala Leu Leu
        40                  45                  50

att agt gcg cct gtg cca ctc gtt atg tct gcg atg ctg gct ctg att   307
Ile Ser Ala Pro Val Pro Leu Val Met Ser Ala Met Leu Ala Leu Ile
    55                  60                  65

gtg gcg ttc cca ttg tcc atg ctg gtg ttc agc aaa ctg cgc atg aat   355
```

```
Val Ala Phe Pro Leu Ser Met Leu Val Phe Ser Lys Leu Arg Met Asn
 70                  75                  80                  85

gcc acc cag gct gtt tcc cag tgg gat gca cag cgc aag gcc cac aag   403
Ala Thr Gln Ala Val Ser Gln Trp Asp Ala Gln Arg Lys Ala His Lys
                 90                  95                 100

gaa tgg gtt cga agc gag ctg gcg gac cgc taaaaaattc ccctcgttct     453
Glu Trp Val Arg Ser Glu Leu Ala Asp Arg
            105                 110

ttg                                                               456


<210> 1732
<211> 111
<212> PRT
<213> Corynebacterium glutamicum

<400> 1732
Val Ser Glu Ser Asn Thr Pro Asn Leu Gln Thr His Gln Ala Pro Glu
  1               5                  10                  15

Leu Asn Pro Glu Leu Gln Lys Ala Ala Arg Lys Asn Val Leu Ile Tyr
             20                  25                  30

Gly Leu Ala Arg Leu Leu Leu Phe Val Val Leu Thr Leu Ile Ile His
         35                  40                  45

Ser Leu Ala Leu Leu Ile Ser Ala Pro Val Pro Leu Val Met Ser Ala
     50                  55                  60

Met Leu Ala Leu Ile Val Ala Phe Pro Leu Ser Met Leu Val Phe Ser
 65                  70                  75                  80

Lys Leu Arg Met Asn Ala Thr Gln Ala Val Ser Gln Trp Asp Ala Gln
                 85                  90                  95

Arg Lys Ala His Lys Glu Trp Val Arg Ser Glu Leu Ala Asp Arg
            100                 105                 110


<210> 1733
<211> 423
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(400)
<223> RXA00395

<400> 1733
actcacatat tcaaccctac tcaatacata ccgataccca agaatgcctc aaagttccgt 60

attgtgggag gttgaagcaa atatttaagg agaggttcaa gtg ggt agg ctt ttg   115
                                               Val Gly Arg Leu Leu
                                                 1               5

ctg att att ttg gtt atc gtc gca atc gtc ttg ctg tgg aag gcc ttc   163
Leu Ile Ile Leu Val Ile Val Ala Ile Val Leu Leu Trp Lys Ala Phe
```

```
                10                  15                  20

aag cca tct aca tgg aag cgt aac gcg gag atc aat cag ggc cag gca   211
Lys Pro Ser Thr Trp Lys Arg Asn Ala Glu Ile Asn Gln Gly Gln Ala
            25                  30                  35

cct cgt gca gtg aaa ggc ccc gac gat gat gaa gaa ttc ttg tgg aat   259
Pro Arg Ala Val Lys Gly Pro Asp Asp Asp Glu Glu Phe Leu Trp Asn
        40                  45                  50

att gaa aag aat cgc ttc aaa cag cgt cgc gcc gac gag gct gcc caa   307
Ile Glu Lys Asn Arg Phe Lys Gln Arg Arg Ala Asp Glu Ala Ala Gln
    55                  60                  65

tta gaa gag gaa gaa cgt ctc aaa cgg gcc agg gaa cgc tac gca aag   355
Leu Glu Glu Glu Glu Arg Leu Lys Arg Ala Arg Glu Arg Tyr Ala Lys
70                  75                  80                  85

cct gaa agc tca gaa gaa ggt cca gag aag ccc act gag gat tct       400
Pro Glu Ser Ser Glu Glu Gly Pro Glu Lys Pro Thr Glu Asp Ser
                90                  95                  100

taaaagggct tctttaaaaa gat                                        423


<210> 1734
<211> 100
<212> PRT
<213> Corynebacterium glutamicum

<400> 1734
Val Gly Arg Leu Leu Leu Ile Ile Leu Val Ile Val Ala Ile Val Leu
  1               5                  10                  15

Leu Trp Lys Ala Phe Lys Pro Ser Thr Trp Lys Arg Asn Ala Glu Ile
            20                  25                  30

Asn Gln Gly Gln Ala Pro Arg Ala Val Lys Gly Pro Asp Asp Asp Glu
        35                  40                  45

Glu Phe Leu Trp Asn Ile Glu Lys Asn Arg Phe Lys Gln Arg Arg Ala
    50                  55                  60

Asp Glu Ala Ala Gln Leu Glu Glu Glu Glu Arg Leu Lys Arg Ala Arg
65                  70                  75                  80

Glu Arg Tyr Ala Lys Pro Glu Ser Ser Glu Glu Gly Pro Glu Lys Pro
                85                  90                  95

Thr Glu Asp Ser
            100


<210> 1735
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(571)
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<223> RXA00396

<400> 1735
atcccttggc gctacaacgg tgtagccatt ggtaccgagg atctgtggta catcggcgca 60

gacaagacct acattttgag ccagcgctaa ggagaaccca gtg aca gaa att gca 115
Val Thr Glu Ile Ala
1 5

gaa aac ctt cag cgc ttg ggt att gaa tta cct gat cta cca gca ccg 163
Glu Asn Leu Gln Arg Leu Gly Ile Glu Leu Pro Asp Leu Pro Ala Pro
10 15 20

cag tat tcc tac gta ccg ttc aac cgc caa gga aac acc ctc tat gta 211
Gln Tyr Ser Tyr Val Pro Phe Asn Arg Gln Gly Asn Thr Leu Tyr Val
25 30 35

tcg ggg cag att tca cga acc gca gcg gga gac atc ctc gcc gga cga 259
Ser Gly Gln Ile Ser Arg Thr Ala Ala Gly Asp Ile Leu Ala Gly Arg
40 45 50

gtt ggc gaa gac gca aca tta gaa gaa gga atc cac gcc gca gag gta 307
Val Gly Glu Asp Ala Thr Leu Glu Glu Gly Ile His Ala Ala Glu Val
55 60 65

gcc acc atc aat ctg ctg gcc aga atc cac caa tcc atc ggt tta gac 355
Ala Thr Ile Asn Leu Leu Ala Arg Ile His Gln Ser Ile Gly Leu Asp
70 75 80 85

aat gtg gcc caa att ctg aaa ctg aat gtg tgg gtc aat agc tcc gat 403
Asn Val Ala Gln Ile Leu Lys Leu Asn Val Trp Val Asn Ser Ser Asp
90 95 100

gac ttt att cag cag cct caa gtg gcc gac ggt gca tcc cag ctc ctt 451
Asp Phe Ile Gln Gln Pro Gln Val Ala Asp Gly Ala Ser Gln Leu Leu
105 110 115

gag gca gtg ttg ggt gag gcc gga aaa cat gca cgc aca gca cta ccc 499
Glu Ala Val Leu Gly Glu Ala Gly Lys His Ala Arg Thr Ala Leu Pro
120 125 130

aca aat act ctc ccc cag gga gca cta gtg gaa ttg gat gct gtc gtt 547
Thr Asn Thr Leu Pro Gln Gly Ala Leu Val Glu Leu Asp Ala Val Val
135 140 145

gcg gtc acc gag gcc gcc gaa gtt taggacgcgt gggcgaaaat ttc 594
Ala Val Thr Glu Ala Ala Glu Val
150 155

<210> 1736
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 1736
Val Thr Glu Ile Ala Glu Asn Leu Gln Arg Leu Gly Ile Glu Leu Pro
1 5 10 15

Asp Leu Pro Ala Pro Gln Tyr Ser Tyr Val Pro Phe Asn Arg Gln Gly
20 25 30

```
Asn Thr Leu Tyr Val Ser Gly Gln Ile Ser Arg Thr Ala Ala Gly Asp
         35                  40                  45

Ile Leu Ala Gly Arg Val Gly Glu Asp Ala Thr Leu Glu Glu Gly Ile
     50                  55                  60

His Ala Ala Glu Val Ala Thr Ile Asn Leu Leu Ala Arg Ile His Gln
 65                  70                  75                  80

Ser Ile Gly Leu Asp Asn Val Ala Gln Ile Leu Lys Leu Asn Val Trp
                 85                  90                  95

Val Asn Ser Ser Asp Asp Phe Ile Gln Gln Pro Gln Val Ala Asp Gly
            100                 105                 110

Ala Ser Gln Leu Leu Glu Ala Val Leu Gly Glu Ala Gly Lys His Ala
        115                 120                 125

Arg Thr Ala Leu Pro Thr Asn Thr Leu Pro Gln Gly Ala Leu Val Glu
    130                 135                 140

Leu Asp Ala Val Val Ala Val Thr Glu Ala Ala Glu Val
145                 150                 155


<210> 1737
<211> 563
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(540)
<223> RXA00397

<400> 1737
aac ctg cac tcc tcc aac aga atg ctc ttc cct gga cct cct gtg gat   48
Asn Leu His Ser Ser Asn Arg Met Leu Phe Pro Gly Pro Pro Val Asp
  1               5                  10                  15

ttc ccg atc aac gca gaa acc cga tgc att cag ctc gac gcc ggt gtt   96
Phe Pro Ile Asn Ala Glu Thr Arg Cys Ile Gln Leu Asp Ala Gly Val
             20                  25                  30

gca gta aag aag gac ggc gtg gtg ctg ggt acc tca gat atg gcg agg   144
Ala Val Lys Lys Asp Gly Val Val Leu Gly Thr Ser Asp Met Ala Arg
         35                  40                  45

tcc ctg cct cga acc gcc gct ggc caa gaa gcc tat gag tac ttc ttc   192
Ser Leu Pro Arg Thr Ala Ala Gly Gln Glu Ala Tyr Glu Tyr Phe Phe
     50                  55                  60

aag gtg gtt cgt gaa ggc atc atc ggg cag ctg cgc ccg ggc gtg atc   240
Lys Val Val Arg Glu Gly Ile Ile Gly Gln Leu Arg Pro Gly Val Ile
 65                  70                  75                  80

tgc gct gac gtg cac gaa gca acc ctt gat tac cta agc ccg cag cta   288
Cys Ala Asp Val His Glu Ala Thr Leu Asp Tyr Leu Ser Pro Gln Leu
                 85                  90                  95
```

```
cct cgc atg att gac atc gga atg ctg ggt gcc gac acc gat ttc aac   336
Pro Arg Met Ile Asp Ile Gly Met Leu Gly Ala Asp Thr Asp Phe Asn
            100                 105                 110

acc atc tac cgc aag cgc aat gtt ggc cac ctc atg ggc aag cag gaa   384
Thr Ile Tyr Arg Lys Arg Asn Val Gly His Leu Met Gly Lys Gln Glu
        115                 120                 125

tcc ttt gcc aat gag ctt cgc cct gga tac aag cac att ctt cac cac   432
Ser Phe Ala Asn Glu Leu Arg Pro Gly Tyr Lys His Ile Leu His His
    130                 135                 140

ggc tcc tat ggt gcc gcg gag atc cct tgg cgc tac aac ggt gta gcc   480
Gly Ser Tyr Gly Ala Ala Glu Ile Pro Trp Arg Tyr Asn Gly Val Ala
145                 150                 155                 160

att ggt acc gag gat ctg tgg tac atc ggc gca gac aag acc tac att   528
Ile Gly Thr Glu Asp Leu Trp Tyr Ile Gly Ala Asp Lys Thr Tyr Ile
                165                 170                 175

ttg agc cag cgc taaggagaac ccagtgacag aaa                        563
Leu Ser Gln Arg
            180
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<210> 1738
<211> 180
<212> PRT
<213> Corynebacterium glutamicum

<400> 1738

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Asn Leu His Ser Ser Asn Arg Met Leu Phe Pro Gly Pro Pro Val Asp
  1               5                  10                  15

Phe Pro Ile Asn Ala Glu Thr Arg Cys Ile Gln Leu Asp Ala Gly Val
             20                  25                  30

Ala Val Lys Lys Asp Gly Val Val Leu Gly Thr Ser Asp Met Ala Arg
         35                  40                  45

Ser Leu Pro Arg Thr Ala Ala Gly Gln Glu Ala Tyr Glu Tyr Phe Phe
     50                  55                  60

Lys Val Val Arg Glu Gly Ile Ile Gly Gln Leu Arg Pro Gly Val Ile
 65                  70                  75                  80

Cys Ala Asp Val His Glu Ala Thr Leu Asp Tyr Leu Ser Pro Gln Leu
                 85                  90                  95

Pro Arg Met Ile Asp Ile Gly Met Leu Gly Ala Asp Thr Asp Phe Asn
            100                 105                 110

Thr Ile Tyr Arg Lys Arg Asn Val Gly His Leu Met Gly Lys Gln Glu
        115                 120                 125

Ser Phe Ala Asn Glu Leu Arg Pro Gly Tyr Lys His Ile Leu His His
    130                 135                 140

Gly Ser Tyr Gly Ala Ala Glu Ile Pro Trp Arg Tyr Asn Gly Val Ala
145                 150                 155                 160
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```
Ile Gly Thr Glu Asp Leu Trp Tyr Ile Gly Ala Asp Lys Thr Tyr Ile
                165                 170                 175

Leu Ser Gln Arg
            180


<210> 1739
<211> 704
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(681)
<223> RXA00398

<400> 1739
tac ctc ccc gag cct ttc acc gtg gag gat tac act gcg cgt gtt gaa   48
Tyr Leu Pro Glu Pro Phe Thr Val Glu Asp Tyr Thr Ala Arg Val Glu
  1               5                  10                  15

ggc ctc gaa gtt gct ggc gga gcg att gtt tcc ggt tct ttc cag gct   96
Gly Leu Glu Val Ala Gly Gly Ala Ile Val Ser Gly Ser Phe Gln Ala
             20                  25                  30

ttc gac cag ggc tac ctc aaa gat gct ctc gca gtg ctt ggc cca ggc   144
Phe Asp Gln Gly Tyr Leu Lys Asp Ala Leu Ala Val Leu Gly Pro Gly
         35                  40                  45

tat gtc ggt gtc act cag atc ccc gca gat acc tct gat cag gag att   192
Tyr Val Gly Val Thr Gln Ile Pro Ala Asp Thr Ser Asp Gln Glu Ile
     50                  55                  60

ctt gat ctg gac aaa gct ggc gtg aag gct gtg cgt tta aac ttg aag   240
Leu Asp Leu Asp Lys Ala Gly Val Lys Ala Val Arg Leu Asn Leu Lys
 65                  70                  75                  80

cgc ggt ggt tcg gca ggt ctt gac gat ctc gag acc ttg gca cgc cga   288
Arg Gly Gly Ser Ala Gly Leu Asp Asp Leu Glu Thr Leu Ala Arg Arg
                 85                  90                  95

gtc cac gac cta gcc ggt tgg cac acc gaa ctc tat gtg gat gct cgc   336
Val His Asp Leu Ala Gly Trp His Thr Glu Leu Tyr Val Asp Ala Arg
            100                 105                 110

gaa cta gac gag ttg gaa tca acc ttg gcc tcc ctc cct gct gtc agc   384
Glu Leu Asp Glu Leu Glu Ser Thr Leu Ala Ser Leu Pro Ala Val Ser
        115                 120                 125

att gat cac tta ggg ctc cac cgc gat gga ctt ccc gca ctt ctt cgc   432
Ile Asp His Leu Gly Leu His Arg Asp Gly Leu Pro Ala Leu Leu Arg
    130                 135                 140

ttg gta gaa aat ggc att aaa gtc aaa gca acc gga ttc gga cgg gta   480
Leu Val Glu Asn Gly Ile Lys Val Lys Ala Thr Gly Phe Gly Arg Val
145                 150                 155                 160

gaa cta gat cca act gaa gtc atc cag gca atc atg gct gtc gat ccc   528
Glu Leu Asp Pro Thr Glu Val Ile Gln Ala Ile Met Ala Val Asp Pro
                165                 170                 175
```

```
act gct ttg atg atc gga act gat ctt cca tcc acc cgc act aag cga   576
Thr Ala Leu Met Ile Gly Thr Asp Leu Pro Ser Thr Arg Thr Lys Arg
            180                 185                 190

cct ttc gaa gac gct gac cta gat ttg atc gct gaa acg gtt ggc gaa   624
Pro Phe Glu Asp Ala Asp Leu Asp Leu Ile Ala Glu Thr Val Gly Glu
        195                 200                 205

gat cat gtc gac aac gtc ttc tgg aac aac gct gca gcg ttc tac ctc   672
Asp His Val Asp Asn Val Phe Trp Asn Asn Ala Ala Ala Phe Tyr Leu
    210                 215                 220

gga gac cag tagttttaag acccgaaatg tct                            704
Gly Asp Gln
225
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<210> 1740
<211> 227
<212> PRT
<213> Corynebacterium glutamicum

<400> 1740

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Tyr Leu Pro Glu Pro Phe Thr Val Glu Asp Tyr Thr Ala Arg Val Glu
  1               5                  10                  15

Gly Leu Glu Val Ala Gly Gly Ala Ile Val Ser Gly Ser Phe Gln Ala
             20                  25                  30

Phe Asp Gln Gly Tyr Leu Lys Asp Ala Leu Ala Val Leu Gly Pro Gly
         35                  40                  45

Tyr Val Gly Val Thr Gln Ile Pro Ala Asp Thr Ser Asp Gln Glu Ile
     50                  55                  60

Leu Asp Leu Asp Lys Ala Gly Val Lys Ala Val Arg Leu Asn Leu Lys
 65                  70                  75                  80

Arg Gly Gly Ser Ala Gly Leu Asp Asp Leu Glu Thr Leu Ala Arg Arg
                 85                  90                  95

Val His Asp Leu Ala Gly Trp His Thr Glu Leu Tyr Val Asp Ala Arg
            100                 105                 110

Glu Leu Asp Glu Leu Glu Ser Thr Leu Ala Ser Leu Pro Ala Val Ser
        115                 120                 125

Ile Asp His Leu Gly Leu His Arg Asp Gly Leu Pro Ala Leu Leu Arg
    130                 135                 140

Leu Val Glu Asn Gly Ile Lys Val Lys Ala Thr Gly Phe Gly Arg Val
145                 150                 155                 160

Glu Leu Asp Pro Thr Glu Val Ile Gln Ala Ile Met Ala Val Asp Pro
                165                 170                 175

Thr Ala Leu Met Ile Gly Thr Asp Leu Pro Ser Thr Arg Thr Lys Arg
            180                 185                 190

Pro Phe Glu Asp Ala Asp Leu Asp Leu Ile Ala Glu Thr Val Gly Glu
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```
        195                 200                 205

Asp His Val Asp Asn Val Phe Trp Asn Asn Ala Ala Ala Phe Tyr Leu
    210                 215                 220

Gly Asp Gln
225
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<210> 1741
<211> 570
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(547)
<223> RXA00408

<400> 1741

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gacaaatacg cacaggcgaa ccccagaacc acatgagggc atg aat cca gtg tca   115
                                            Met Asn Pro Val Ser
                                              1               5

cca aaa ctg acc acg gcc agg tac ctc acc cgc att cca tgg ctg ctg   163
Pro Lys Leu Thr Thr Ala Arg Tyr Leu Thr Arg Ile Pro Trp Leu Leu
                10                  15                  20

atc agc gcg att gtg ttt ggg gtg ctt gga gtt ttt gtg tct tcg tgg   211
Ile Ser Ala Ile Val Phe Gly Val Leu Gly Val Phe Val Ser Ser Trp
            25                  30                  35

ttt tac gcc ggt gtg atc gta gtt gcc gtc att ctt atc tgg cag ctg   259
Phe Tyr Ala Gly Val Ile Val Val Ala Val Ile Leu Ile Trp Gln Leu
        40                  45                  50

tgg ctg atc ccg cag cag gtc aag cga ctg gga tgg ctg gaa acc tcc   307
Trp Leu Ile Pro Gln Gln Val Lys Arg Leu Gly Trp Leu Glu Thr Ser
    55                  60                  65

gat gag ctg ctg atc acc aag gga aaa ctg tgg cac acc ttc acg gtt   355
Asp Glu Leu Leu Ile Thr Lys Gly Lys Leu Trp His Thr Phe Thr Val
70                  75                  80                  85

gtt ccc tat ggc cgc atc cag ttt gtt gat gtc acc gca ggt ccc ctc   403
Val Pro Tyr Gly Arg Ile Gln Phe Val Asp Val Thr Ala Gly Pro Leu
                90                  95                  100

gag cgc gcg ttt ggc atg aaa caa gtg caa ttg cat acc gcg tcg gcg   451
Glu Arg Ala Phe Gly Met Lys Gln Val Gln Leu His Thr Ala Ser Ala
            105                 110                 115

tcc tct gac tcc acc att caa ggc ctg cct gtc gcg gaa gcc gat gcc   499
Ser Ser Asp Ser Thr Ile Gln Gly Leu Pro Val Ala Glu Ala Asp Ala
        120                 125                 130

tta cgt gag cga ctg gct att aag gcc cgg gag agg atg agc gga cta   547
Leu Arg Glu Arg Leu Ala Ile Lys Ala Arg Glu Arg Met Ser Gly Leu
    135                 140                 145
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tgagcagcct tgaagggttt cga 570

<210> 1742
<211> 149
<212> PRT
<213> Corynebacterium glutamicum

<400> 1742
Met Asn Pro Val Ser Pro Lys Leu Thr Thr Ala Arg Tyr Leu Thr Arg
1 5 10 15

Ile Pro Trp Leu Leu Ile Ser Ala Ile Val Phe Gly Val Leu Gly Val
20 25 30

Phe Val Ser Ser Trp Phe Tyr Ala Gly Val Ile Val Val Ala Val Ile
35 40 45

Leu Ile Trp Gln Leu Trp Leu Ile Pro Gln Gln Val Lys Arg Leu Gly
50 55 60

Trp Leu Glu Thr Ser Asp Glu Leu Leu Ile Thr Lys Gly Lys Leu Trp
65 70 75 80

His Thr Phe Thr Val Val Pro Tyr Gly Arg Ile Gln Phe Val Asp Val
85 90 95

Thr Ala Gly Pro Leu Glu Arg Ala Phe Gly Met Lys Gln Val Gln Leu
100 105 110

His Thr Ala Ser Ala Ser Ser Asp Ser Thr Ile Gln Gly Leu Pro Val
115 120 125

Ala Glu Ala Asp Ala Leu Arg Glu Arg Leu Ala Ile Lys Ala Arg Glu
130 135 140

Arg Met Ser Gly Leu
145

<210> 1743
<211> 1536
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1513)
<223> RXA00409

<400> 1743
cggcgtcctc tgactccacc attcaaggcc tgcctgtcgc ggaagccgat gccttacgtg 60

agcgactggc tattaaggcc cgggagagga tgagcggact atg agc agc ctt gaa 115
Met Ser Ser Leu Glu
1 5

ggg ttt cga aaa gtc cac cgc gcc acc cca ttc ctt cgc atc tgg acc 163
Gly Phe Arg Lys Val His Arg Ala Thr Pro Phe Leu Arg Ile Trp Thr
10 15 20

```
atc atc gtc gca gtt ctc gcg gca ttc gca ttc aat tcc ggc gca tcc   211
Ile Ile Val Ala Val Leu Ala Ala Phe Ala Phe Asn Ser Gly Ala Ser
             25                  30                  35

gtt tta agt ttc atc tgg ggt gtc gtc acc ggc gaa tac gga ttc gca   259
Val Leu Ser Phe Ile Trp Gly Val Val Thr Gly Glu Tyr Gly Phe Ala
         40                  45                  50

gtg ctg ccg att cta ttg acc gtc ggt ggc gcc gtc att gtg gtg gca   307
Val Leu Pro Ile Leu Leu Thr Val Gly Gly Ala Val Ile Val Val Ala
     55                  60                  65

ctg gcc tgg att atc acc gga att tgg tgg aaa gcc gtc gga ttc cgc   355
Leu Ala Trp Ile Ile Thr Gly Ile Trp Trp Lys Ala Val Gly Phe Arg
 70                  75                  80                  85

atc acc aat gaa gag gtg cag ctg caa cgc gga gtg atc agc aaa gac   403
Ile Thr Asn Glu Glu Val Gln Leu Gln Arg Gly Val Ile Ser Lys Asp
                 90                  95                 100

ctc cgc acc gcc cga ttt gac cgt atc caa gcc gtt gac ctg gtg gaa   451
Leu Arg Thr Ala Arg Phe Asp Arg Ile Gln Ala Val Asp Leu Val Glu
            105                 110                 115

tca ttc atc gcc cgt atc ttc cga ctg gca gaa gtc cgc atc gaa acc   499
Ser Phe Ile Ala Arg Ile Phe Arg Leu Ala Glu Val Arg Ile Glu Thr
        120                 125                 130

gcc ggc ggc agc gac tcc gcc atc agc att ggc ttt tta aga aaa agc   547
Ala Gly Gly Ser Asp Ser Ala Ile Ser Ile Gly Phe Leu Arg Lys Ser
    135                 140                 145

gag gcc gag gcc cta aaa agg gag ctt ctc gac gcc tcc cag cac tca   595
Glu Ala Glu Ala Leu Lys Arg Glu Leu Leu Asp Ala Ser Gln His Ser
150                 155                 160                 165

gtc gcc acc acc cca gcc gga gtt ccg gct gag cct ggg gta ggg gag   643
Val Ala Thr Thr Pro Ala Gly Val Pro Ala Glu Pro Gly Val Gly Glu
                170                 175                 180

acc gtt gta gtt gag agc gcg ggc gat gtt ctg gtt cca caa atc ccc   691
Thr Val Val Val Glu Ser Ala Gly Asp Val Leu Val Pro Gln Ile Pro
            185                 190                 195

gtg caa cgc acc ctc gcc agc acc gcc tta tca cta gca acc atc atc   739
Val Gln Arg Thr Leu Ala Ser Thr Ala Leu Ser Leu Ala Thr Ile Ile
        200                 205                 210

acc gcg atc ggt att gtg att ttg ctc ttc gtt cct ttc gga gtg agc   787
Thr Ala Ile Gly Ile Val Ile Leu Leu Phe Val Pro Phe Gly Val Ser
    215                 220                 225

att gcc gtg ccg ttc ttt gta ggc atg gtg cca gcg gtc tgg aac ttg   835
Ile Ala Val Pro Phe Phe Val Gly Met Val Pro Ala Val Trp Asn Leu
230                 235                 240                 245

atc gat aag tcg tgg caa ttc acc gca aca cag cgc aac gat gtc ctg   883
Ile Asp Lys Ser Trp Gln Phe Thr Ala Thr Gln Arg Asn Asp Val Leu
                250                 255                 260
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cat gtc agc tat gga ctt gcc aac cgc cgc aaa caa tca atc cca ctg   931
His Val Ser Tyr Gly Leu Ala Asn Arg Arg Lys Gln Ser Ile Pro Leu
            265                 270                 275

gga cgc atc cac gca gtg aaa cta aaa cag cca ttg ctg tgg cga ctg   979
Gly Arg Ile His Ala Val Lys Leu Lys Gln Pro Leu Leu Trp Arg Leu
        280                 285                 290

gtt ggc tgg tgg acc gtg acc gtg cct gta gtt ggc tac ggc gac acc   1027
Val Gly Trp Trp Thr Val Thr Val Pro Val Val Gly Tyr Gly Asp Thr
    295                 300                 305

acc caa ggc gga acc tcc aaa atc ttg ccc gtg ggt tcc aaa gaa ctc   1075
Thr Gln Gly Gly Thr Ser Lys Ile Leu Pro Val Gly Ser Lys Glu Leu
310                 315                 320                 325

gca cta aaa gtc ctt gaa gcg gtg ggg cca cta aac agc gcc gac atc   1123
Ala Leu Lys Val Leu Glu Ala Val Gly Pro Leu Asn Ser Ala Asp Ile
                330                 335                 340

gcc gaa tct gca gac cca tca cat atg agc aga ccc cag tac aca cca   1171
Ala Glu Ser Ala Asp Pro Ser His Met Ser Arg Pro Gln Tyr Thr Pro
            345                 350                 355

cca gtt gct gca cgc ctg ctc aca cca gtc gat cgg acc cgc caa ggc   1219
Pro Val Ala Ala Arg Leu Leu Thr Pro Val Asp Arg Thr Arg Gln Gly
        360                 365                 370

gtc acg ttg att ggt gtg gct ggt gcc cct ggt gcg gtg gtc gtg cat   1267
Val Thr Leu Ile Gly Val Ala Gly Ala Pro Gly Ala Val Val Val His
    375                 380                 385

gaa ggc aga ttc atg cca cgt atg tct gtg att gat acc tcc cac atc   1315
Glu Gly Arg Phe Met Pro Arg Met Ser Val Ile Asp Thr Ser His Ile
390                 395                 400                 405

caa gaa ctc acc ctt aaa cac ggg ccg atc caa aga ata ctg gga ctc   1363
Gln Glu Leu Thr Leu Lys His Gly Pro Ile Gln Arg Ile Leu Gly Leu
                410                 415                 420

tcc acc gtt gtg ttt aac ctg gtc caa ggg cca gtg gga atg gcc gca   1411
Ser Thr Val Val Phe Asn Leu Val Gln Gly Pro Val Gly Met Ala Ala
            425                 430                 435

tcg gat ctc agt gca gct gat gga aaa gaa ctt ctc aac att ctc cgc   1459
Ser Asp Leu Ser Ala Ala Asp Gly Lys Glu Leu Leu Asn Ile Leu Arg
        440                 445                 450

aac aga aaa cta ccc gca ctg gaa tca gct ccg ctg gga caa aac agc   1507
Asn Arg Lys Leu Pro Ala Leu Glu Ser Ala Pro Leu Gly Gln Asn Ser
    455                 460                 465

ctg gac taaggtgtaa tcatgcacat ctc                                1536
Leu Asp
470
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<210> 1744
<211> 471
<212> PRT
<213> Corynebacterium glutamicum

<400> 1744

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Met Ser Ser Leu Glu Gly Phe Arg Lys Val His Arg Ala Thr Pro Phe
  1               5                  10                  15

Leu Arg Ile Trp Thr Ile Ile Val Ala Val Leu Ala Ala Phe Ala Phe
             20                  25                  30

Asn Ser Gly Ala Ser Val Leu Ser Phe Ile Trp Gly Val Val Thr Gly
         35                  40                  45

Glu Tyr Gly Phe Ala Val Leu Pro Ile Leu Leu Thr Val Gly Gly Ala
     50                  55                  60

Val Ile Val Val Ala Leu Ala Trp Ile Ile Thr Gly Ile Trp Trp Lys
 65                  70                  75                  80

Ala Val Gly Phe Arg Ile Thr Asn Glu Glu Val Gln Leu Gln Arg Gly
                 85                  90                  95

Val Ile Ser Lys Asp Leu Arg Thr Ala Arg Phe Asp Arg Ile Gln Ala
            100                 105                 110

Val Asp Leu Val Glu Ser Phe Ile Ala Arg Ile Phe Arg Leu Ala Glu
        115                 120                 125

Val Arg Ile Glu Thr Ala Gly Gly Ser Asp Ser Ala Ile Ser Ile Gly
    130                 135                 140

Phe Leu Arg Lys Ser Glu Ala Glu Ala Leu Lys Arg Glu Leu Leu Asp
145                 150                 155                 160

Ala Ser Gln His Ser Val Ala Thr Thr Pro Ala Gly Val Pro Ala Glu
                165                 170                 175

Pro Gly Val Gly Glu Thr Val Val Val Glu Ser Ala Gly Asp Val Leu
            180                 185                 190

Val Pro Gln Ile Pro Val Gln Arg Thr Leu Ala Ser Thr Ala Leu Ser
        195                 200                 205

Leu Ala Thr Ile Ile Thr Ala Ile Gly Ile Val Ile Leu Leu Phe Val
    210                 215                 220

Pro Phe Gly Val Ser Ile Ala Val Pro Phe Phe Val Gly Met Val Pro
225                 230                 235                 240

Ala Val Trp Asn Leu Ile Asp Lys Ser Trp Gln Phe Thr Ala Thr Gln
                245                 250                 255

Arg Asn Asp Val Leu His Val Ser Tyr Gly Leu Ala Asn Arg Arg Lys
            260                 265                 270

Gln Ser Ile Pro Leu Gly Arg Ile His Ala Val Lys Leu Lys Gln Pro
        275                 280                 285

Leu Leu Trp Arg Leu Val Gly Trp Trp Thr Val Thr Val Pro Val Val
    290                 295                 300

Gly Tyr Gly Asp Thr Thr Gln Gly Gly Thr Ser Lys Ile Leu Pro Val
305                 310                 315                 320
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```
Gly Ser Lys Glu Leu Ala Leu Lys Val Leu Glu Ala Val Gly Pro Leu
               325                 330                 335

Asn Ser Ala Asp Ile Ala Glu Ser Ala Asp Pro Ser His Met Ser Arg
            340                 345                 350

Pro Gln Tyr Thr Pro Pro Val Ala Ala Arg Leu Leu Thr Pro Val Asp
        355                 360                 365

Arg Thr Arg Gln Gly Val Thr Leu Ile Gly Val Ala Gly Ala Pro Gly
    370                 375                 380

Ala Val Val Val His Glu Gly Arg Phe Met Pro Arg Met Ser Val Ile
385                 390                 395                 400

Asp Thr Ser His Ile Gln Glu Leu Thr Leu Lys His Gly Pro Ile Gln
               405                 410                 415

Arg Ile Leu Gly Leu Ser Thr Val Val Phe Asn Leu Val Gln Gly Pro
            420                 425                 430

Val Gly Met Ala Ala Ser Asp Leu Ser Ala Ala Asp Gly Lys Glu Leu
        435                 440                 445

Leu Asn Ile Leu Arg Asn Arg Lys Leu Pro Ala Leu Glu Ser Ala Pro
    450                 455                 460

Leu Gly Gln Asn Ser Leu Asp
465                 470


<210> 1745
<211> 798
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(775)
<223> RXA00411

<400> 1745
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aaaccttgac caagaccacg accatcaagg agatcacccg atg aac gag atg atc   115
                                              Met Asn Glu Met Ile
                                                1               5

ctc gca gct gac tgg aac cgg cta gga ccc acc ttc caa aca gcc atc   163
Leu Ala Ala Asp Trp Asn Arg Leu Gly Pro Thr Phe Gln Thr Ala Ile
                10                  15                  20

att gac acc ctg ttg atg gtc atc atc acc atg gtg gtg gct ggc tta   211
Ile Asp Thr Leu Leu Met Val Ile Ile Thr Met Val Val Ala Gly Leu
            25                  30                  35

ctg ggt ctt gtc gtc ggc ctg ctg ctt tac acc acc cgc gct ggt gga   259
Leu Gly Leu Val Val Gly Leu Leu Leu Tyr Thr Thr Arg Ala Gly Gly
        40                  45                  50
```

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atc ttg aag aac aag gtc atc tac acc att ttg aat gtg ctg gtg aac   307
Ile Leu Lys Asn Lys Val Ile Tyr Thr Ile Leu Asn Val Leu Val Asn
     55                  60                  65

ttt gtt cga ccc atc cca ttc att att ttg atc gcc gcc atc aag cca   355
Phe Val Arg Pro Ile Pro Phe Ile Ile Leu Ile Ala Ala Ile Lys Pro
 70                  75                  80                  85

cta acg gtc gcc gtc atg ggc acc tcc atc ggc cga gat gcc ggc atc   403
Leu Thr Val Ala Val Met Gly Thr Ser Ile Gly Arg Asp Ala Gly Ile
                90                  95                 100

ttc gtc atg gtt gtc gca gcg att ttc tct gtg gct cga atc gtg gag   451
Phe Val Met Val Val Ala Ala Ile Phe Ser Val Ala Arg Ile Val Glu
            105                 110                 115

caa aac ttg gtc tcc att gat cct ggt gtc atc gag gca gct cgc tcc   499
Gln Asn Leu Val Ser Ile Asp Pro Gly Val Ile Glu Ala Ala Arg Ser
        120                 125                 130

atg ggt gcg tcc ccg atg cgc atc atc gcc acc gtg atc att cca gaa   547
Met Gly Ala Ser Pro Met Arg Ile Ile Ala Thr Val Ile Ile Pro Glu
    135                 140                 145

gca ctt gga cca ttg gtt ctg ggt tac acc ttc ctg ttc atc gcg atc   595
Ala Leu Gly Pro Leu Val Leu Gly Tyr Thr Phe Leu Phe Ile Ala Ile
150                 155                 160                 165

gtc gat atg tcc gca atg gtc ggc tac atc ggt ggc ggt ggt ctt ggt   643
Val Asp Met Ser Ala Met Val Gly Tyr Ile Gly Gly Gly Gly Leu Gly
                170                 175                 180

gac ttc gcc att gtt tac ggc tac cgc gcc ttc gac aac gaa gtt atg   691
Asp Phe Ala Ile Val Tyr Gly Tyr Arg Ala Phe Asp Asn Glu Val Met
            185                 190                 195

tac gtt gcc gtc ctg gtt atc gtc atc atc gtg cag gca gcc cag ctt   739
Tyr Val Ala Val Leu Val Ile Val Ile Ile Val Gln Ala Ala Gln Leu
        200                 205                 210

ctg ggc aat tgg ctg tcc aag aag atc atg cgc cgc taaacctctt        785
Leu Gly Asn Trp Leu Ser Lys Lys Ile Met Arg Arg
    215                 220                 225

gcatagaaaa acc                                                   798


<210> 1746
<211> 225
<212> PRT
<213> Corynebacterium glutamicum

<400> 1746
Met Asn Glu Met Ile Leu Ala Ala Asp Trp Asn Arg Leu Gly Pro Thr
  1               5                  10                  15

Phe Gln Thr Ala Ile Ile Asp Thr Leu Leu Met Val Ile Ile Thr Met
             20                  25                  30

Val Val Ala Gly Leu Leu Gly Leu Val Val Gly Leu Leu Leu Tyr Thr
         35                  40                  45
```

```
Thr Arg Ala Gly Gly Ile Leu Lys Asn Lys Val Ile Tyr Thr Ile Leu
     50                  55                  60

Asn Val Leu Val Asn Phe Val Arg Pro Ile Pro Phe Ile Ile Leu Ile
 65                  70                  75                  80

Ala Ala Ile Lys Pro Leu Thr Val Ala Val Met Gly Thr Ser Ile Gly
                 85                  90                  95

Arg Asp Ala Gly Ile Phe Val Met Val Val Ala Ala Ile Phe Ser Val
            100                 105                 110

Ala Arg Ile Val Glu Gln Asn Leu Val Ser Ile Asp Pro Gly Val Ile
        115                 120                 125

Glu Ala Ala Arg Ser Met Gly Ala Ser Pro Met Arg Ile Ile Ala Thr
    130                 135                 140

Val Ile Ile Pro Glu Ala Leu Gly Pro Leu Val Leu Gly Tyr Thr Phe
145                 150                 155                 160

Leu Phe Ile Ala Ile Val Asp Met Ser Ala Met Val Gly Tyr Ile Gly
                165                 170                 175

Gly Gly Gly Leu Gly Asp Phe Ala Ile Val Tyr Gly Tyr Arg Ala Phe
            180                 185                 190

Asp Asn Glu Val Met Tyr Val Ala Val Leu Val Ile Val Ile Ile Val
        195                 200                 205

Gln Ala Ala Gln Leu Leu Gly Asn Trp Leu Ser Lys Lys Ile Met Arg
    210                 215                 220

Arg
225
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<210> 1747
<211> 576
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(553)
<223> RXA00423

<400> 1747
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cttttattta cgcaatctgt gagctggagg cccgcacaaa atg acc tat ccc gtg   115
                                              Met Thr Tyr Pro Val
                                                1               5

ttg agt gtt ttg gat aat tct ggc gat cac aac atc atc tgg cat gtg   163
Leu Ser Val Leu Asp Asn Ser Gly Asp His Asn Ile Ile Trp His Val
                10                  15                  20

caa act tat ccc gcg gcg ctg ccc acc ggg gcg tgg att gcc gat gag   211
Gln Thr Tyr Pro Ala Ala Leu Pro Thr Gly Ala Trp Ile Ala Asp Glu
```

```
            25                  30                  35

caa caa ctg act gac ctg ctg aaa gac aca gta gtg ttc ctt acc cct   259
Gln Gln Leu Thr Asp Leu Leu Lys Asp Thr Val Val Phe Leu Thr Pro
        40                  45                  50

ggg agc acc gct ccg gaa aat gcc ccc gtg gcg acg ata gaa ggg gtg   307
Gly Ser Thr Ala Pro Glu Asn Ala Pro Val Ala Thr Ile Glu Gly Val
    55                  60                  65

cgg gtt gac gtc gat aag cag gtg gca gag tac aac aaa cat ggg atc   355
Arg Val Asp Val Asp Lys Gln Val Ala Glu Tyr Asn Lys His Gly Ile
70                  75                  80                  85

cgc ctg ccc agc ttg ggc gcg cgc act gtg gag gcg cag tac cgc ggc   403
Arg Leu Pro Ser Leu Gly Ala Arg Thr Val Glu Ala Gln Tyr Arg Gly
                90                  95                  100

gag ccg gag gca gag gct gcg tgg cgc acg gcg atg gag ctc gta gag   451
Glu Pro Glu Ala Glu Ala Ala Trp Arg Thr Ala Met Glu Leu Val Glu
            105                 110                 115

atc gca ggc ggc tgg cta gaa att gaa gcc aag cgc cgg gcg cgg aag   499
Ile Ala Gly Gly Trp Leu Glu Ile Glu Ala Lys Arg Arg Ala Arg Lys
        120                 125                 130

gcg ctg gct gag gcc ttc ggc gcg gag gtc cag cca ctg ccg ctt gac   547
Ala Leu Ala Glu Ala Phe Gly Ala Glu Val Gln Pro Leu Pro Leu Asp
    135                 140                 145

acc gaa taggacaaat gggtctatcc tgg                                576
Thr Glu
150
```

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<210> 1748
<211> 151
<212> PRT
<213> Corynebacterium glutamicum

<400> 1748
Met Thr Tyr Pro Val Leu Ser Val Leu Asp Asn Ser Gly Asp His Asn
  1               5                  10                  15

Ile Ile Trp His Val Gln Thr Tyr Pro Ala Ala Leu Pro Thr Gly Ala
             20                  25                  30

Trp Ile Ala Asp Glu Gln Gln Leu Thr Asp Leu Leu Lys Asp Thr Val
         35                  40                  45

Val Phe Leu Thr Pro Gly Ser Thr Ala Pro Glu Asn Ala Pro Val Ala
     50                  55                  60

Thr Ile Glu Gly Val Arg Val Asp Val Asp Lys Gln Val Ala Glu Tyr
 65                  70                  75                  80

Asn Lys His Gly Ile Arg Leu Pro Ser Leu Gly Ala Arg Thr Val Glu
                 85                  90                  95

Ala Gln Tyr Arg Gly Glu Pro Glu Ala Glu Ala Ala Trp Arg Thr Ala
            100                 105                 110
```

```
Met Glu Leu Val Glu Ile Ala Gly Gly Trp Leu Glu Ile Glu Ala Lys
        115                 120                 125

Arg Arg Ala Arg Lys Ala Leu Ala Glu Ala Phe Gly Ala Glu Val Gln
    130                 135                 140

Pro Leu Pro Leu Asp Thr Glu
145                 150


<210> 1749
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(571)
<223> RXA00424

<400> 1749
gcgatgtgga cctcgggagc cttggctttt ttgaatcttt caaacatgcc caccacctta 60

atcagtgagt agtcttggca acatggatac caggatgaga ttg cag gta gca gca   115
                                          Leu Gln Val Ala Ala
                                            1               5

ggt tcc gcg ctg att ggt gct ggg gtt gcg gtt aat gat tac gta caa   163
Gly Ser Ala Leu Ile Gly Ala Gly Val Ala Val Asn Asp Tyr Val Gln
                10                  15                  20

agc cca gtc cgc cgg gcc atc agt tat ggt gcg ttg gcg ctt tct ggg   211
Ser Pro Val Arg Arg Ala Ile Ser Tyr Gly Ala Leu Ala Leu Ser Gly
            25                  30                  35

gcg acg gtg att gcg atg ggt cag gac ccg act ggg gag cgg tcc atc   259
Ala Thr Val Ile Ala Met Gly Gln Asp Pro Thr Gly Glu Arg Ser Ile
        40                  45                  50

att gcg aaa gat tcc gcg acg atg gtt gat caa atc cgc cag gag atc   307
Ile Ala Lys Asp Ser Ala Thr Met Val Asp Gln Ile Arg Gln Glu Ile
    55                  60                  65

ggc gat ttg ggt gtc acg cct ggt cca gaa tct gat gtg gat gcc atc   355
Gly Asp Leu Gly Val Thr Pro Gly Pro Glu Ser Asp Val Asp Ala Ile
70                  75                  80                  85

acg gag cga ggt ccg ctg gtg acg tgg ctg ttg ctt gct gtt ttt gtc   403
Thr Glu Arg Gly Pro Leu Val Thr Trp Leu Leu Leu Ala Val Phe Val
                90                  95                  100

gtg gca ttt ttc acc ttg gcg tat ttc tcc atg cgc atg gat gtg gcg   451
Val Ala Phe Phe Thr Leu Ala Tyr Phe Ser Met Arg Met Asp Val Ala
            105                 110                 115

gtg atg aga agg atc gct aag ttc ttt gaa aaa cgt ggc gct tcc agg   499
Val Met Arg Arg Ile Ala Lys Phe Phe Glu Lys Arg Gly Ala Ser Arg
        120                 125                 130

cca ttc acc tgc act ggc atg gtg tac gcc gct ttt att tac gca atc   547
```

```
Pro Phe Thr Cys Thr Gly Met Val Tyr Ala Ala Phe Ile Tyr Ala Ile
    135                 140                 145

tgt gag ctg gag gcc cgc aca aaa tgacctatcc cgtgttgagt gtt         594
Cys Glu Leu Glu Ala Arg Thr Lys
150                 155


<210> 1750
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 1750
Leu Gln Val Ala Ala Gly Ser Ala Leu Ile Gly Ala Gly Val Ala Val
  1               5                  10                  15

Asn Asp Tyr Val Gln Ser Pro Val Arg Arg Ala Ile Ser Tyr Gly Ala
             20                  25                  30

Leu Ala Leu Ser Gly Ala Thr Val Ile Ala Met Gly Gln Asp Pro Thr
         35                  40                  45

Gly Glu Arg Ser Ile Ile Ala Lys Asp Ser Ala Thr Met Val Asp Gln
     50                  55                  60

Ile Arg Gln Glu Ile Gly Asp Leu Gly Val Thr Pro Gly Pro Glu Ser
 65                  70                  75                  80

Asp Val Asp Ala Ile Thr Glu Arg Gly Pro Leu Val Thr Trp Leu Leu
                 85                  90                  95

Leu Ala Val Phe Val Val Ala Phe Phe Thr Leu Ala Tyr Phe Ser Met
            100                 105                 110

Arg Met Asp Val Ala Val Met Arg Arg Ile Ala Lys Phe Phe Glu Lys
        115                 120                 125

Arg Gly Ala Ser Arg Pro Phe Thr Cys Thr Gly Met Val Tyr Ala Ala
    130                 135                 140

Phe Ile Tyr Ala Ile Cys Glu Leu Glu Ala Arg Thr Lys
145                 150                 155


<210> 1751
<211> 348
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(325)
<223> RXA00425

<400> 1751
accgcaaccc cagcaccaat cagcgcggaa cctgctgcta cctgcaatct catcctggta 60

tccatgttgc caagactact cactgattaa ggtggtgggc atg ttt gaa aga ttc   115
                                            Met Phe Glu Arg Phe
                                              1               5
```

```
aaa aaa gcc aag gct ccc gag gtc cac atc gcg gcg gaa cgc acc aac   163
Lys Lys Ala Lys Ala Pro Glu Val His Ile Ala Ala Glu Arg Thr Asn
                10                  15                  20

ctt ccg ctt aac gat ttc atg acc cgc ctc ttc gcc cag gaa ctc ccc   211
Leu Pro Leu Asn Asp Phe Met Thr Arg Leu Phe Ala Gln Glu Leu Pro
            25                  30                  35

ctg ctc gat agc acc tca cgt tca gag gtc tac cgc ctg ctt cgg gaa   259
Leu Leu Asp Ser Thr Ser Arg Ser Glu Val Tyr Arg Leu Leu Arg Glu
        40                  45                  50

tac gac ggc cca aca att agc tcc cag gaa gaa atc ccc gca gag att   307
Tyr Asp Gly Pro Thr Ile Ser Ser Gln Glu Glu Ile Pro Ala Glu Ile
    55                  60                  65

cgt gaa ctc atg gat ctt taggcaataa atgtgagatt gga                348
Arg Glu Leu Met Asp Leu
70                  75
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<210> 1752
<211> 75
<212> PRT
<213> Corynebacterium glutamicum

<400> 1752

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Met Phe Glu Arg Phe Lys Lys Ala Lys Ala Pro Glu Val His Ile Ala
  1               5                  10                  15

Ala Glu Arg Thr Asn Leu Pro Leu Asn Asp Phe Met Thr Arg Leu Phe
            20                  25                  30

Ala Gln Glu Leu Pro Leu Leu Asp Ser Thr Ser Arg Ser Glu Val Tyr
        35                  40                  45

Arg Leu Leu Arg Glu Tyr Asp Gly Pro Thr Ile Ser Ser Gln Glu Glu
    50                  55                  60

Ile Pro Ala Glu Ile Arg Glu Leu Met Asp Leu
65                  70                  75
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<210> 1753
<211> 756
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(733)
<223> RXA00428

<400> 1753

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agcgtcgcag ggatcggcgc gatcttcctc cttccgatcg gcatcatcat gtgcctcatc 60

gccggattca accgctacta cgcagccctt aaggtctaaa atg ccc ggt cta gtt   115
                                                Met Pro Gly Leu Val
                                                  1               5
```

```
ctc tcc aca aac gtc gcc cat atc caa caa gac cca ggt ggc gat gac   163
Leu Ser Thr Asn Val Ala His Ile Gln Gln Asp Pro Gly Gly Asp Asp
                10                  15                  20

cgc atc agc ggc atc aac aaa ctc ccc gtc gcc acc ggc atc gat gta   211
Arg Ile Ser Gly Ile Asn Lys Leu Pro Val Ala Thr Gly Ile Asp Val
            25                  30                  35

ttc atc ccc gga ccc aac tac ggc gac ggc tcc ggc gta gtc ggc gac   259
Phe Ile Pro Gly Pro Asn Tyr Gly Asp Gly Ser Gly Val Val Gly Asp
        40                  45                  50

gcc atc ggc gat tcc ctc cac cac ggc ggc gcc cac aaa gcc atc tac   307
Ala Ile Gly Asp Ser Leu His His Gly Gly Ala His Lys Ala Ile Tyr
    55                  60                  65

gcc tac agc cgc gaa gaa ctc gac ttc ttt gac ccc acc tac cgc aac   355
Ala Tyr Ser Arg Glu Glu Leu Asp Phe Phe Asp Pro Thr Tyr Arg Asn
70                  75                  80                  85

gga tac ttc ggc gaa aac ctc acc acc agc gga atc gtg ttg gaa gac   403
Gly Tyr Phe Gly Glu Asn Leu Thr Thr Ser Gly Ile Val Leu Glu Asp
                90                  95                  100

ctc ctg atc aac caa caa gtg cgc atc ggc acc acg ctg ctc gaa gtc   451
Leu Leu Ile Asn Gln Gln Val Arg Ile Gly Thr Thr Leu Leu Glu Val
            105                 110                 115

tcc att ccc cgc cga ccc tgc cgc acg ttc gcc cac tgg ctc gac atc   499
Ser Ile Pro Arg Arg Pro Cys Arg Thr Phe Ala His Trp Leu Asp Ile
        120                 125                 130

aaa ggc tgg cta aaa acc ttc acc caa cgc ggc ctc ccc ggc agc tac   547
Lys Gly Trp Leu Lys Thr Phe Thr Gln Arg Gly Leu Pro Gly Ser Tyr
    135                 140                 145

ttc cga gtc atc gaa gaa ggc cac atc aac ccc ggc gac ccc att gaa   595
Phe Arg Val Ile Glu Glu Gly His Ile Asn Pro Gly Asp Pro Ile Glu
150                 155                 160                 165

gtt ctg cag gcc ccc gac cac gac atc acc atg tcc atg gcc ttc cgt   643
Val Leu Gln Ala Pro Asp His Asp Ile Thr Met Ser Met Ala Phe Arg
                170                 175                 180

gca aaa atg gga aac aaa gac ctc gcg cgc cgg gtt gtt gca gcc aac   691
Ala Lys Met Gly Asn Lys Asp Leu Ala Arg Arg Val Val Ala Ala Asn
            185                 190                 195

tgt ctc cca gcg cgc tac cac gag gaa cta cta aaa ctg atc           733
Cys Leu Pro Ala Arg Tyr His Glu Glu Leu Leu Lys Leu Ile
        200                 205                 210

tagggcctat tgaatttctc gtc                                       756
```

<210> 1754
<211> 211
<212> PRT
<213> Corynebacterium glutamicum

<400> 1754

```
Met Pro Gly Leu Val Leu Ser Thr Asn Val Ala His Ile Gln Gln Asp
  1               5                  10                  15

Pro Gly Gly Asp Asp Arg Ile Ser Gly Ile Asn Lys Leu Pro Val Ala
             20                  25                  30

Thr Gly Ile Asp Val Phe Ile Pro Gly Pro Asn Tyr Gly Asp Gly Ser
         35                  40                  45

Gly Val Val Gly Asp Ala Ile Gly Asp Ser Leu His His Gly Gly Ala
     50                  55                  60

His Lys Ala Ile Tyr Ala Tyr Ser Arg Glu Glu Leu Asp Phe Phe Asp
 65                  70                  75                  80

Pro Thr Tyr Arg Asn Gly Tyr Phe Gly Glu Asn Leu Thr Thr Ser Gly
                 85                  90                  95

Ile Val Leu Glu Asp Leu Leu Ile Asn Gln Gln Val Arg Ile Gly Thr
            100                 105                 110

Thr Leu Leu Glu Val Ser Ile Pro Arg Arg Pro Cys Arg Thr Phe Ala
        115                 120                 125

His Trp Leu Asp Ile Lys Gly Trp Leu Lys Thr Phe Thr Gln Arg Gly
    130                 135                 140

Leu Pro Gly Ser Tyr Phe Arg Val Ile Glu Glu Gly His Ile Asn Pro
145                 150                 155                 160

Gly Asp Pro Ile Glu Val Leu Gln Ala Pro Asp His Asp Ile Thr Met
                165                 170                 175

Ser Met Ala Phe Arg Ala Lys Met Gly Asn Lys Asp Leu Ala Arg Arg
            180                 185                 190

Val Val Ala Ala Asn Cys Leu Pro Ala Arg Tyr His Glu Glu Leu Leu
        195                 200                 205

Lys Leu Ile
    210
```

<210> 1755
<211> 525
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(502)
<223> RXA00429

<400> 1755
cgatggtggt cgccttcgtg atcgcccaag gcacccggaa cggtcatcaa cttcatcgtc 60

caaagaacca tcattttccg agtgaagtaa ggtacccctc atg aag acc ttc aat 115
                                                Met Lys Thr Phe Asn
                                                  1   5

ccc acc atg att gcc gga ctc atc ggc gta ctc tac ttc gtg ctg ctc 163

```
Pro Thr Met Ile Ala Gly Leu Ile Gly Val Leu Tyr Phe Val Leu Leu
                10                  15                  20

acc ctg att ttc tcc atc caa gac atg gaa cta gca gca gaa atc gcc   211
Thr Leu Ile Phe Ser Ile Gln Asp Met Glu Leu Ala Ala Glu Ile Ala
            25                  30                  35

ttc gga atc gtc acc atc gtc ggc ctg atc gcg gtg tgg gac aac ttc   259
Phe Gly Ile Val Thr Ile Val Gly Leu Ile Ala Val Trp Asp Asn Phe
        40                  45                  50

cgc gac cgc aac aac tcc acc tgg aaa acc tgg acc ggc ctc gtc ggc   307
Arg Asp Arg Asn Asn Ser Thr Trp Lys Thr Trp Thr Gly Leu Val Gly
    55                  60                  65

gga ctg cta atc gcc gtc ccc gga atc tgc ctt ctt gtg gga aac ctc   355
Gly Leu Leu Ile Ala Val Pro Gly Ile Cys Leu Leu Val Gly Asn Leu
70                  75                  80                  85

gtg ctc ctc gca gtc gac ggc aac ccc tca acc atg gtg aac acc ctg   403
Val Leu Leu Ala Val Asp Gly Asn Pro Ser Thr Met Val Asn Thr Leu
                90                  95                  100

ctc agc gtc gca ggg atc ggc gcg atc ttc ctc ctt ccg atc ggc atc   451
Leu Ser Val Ala Gly Ile Gly Ala Ile Phe Leu Leu Pro Ile Gly Ile
            105                 110                 115

atc atg tgc ctc atc gcc gga ttc aac cgc tac tac gca gcc ctt aag   499
Ile Met Cys Leu Ile Ala Gly Phe Asn Arg Tyr Tyr Ala Ala Leu Lys
        120                 125                 130

gtc taaaatgccc ggtctagttc tct                                    525
Val
```

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<210> 1756
<211> 134
<212> PRT
<213> Corynebacterium glutamicum

<400> 1756

```
Met Lys Thr Phe Asn Pro Thr Met Ile Ala Gly Leu Ile Gly Val Leu
  1               5                  10                  15

Tyr Phe Val Leu Leu Thr Leu Ile Phe Ser Ile Gln Asp Met Glu Leu
            20                  25                  30

Ala Ala Glu Ile Ala Phe Gly Ile Val Thr Ile Val Gly Leu Ile Ala
        35                  40                  45

Val Trp Asp Asn Phe Arg Asp Arg Asn Asn Ser Thr Trp Lys Thr Trp
    50                  55                  60

Thr Gly Leu Val Gly Gly Leu Leu Ile Ala Val Pro Gly Ile Cys Leu
65                  70                  75                  80

Leu Val Gly Asn Leu Val Leu Leu Ala Val Asp Gly Asn Pro Ser Thr
                85                  90                  95

Met Val Asn Thr Leu Leu Ser Val Ala Gly Ile Gly Ala Ile Phe Leu
```

```
            100                 105                 110

Leu Pro Ile Gly Ile Ile Met Cys Leu Ile Ala Gly Phe Asn Arg Tyr
        115                 120                 125

Tyr Ala Ala Leu Lys Val
    130


<210> 1757
<211> 534
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(511)
<223> RXA00430

<400> 1757
tgcccccgtg gatcgcctgg acatttatag ggagctgctg tgtttctagg tattgtgtaa 60

cctcgtgtcc gaaaatcttg atgttacgat cgtccgacca atg agc ctg aaa acc   115
                                            Met Ser Leu Lys Thr
                                              1               5

caa gct ttc cgg ttc atc ctc acc ggt ggc ctc tca gcc atc gtg gac   163
Gln Ala Phe Arg Phe Ile Leu Thr Gly Gly Leu Ser Ala Ile Val Asp
                10                  15                  20

ctc ggc ctg ctg tca ctt ttg cag cta gtg ttc ggc ctt ccc gta cct   211
Leu Gly Leu Leu Ser Leu Leu Gln Leu Val Phe Gly Leu Pro Val Pro
            25                  30                  35

gtt gcc cgc acg atc tcc ttc atc gcc ggc acc acc acc gcc tac atg   259
Val Ala Arg Thr Ile Ser Phe Ile Ala Gly Thr Thr Thr Ala Tyr Met
        40                  45                  50

atc aac cgc cgg tgg acc ttc caa gca gaa agc tcc acc tcc agg ttc   307
Ile Asn Arg Arg Trp Thr Phe Gln Ala Glu Ser Ser Thr Ser Arg Phe
    55                  60                  65

ctt gct gtg gtg gcc ctc tac ggc gtg acc ttc ctg atc aac att gga   355
Leu Ala Val Val Ala Leu Tyr Gly Val Thr Phe Leu Ile Asn Ile Gly
70                  75                  80                  85

ctg caa acc ctc tgc tcc gca ttg ttt gag aat tgg ggc tgg aac gaa   403
Leu Gln Thr Leu Cys Ser Ala Leu Phe Glu Asn Trp Gly Trp Asn Glu
                90                  95                  100

gcc gtc gcg atg gtg gtc gcc ttc gtg atc gcc caa ggc acc cgg aac   451
Ala Val Ala Met Val Val Ala Phe Val Ile Ala Gln Gly Thr Arg Asn
            105                 110                 115

ggt cat caa ctt cat cgt cca aag aac cat cat ttt ccg agt gaa gta   499
Gly His Gln Leu His Arg Pro Lys Asn His His Phe Pro Ser Glu Val
        120                 125                 130

agg tac ccc tca tgaagacctt caatcccacc atg                        534
Arg Tyr Pro Ser
    135
```

<210> 1758
<211> 137
<212> PRT
<213> Corynebacterium glutamicum

<400> 1758

```
Met Ser Leu Lys Thr Gln Ala Phe Arg Phe Ile Leu Thr Gly Gly Leu
  1               5                  10                  15

Ser Ala Ile Val Asp Leu Gly Leu Leu Ser Leu Leu Gln Leu Val Phe
             20                  25                  30

Gly Leu Pro Val Pro Val Ala Arg Thr Ile Ser Phe Ile Ala Gly Thr
         35                  40                  45

Thr Thr Ala Tyr Met Ile Asn Arg Arg Trp Thr Phe Gln Ala Glu Ser
     50                  55                  60

Ser Thr Ser Arg Phe Leu Ala Val Val Ala Leu Tyr Gly Val Thr Phe
 65                  70                  75                  80

Leu Ile Asn Ile Gly Leu Gln Thr Leu Cys Ser Ala Leu Phe Glu Asn
                 85                  90                  95

Trp Gly Trp Asn Glu Ala Val Ala Met Val Val Ala Phe Val Ile Ala
            100                 105                 110

Gln Gly Thr Arg Asn Gly His Gln Leu His Arg Pro Lys Asn His His
        115                 120                 125

Phe Pro Ser Glu Val Arg Tyr Pro Ser
    130                 135
```

<210> 1759
<211> 648
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(625)
<223> RXA00433

<400> 1759

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gtctccagcg actcaaacat caaaaattga tatttgcgac aagttgaaat catacccgat 60

agtctcgaac atactaaatc acctaatcag ggggaattac atg gat gtg tta aag   115
                                          Met Asp Val Leu Lys
                                            1               5

atc gcc atc atc gct gca gcc atg att ggt gtg ccg gtt ctg gtg gtt   163
Ile Ala Ile Ile Ala Ala Ala Met Ile Gly Val Pro Val Leu Val Val
                 10                  15                  20

ttc ctc att gtg ttt gcg gtg cac aag ttg gct aag gaa gtg ccg cgg   211
Phe Leu Ile Val Phe Ala Val His Lys Leu Ala Lys Glu Val Pro Arg
             25                  30                  35
```

```
tct ggt cgt cgt ccg ggt att ggg ttg ggg ttg ttg ctt ggt ttt gtt   259
Ser Gly Arg Arg Pro Gly Ile Gly Leu Gly Leu Leu Leu Gly Phe Val
         40                  45                  50

gcg ggg ctc atc gtg tgg ttt gtg tgg ttg agt tgg ggt ggt tat tac   307
Ala Gly Leu Ile Val Trp Phe Val Trp Leu Ser Trp Gly Gly Tyr Tyr
     55                  60                  65

gag aat gag ttt ggg cag atg caa ggt ccg tat cgt ccg tgg cag gtt   355
Glu Asn Glu Phe Gly Gln Met Gln Gly Pro Tyr Arg Pro Trp Gln Val
 70                  75                  80                  85

gtt gct tgt ggt gtc acg atg gtc gcg gtc act gtg att ctt ggt ctg   403
Val Ala Cys Gly Val Thr Met Val Ala Val Thr Val Ile Leu Gly Leu
                 90                  95                 100

tgg act agg tgg act gcg tct ggt ccg ttt tat tcg gcg ttg ggt ggt   451
Trp Thr Arg Trp Thr Ala Ser Gly Pro Phe Tyr Ser Ala Leu Gly Gly
            105                 110                 115

gcg tcg ggg ttt agt ttc gcg tgg gcc atg gat gcc att cct cag gat   499
Ala Ser Gly Phe Ser Phe Ala Trp Ala Met Asp Ala Ile Pro Gln Asp
        120                 125                 130

gaa acc gga ttg tcg gcg ttt ggc tta gtg atg gtc att gtt ggt gtt   547
Glu Thr Gly Leu Ser Ala Phe Gly Leu Val Met Val Ile Val Gly Val
    135                 140                 145

ggt gcg ggg cta aat gtg gtg gca act ctg acg tca atc ggc gca acg   595
Gly Ala Gly Leu Asn Val Val Ala Thr Leu Thr Ser Ile Gly Ala Thr
150                 155                 160                 165

atc tgg aat aac cgg cta ccc tcg aat gca tgactaaaac cacgcgccaa     645
Ile Trp Asn Asn Arg Leu Pro Ser Asn Ala
                170                 175

acc                                                              648
```

<210> 1760
<211> 175
<212> PRT
<213> Corynebacterium glutamicum

<400> 1760

```
Met Asp Val Leu Lys Ile Ala Ile Ile Ala Ala Ala Met Ile Gly Val
  1               5                  10                  15

Pro Val Leu Val Val Phe Leu Ile Val Phe Ala Val His Lys Leu Ala
             20                  25                  30

Lys Glu Val Pro Arg Ser Gly Arg Arg Pro Gly Ile Gly Leu Gly Leu
         35                  40                  45

Leu Leu Gly Phe Val Ala Gly Leu Ile Val Trp Phe Val Trp Leu Ser
     50                  55                  60

Trp Gly Gly Tyr Tyr Glu Asn Glu Phe Gly Gln Met Gln Gly Pro Tyr
 65                  70                  75                  80

Arg Pro Trp Gln Val Val Ala Cys Gly Val Thr Met Val Ala Val Thr
```

```
                85                  90                  95

Val Ile Leu Gly Leu Trp Thr Arg Trp Thr Ala Ser Gly Pro Phe Tyr
            100                 105                 110

Ser Ala Leu Gly Gly Ala Ser Gly Phe Ser Phe Ala Trp Ala Met Asp
        115                 120                 125

Ala Ile Pro Gln Asp Glu Thr Gly Leu Ser Ala Phe Gly Leu Val Met
    130                 135                 140

Val Ile Val Gly Val Gly Ala Gly Leu Asn Val Val Ala Thr Leu Thr
145                 150                 155                 160

Ser Ile Gly Ala Thr Ile Trp Asn Asn Arg Leu Pro Ser Asn Ala
                165                 170                 175


<210> 1761
<211> 615
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(592)
<223> RXA00451

<400> 1761
ggatccgccg atgaggccga ggcccaggat gcatactggg cgggaaatgt ctttggtagt 60

cacctgacaa gtgtggcaca tacctactac ggttatctct atg aac act gaa gag   115
                                          Met Asn Thr Glu Glu
                                            1               5

gat ggc ctg agc ttt gca gtt acg gct acc tta gtt gaa ggt aaa tgg   163
Asp Gly Leu Ser Phe Ala Val Thr Ala Thr Leu Val Glu Gly Lys Trp
                10                  15                  20

cag gta cgc gag ttt gag gat cac ttc tcc aag ctc tct acc tct att   211
Gln Val Arg Glu Phe Glu Asp His Phe Ser Lys Leu Ser Thr Ser Ile
            25                  30                  35

aat gcg gtt cgc tcg ctg cgt agc gag ggg ccg gcg ttt gcg ctg ttg   259
Asn Ala Val Arg Ser Leu Arg Ser Glu Gly Pro Ala Phe Ala Leu Leu
        40                  45                  50

tgc gtt gat gat gaa tat ttt gtg atg gtg cgt ccc acc cca agt agg   307
Cys Val Asp Asp Glu Tyr Phe Val Met Val Arg Pro Thr Pro Ser Arg
    55                  60                  65

gta ttc ctt ttc ctt tcg gat gcg ccg atg gct gtc gac gat gat ttc   355
Val Phe Leu Phe Leu Ser Asp Ala Pro Met Ala Val Asp Asp Asp Phe
70                  75                  80                  85

gcc gcc gcg gtg atg gat gaa ctc gat gcg gat ctt cca gat atc aac   403
Ala Ala Ala Val Met Asp Glu Leu Asp Ala Asp Leu Pro Asp Ile Asn
                90                  95                  100

cct gat gat ttg gac gac atc gat cca tgg cca gaa ggt gat ttc gat   451
Pro Asp Asp Leu Asp Asp Ile Asp Pro Trp Pro Glu Gly Asp Phe Asp
```

```
            105                 110                 115

att ttg gcg gat ttg ggg ctg tct gag gag gtt ctt tcc gtg att tgc   499
Ile Leu Ala Asp Leu Gly Leu Ser Glu Glu Val Leu Ser Val Ile Cys
        120                 125                 130

gat gac atg gat ttg gat cct tcc gaa caa ttg ctg cgc atc gcg gaa   547
Asp Asp Met Asp Leu Asp Pro Ser Glu Gln Leu Leu Arg Ile Ala Glu
    135                 140                 145

gaa ctc ggt ttt gat aat gat ctg gct cgg gtg gtg gga ttc gac       592
Glu Leu Gly Phe Asp Asn Asp Leu Ala Arg Val Val Gly Phe Asp
150                 155                 160

tagtgggcgt tttacctgtg cag                                        615
```

<210> 1762
<211> 164
<212> PRT
<213> Corynebacterium glutamicum

<400> 1762

```
Met Asn Thr Glu Glu Asp Gly Leu Ser Phe Ala Val Thr Ala Thr Leu
  1               5                  10                  15

Val Glu Gly Lys Trp Gln Val Arg Glu Phe Glu Asp His Phe Ser Lys
             20                  25                  30

Leu Ser Thr Ser Ile Asn Ala Val Arg Ser Leu Arg Ser Glu Gly Pro
         35                  40                  45

Ala Phe Ala Leu Leu Cys Val Asp Asp Glu Tyr Phe Val Met Val Arg
     50                  55                  60

Pro Thr Pro Ser Arg Val Phe Leu Phe Leu Ser Asp Ala Pro Met Ala
 65                  70                  75                  80

Val Asp Asp Asp Phe Ala Ala Ala Val Met Asp Glu Leu Asp Ala Asp
                 85                  90                  95

Leu Pro Asp Ile Asn Pro Asp Asp Leu Asp Asp Ile Asp Pro Trp Pro
            100                 105                 110

Glu Gly Asp Phe Asp Ile Leu Ala Asp Leu Gly Leu Ser Glu Glu Val
        115                 120                 125

Leu Ser Val Ile Cys Asp Asp Met Asp Leu Asp Pro Ser Glu Gln Leu
    130                 135                 140

Leu Arg Ile Ala Glu Glu Leu Gly Phe Asp Asn Asp Leu Ala Arg Val
145                 150                 155                 160

Val Gly Phe Asp
```

<210> 1763
<211> 1203
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1180)
<223> RXA00457

<400> 1763
aaactctcat gttggtttca tcgtggtttc atgaggcggg atttaactag agattgttag 60

ccaatcggcc agacacttcc tcctagaaag gtccctcctc atg acc att gct ctt 115
Met Thr Ile Ala Leu
1 5

gaa cac cca gta ctg cac tcc acg gcg atc gcg ttg cct gct cgt ttt 163
Glu His Pro Val Leu His Ser Thr Ala Ile Ala Leu Pro Ala Arg Phe
10 15 20

cag gcg agc tat acg acg cgt ttg gtg gcg gtg ggc gtc gat aag cgt 211
Gln Ala Ser Tyr Thr Thr Arg Leu Val Ala Val Gly Val Asp Lys Arg
25 30 35

cct tct gat ttt tgg ttg gaa aca gcc ggc acg ccg cag gcg ggc gat 259
Pro Ser Asp Phe Trp Leu Glu Thr Ala Gly Thr Pro Gln Ala Gly Asp
40 45 50

gtg gtg att gcg cgg gtg acg gcg att aat aat cac aag cgg gtg gag 307
Val Val Ile Ala Arg Val Thr Ala Ile Asn Asn His Lys Arg Val Glu
55 60 65

acg ccg gag tcg cgc aag gcc att ttg ttt gag ggg gtg ttg gtg atg 355
Thr Pro Glu Ser Arg Lys Ala Ile Leu Phe Glu Gly Val Leu Val Met
70 75 80 85

ttg gcg tat ggg cac cgg tat gcg gcg gat cag ttt tta gcg cat gta 403
Leu Ala Tyr Gly His Arg Tyr Ala Ala Asp Gln Phe Leu Ala His Val
90 95 100

ccg gag gat ttg ggg cca tgc cat ttg gtg gcg gct ggt ggc atc gcg 451
Pro Glu Asp Leu Gly Pro Cys His Leu Val Ala Ala Gly Gly Ile Ala
105 110 115

gga acg gtg acg gcg ctg cac gat cgg gtg gat gaa ccc aca gag att 499
Gly Thr Val Thr Ala Leu His Asp Arg Val Asp Glu Pro Thr Glu Ile
120 125 130

gaa ccg ttg gga ttg ctc acc aat gcg cgc gga act gtg aat gta cgg 547
Glu Pro Leu Gly Leu Leu Thr Asn Ala Arg Gly Thr Val Asn Val Arg
135 140 145

gac ttt gcg gct ttt gat aat cct ttg aaa gtg gag gct ccc aac aag 595
Asp Phe Ala Ala Phe Asp Asn Pro Leu Lys Val Glu Ala Pro Asn Lys
150 155 160 165

cgt gcg cag gtg atc gcg gtg ctg gga acg tcg atg aac tct gga aaa 643
Arg Ala Gln Val Ile Ala Val Leu Gly Thr Ser Met Asn Ser Gly Lys
170 175 180

tcc acc acg ctt gcc tgc ttg gtc aat ggt ttg gct gcg gcg ggg cag 691
Ser Thr Thr Leu Ala Cys Leu Val Asn Gly Leu Ala Ala Ala Gly Gln
185 190 195

```
aag gtg gcg gct gga aag atc acg ggc act ggt gct gga aat gac cgc   739
Lys Val Ala Ala Gly Lys Ile Thr Gly Thr Gly Ala Gly Asn Asp Arg
        200                 205                 210

atg att tat cac gat gct ggt gct cac agc gtt att gat ttc acc gac   787
Met Ile Tyr His Asp Ala Gly Ala His Ser Val Ile Asp Phe Thr Asp
    215                 220                 225

ttt ggc tac cca act acg ttc aag ctg aat ttc gcg gag att cgt gcg   835
Phe Gly Tyr Pro Thr Thr Phe Lys Leu Asn Phe Ala Glu Ile Arg Ala
230                 235                 240                 245

ctg agc gtc aac atg att aat gtg ctg gct gat tct ggt gcg gat acc   883
Leu Ser Val Asn Met Ile Asn Val Leu Ala Asp Ser Gly Ala Asp Thr
                250                 255                 260

gtg atc gtg gaa atc gcg gac gga att tat cag ggc gaa acc tcg cgg   931
Val Ile Val Glu Ile Ala Asp Gly Ile Tyr Gln Gly Glu Thr Ser Arg
            265                 270                 275

ctg ttg cgc gat caa gtg ttc cag gaa gcc gtg gat cat gtg gtg ttc   979
Leu Leu Arg Asp Gln Val Phe Gln Glu Ala Val Asp His Val Val Phe
        280                 285                 290

tcc gct gtt gat gcc ttg ggc gcg aag gcc ggt gtg cag gaa ctg cag   1027
Ser Ala Val Asp Ala Leu Gly Ala Lys Ala Gly Val Gln Glu Leu Gln
    295                 300                 305

gcg gcg ggg ctt cat gtg gct gcg gcc tcc gga gtg atg acg gct tcg   1075
Ala Ala Gly Leu His Val Ala Ala Ala Ser Gly Val Met Thr Ala Ser
310                 315                 320                 325

ccg ctg gcc acc gcg gaa gct gcc gct gtg ctt gaa gtt cca gtg gtg   1123
Pro Leu Ala Thr Ala Glu Ala Ala Ala Val Leu Glu Val Pro Val Val
                330                 335                 340

ccc act ttt gat ctc acc aac ccg gag atc gtc aca gcg gtg cta acg   1171
Pro Thr Phe Asp Leu Thr Asn Pro Glu Ile Val Thr Ala Val Leu Thr
            345                 350                 355

gat cat gcc tagcttatgg cgtgctcgtc gca                            1203
Asp His Ala
        360
```

<210> 1764
<211> 360
<212> PRT
<213> Corynebacterium glutamicum

<400> 1764

```
Met Thr Ile Ala Leu Glu His Pro Val Leu His Ser Thr Ala Ile Ala
  1               5                  10                  15

Leu Pro Ala Arg Phe Gln Ala Ser Tyr Thr Thr Arg Leu Val Ala Val
             20                  25                  30

Gly Val Asp Lys Arg Pro Ser Asp Phe Trp Leu Glu Thr Ala Gly Thr
         35                  40                  45

Pro Gln Ala Gly Asp Val Val Ile Ala Arg Val Thr Ala Ile Asn Asn
```

```
     50                  55                  60

His Lys Arg Val Glu Thr Pro Glu Ser Arg Lys Ala Ile Leu Phe Glu
 65                  70                  75                  80

Gly Val Leu Val Met Leu Ala Tyr Gly His Arg Tyr Ala Ala Asp Gln
                 85                  90                  95

Phe Leu Ala His Val Pro Glu Asp Leu Gly Pro Cys His Leu Val Ala
            100                 105                 110

Ala Gly Gly Ile Ala Gly Thr Val Thr Ala Leu His Asp Arg Val Asp
        115                 120                 125

Glu Pro Thr Glu Ile Glu Pro Leu Gly Leu Leu Thr Asn Ala Arg Gly
    130                 135                 140

Thr Val Asn Val Arg Asp Phe Ala Ala Phe Asp Asn Pro Leu Lys Val
145                 150                 155                 160

Glu Ala Pro Asn Lys Arg Ala Gln Val Ile Ala Val Leu Gly Thr Ser
                165                 170                 175

Met Asn Ser Gly Lys Ser Thr Thr Leu Ala Cys Leu Val Asn Gly Leu
            180                 185                 190

Ala Ala Ala Gly Gln Lys Val Ala Ala Gly Lys Ile Thr Gly Thr Gly
        195                 200                 205

Ala Gly Asn Asp Arg Met Ile Tyr His Asp Ala Gly Ala His Ser Val
    210                 215                 220

Ile Asp Phe Thr Asp Phe Gly Tyr Pro Thr Thr Phe Lys Leu Asn Phe
225                 230                 235                 240

Ala Glu Ile Arg Ala Leu Ser Val Asn Met Ile Asn Val Leu Ala Asp
                245                 250                 255

Ser Gly Ala Asp Thr Val Ile Val Glu Ile Ala Asp Gly Ile Tyr Gln
            260                 265                 270

Gly Glu Thr Ser Arg Leu Leu Arg Asp Gln Val Phe Gln Glu Ala Val
        275                 280                 285

Asp His Val Val Phe Ser Ala Val Asp Ala Leu Gly Ala Lys Ala Gly
    290                 295                 300

Val Gln Glu Leu Gln Ala Ala Gly Leu His Val Ala Ala Ala Ser Gly
305                 310                 315                 320

Val Met Thr Ala Ser Pro Leu Ala Thr Ala Glu Ala Ala Ala Val Leu
                325                 330                 335

Glu Val Pro Val Val Pro Thr Phe Asp Leu Thr Asn Pro Glu Ile Val
            340                 345                 350

Thr Ala Val Leu Thr Asp His Ala
        355                 360
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<210> 1765

<211> 1503
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1480)
<223> RXA00462

<400> 1765
tgaagccttg tcatttttcta catgtgcatc cgctttgact accgcccttt tccgcccagt 60

```
cctttttagaa accagcaaca cagaaagcaa gtgatcattt atg gaa gct att gcc   115
                                              Met Glu Ala Ile Ala
                                                1               5

ata cta ttt gtc att ggg gcg att ctt gtc gtc gcg gtc att gtc ctc   163
Ile Leu Phe Val Ile Gly Ala Ile Leu Val Val Ala Val Ile Val Leu
                 10                  15                  20

ggt att ttc ttc tta act tca cgc acc tgg atc aag gtg gct gca gct   211
Gly Ile Phe Phe Leu Thr Ser Arg Thr Trp Ile Lys Val Ala Ala Ala
             25                  30                  35

gat gaa gcg ctc att gtc tct gcg aag aag aag ggg gaa tcg cag gtc   259
Asp Glu Ala Leu Ile Val Ser Ala Lys Lys Lys Gly Glu Ser Gln Val
         40                  45                  50

att gtc cac ggc aaa gct gtg gta atg cct att acc cag act cac cag   307
Ile Val His Gly Lys Ala Val Val Met Pro Ile Thr Gln Thr His Gln
     55                  60                  65

aag atc tct ctg cgt tcc cgt cag gta aat atg cag gtg acg gca caa   355
Lys Ile Ser Leu Arg Ser Arg Gln Val Asn Met Gln Val Thr Ala Gln
 70                  75                  80                  85

agc gat gac aat gtc acg ttg aat gtc gag gct gtt gcg ctg gtg aag   403
Ser Asp Asp Asn Val Thr Leu Asn Val Glu Ala Val Ala Leu Val Lys
                 90                  95                 100

atc ggt tcc gaa gct gag ttt att cgt cgc gct gcc cag cgc ttc gct   451
Ile Gly Ser Glu Ala Glu Phe Ile Arg Arg Ala Ala Gln Arg Phe Ala
            105                 110                 115

tcc agt gac aaa gaa att gtt cgg ttc aca cag gat cag ctg gaa ggt   499
Ser Ser Asp Lys Glu Ile Val Arg Phe Thr Gln Asp Gln Leu Glu Gly
        120                 125                 130

gtg ctt cgt ggt gtc gtg gcg cag caa aca gtc acg tcg ctc atg cgt   547
Val Leu Arg Gly Val Val Ala Gln Gln Thr Val Thr Ser Leu Met Arg
    135                 140                 145

gag cgt aaa aaa ttc tcc gag cag atc gct gaa aca gtc atc ccc gag   595
Glu Arg Lys Lys Phe Ser Glu Gln Ile Ala Glu Thr Val Ile Pro Glu
150                 155                 160                 165

cta gag aag cag ggt ttg att ctt gac tcc ttc cag att cgt ggc atc   643
Leu Glu Lys Gln Gly Leu Ile Leu Asp Ser Phe Gln Ile Arg Gly Ile
                170                 175                 180

acc gat gat gtg gga tac atc aaa tcc ctc ggc gca ccg gaa att cag   691
```

```
Thr Asp Asp Val Gly Tyr Ile Lys Ser Leu Gly Ala Pro Glu Ile Gln
            185                 190                 195

gca aag aag cag gct gcg gaa att gca gaa act gaa gct gct cgt gcg   739
Ala Lys Lys Gln Ala Ala Glu Ile Ala Glu Thr Glu Ala Ala Arg Ala
        200                 205                 210

atc gct aaa tca cgc att gct aac caa gag gca gat ctg gtt gaa cag   787
Ile Ala Lys Ser Arg Ile Ala Asn Gln Glu Ala Asp Leu Val Glu Gln
    215                 220                 225

acc caa ctt gat gcc aac aag gct gcc gct gat gct cag gtc ggt gaa   835
Thr Gln Leu Asp Ala Asn Lys Ala Ala Ala Asp Ala Gln Val Gly Glu
230                 235                 240                 245

gcc cgt gcc cag gct atg cag gct gaa cgc ctt gcc gat gaa aaa gct   883
Ala Arg Ala Gln Ala Met Gln Ala Glu Arg Leu Ala Asp Glu Lys Ala
                250                 255                 260

cga cta gag gtt ctt cgc caa cag gct gaa aat aag cag atc gag ctg   931
Arg Leu Glu Val Leu Arg Gln Gln Ala Glu Asn Lys Gln Ile Glu Leu
            265                 270                 275

gaa gcc gaa gtg aac aag gtg gcc gac gct gaa cgc tac cgc cgc aag   979
Glu Ala Glu Val Asn Lys Val Ala Asp Ala Glu Arg Tyr Arg Arg Lys
        280                 285                 290

cag gaa gtc gaa gcc gat act ttc gag caa acc agg cgc gca cag gct  1027
Gln Glu Val Glu Ala Asp Thr Phe Glu Gln Thr Arg Arg Ala Gln Ala
    295                 300                 305

cag gtc gaa atc gca gaa gcc gaa gct acc gct gca aag gtt cgt gca  1075
Gln Val Glu Ile Ala Glu Ala Glu Ala Thr Ala Ala Lys Val Arg Ala
310                 315                 320                 325

atg gct gaa gcc gaa gct gtt cga ttg aag gga cag gca gag gca gac  1123
Met Ala Glu Ala Glu Ala Val Arg Leu Lys Gly Gln Ala Glu Ala Asp
                330                 335                 340

gct atc aag gca aag gcc gag gcc tac cgc gaa aac caa gaa gca cta  1171
Ala Ile Lys Ala Lys Ala Glu Ala Tyr Arg Glu Asn Gln Glu Ala Leu
            345                 350                 355

ctc gcc cag caa gcc atg gaa atc ctg ccg gaa ctc atg agc aac ttc  1219
Leu Ala Gln Gln Ala Met Glu Ile Leu Pro Glu Leu Met Ser Asn Phe
        360                 365                 370

gcc tct gga tac gca aac att gga tcc atg aca gtg ctc tcc ggt gga  1267
Ala Ser Gly Tyr Ala Asn Ile Gly Ser Met Thr Val Leu Ser Gly Gly
    375                 380                 385

gaa gga tcc gag aat tcc gtg ggt tca cgt ttt gcc ggt gaa caa gca  1315
Glu Gly Ser Glu Asn Ser Val Gly Ser Arg Phe Ala Gly Glu Gln Ala
390                 395                 400                 405

ctt gga ctg aaa tcc att att gaa tca gtc aag caa acc acc ggc att  1363
Leu Gly Leu Lys Ser Ile Ile Glu Ser Val Lys Gln Thr Thr Gly Ile
                410                 415                 420

gat cta gct gag atc atc caa ggc cgt gct gct gga cat gca cag ggc  1411
Asp Leu Ala Glu Ile Ile Gln Gly Arg Ala Ala Gly His Ala Gln Gly
```

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            425                 430                 435

tcc gct cag ggt gca gcg att gct gaa gcg ctt tca cgc gat gaa act   1459
Ser Ala Gln Gly Ala Ala Ile Ala Glu Ala Leu Ser Arg Asp Glu Thr
        440                 445                 450

gtg gaa gat cgc tct gaa aaa taatctagct gcccagcgca tcg             1503
Val Glu Asp Arg Ser Glu Lys
    455                 460


<210> 1766
<211> 460
<212> PRT
<213> Corynebacterium glutamicum

<400> 1766
Met Glu Ala Ile Ala Ile Leu Phe Val Ile Gly Ala Ile Leu Val Val
  1               5                  10                  15

Ala Val Ile Val Leu Gly Ile Phe Phe Leu Thr Ser Arg Thr Trp Ile
             20                  25                  30

Lys Val Ala Ala Ala Asp Glu Ala Leu Ile Val Ser Ala Lys Lys Lys
         35                  40                  45

Gly Glu Ser Gln Val Ile Val His Gly Lys Ala Val Val Met Pro Ile
     50                  55                  60

Thr Gln Thr His Gln Lys Ile Ser Leu Arg Ser Arg Gln Val Asn Met
 65                  70                  75                  80

Gln Val Thr Ala Gln Ser Asp Asp Asn Val Thr Leu Asn Val Glu Ala
                 85                  90                  95

Val Ala Leu Val Lys Ile Gly Ser Glu Ala Glu Phe Ile Arg Arg Ala
            100                 105                 110

Ala Gln Arg Phe Ala Ser Ser Asp Lys Glu Ile Val Arg Phe Thr Gln
        115                 120                 125

Asp Gln Leu Glu Gly Val Leu Arg Gly Val Val Ala Gln Gln Thr Val
    130                 135                 140

Thr Ser Leu Met Arg Glu Arg Lys Lys Phe Ser Glu Gln Ile Ala Glu
145                 150                 155                 160

Thr Val Ile Pro Glu Leu Glu Lys Gln Gly Leu Ile Leu Asp Ser Phe
                165                 170                 175

Gln Ile Arg Gly Ile Thr Asp Asp Val Gly Tyr Ile Lys Ser Leu Gly
            180                 185                 190

Ala Pro Glu Ile Gln Ala Lys Lys Gln Ala Ala Glu Ile Ala Glu Thr
        195                 200                 205

Glu Ala Ala Arg Ala Ile Ala Lys Ser Arg Ile Ala Asn Gln Glu Ala
    210                 215                 220

Asp Leu Val Glu Gln Thr Gln Leu Asp Ala Asn Lys Ala Ala Ala Asp
225                 230                 235                 240
```

```
Ala Gln Val Gly Glu Ala Arg Ala Gln Ala Met Gln Ala Glu Arg Leu
               245                 250                 255

Ala Asp Glu Lys Ala Arg Leu Glu Val Leu Arg Gln Gln Ala Glu Asn
            260                 265                 270

Lys Gln Ile Glu Leu Glu Ala Glu Val Asn Lys Val Ala Asp Ala Glu
        275                 280                 285

Arg Tyr Arg Arg Lys Gln Glu Val Glu Ala Asp Thr Phe Glu Gln Thr
    290                 295                 300

Arg Arg Ala Gln Ala Gln Val Glu Ile Ala Glu Ala Glu Ala Thr Ala
305                 310                 315                 320

Ala Lys Val Arg Ala Met Ala Glu Ala Glu Ala Val Arg Leu Lys Gly
                325                 330                 335

Gln Ala Glu Ala Asp Ala Ile Lys Ala Lys Ala Glu Ala Tyr Arg Glu
            340                 345                 350

Asn Gln Glu Ala Leu Leu Ala Gln Gln Ala Met Glu Ile Leu Pro Glu
        355                 360                 365

Leu Met Ser Asn Phe Ala Ser Gly Tyr Ala Asn Ile Gly Ser Met Thr
    370                 375                 380

Val Leu Ser Gly Gly Glu Gly Ser Glu Asn Ser Val Gly Ser Arg Phe
385                 390                 395                 400

Ala Gly Glu Gln Ala Leu Gly Leu Lys Ser Ile Ile Glu Ser Val Lys
                405                 410                 415

Gln Thr Thr Gly Ile Asp Leu Ala Glu Ile Ile Gln Gly Arg Ala Ala
            420                 425                 430

Gly His Ala Gln Gly Ser Ala Gln Gly Ala Ala Ile Ala Glu Ala Leu
        435                 440                 445

Ser Arg Asp Glu Thr Val Glu Asp Arg Ser Glu Lys
    450                 455                 460
```

<210> 1767
<211> 945
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(922)
<223> RXA00463

<400> 1767
taccacgcta gtcgccagca ctctcggatt aagcggatgt acctccgtaa cttccagtgc 60

tacgagctcc cctgaaccgc cgactaaagt tgcggcggca atg cag aca acg act 115
                                    Met Gln Thr Thr Thr
                                      1   5

```
ggg gag acg tcg ata agc aat gaa acc tcg ttt aac gcc tca cgc gaa   163
Gly Glu Thr Ser Ile Ser Asn Glu Thr Ser Phe Asn Ala Ser Arg Glu
                 10                  15                  20

acc tcg ctg acg gcg ctg ggt ttc ttg gac tat ctt gac gag gag caa   211
Thr Ser Leu Thr Ala Leu Gly Phe Leu Asp Tyr Leu Asp Glu Glu Gln
             25                  30                  35

cgc gcc gcc ttg ctc ggt gaa ggc ctg gac atc agc acg ctg acc tgg   259
Arg Ala Ala Leu Leu Gly Glu Gly Leu Asp Ile Ser Thr Leu Thr Trp
         40                  45                  50

gcc aac cag gtt acc gcg ctg cgt gtg ctg gaa tcc ctc ttc aat gag   307
Ala Asn Gln Val Thr Ala Leu Arg Val Leu Glu Ser Leu Phe Asn Glu
     55                  60                  65

cat gca tac gag ctg gtt tct gca gtg att cag cat gta gct caa gaa   355
His Ala Tyr Glu Leu Val Ser Ala Val Ile Gln His Val Ala Gln Glu
 70                  75                  80                  85

cct ggc gat aat cca cac cac ttt ctg aag ttc tcg cct gaa cca tcc   403
Pro Gly Asp Asn Pro His His Phe Leu Lys Phe Ser Pro Glu Pro Ser
                 90                  95                 100

acc gag aat tct tgg gaa ttg acc ctg gat gga cca act gtc gga ttg   451
Thr Glu Asn Ser Trp Glu Leu Thr Leu Asp Gly Pro Thr Val Gly Leu
            105                 110                 115

aaa gtc act ttc gat ccg gac ggt cag atc act ttc aag gat gct cat   499
Lys Val Thr Phe Asp Pro Asp Gly Gln Ile Thr Phe Lys Asp Ala His
        120                 125                 130

ttg ggc ctg agc cca gct gag gtc gtt agt gtc act gag gcg tta gat   547
Leu Gly Leu Ser Pro Ala Glu Val Val Ser Val Thr Glu Ala Leu Asp
    135                 140                 145

acc tcc tat tcg gaa tcg caa atc aaa aaa gct gcg gaa caa ctg gtg   595
Thr Ser Tyr Ser Glu Ser Gln Ile Lys Lys Ala Ala Glu Gln Leu Val
150                 155                 160                 165

gga agc ctc aat cca acc cag cag gca gcg ctc caa gga tcc ggt ttg   643
Gly Ser Leu Asn Pro Thr Gln Gln Ala Ala Leu Gln Gly Ser Gly Leu
                170                 175                 180

cga gga gca cag ctc act gaa gag caa aag acc ctg ttc tta aag atg   691
Arg Gly Ala Gln Leu Thr Glu Glu Gln Lys Thr Leu Phe Leu Lys Met
            185                 190                 195

acc tcc aac tgg atc gac ctt gcc aat ggc gat tcc ggc tct gaa cag   739
Thr Ser Asn Trp Ile Asp Leu Ala Asn Gly Asp Ser Gly Ser Glu Gln
        200                 205                 210

caa gaa gaa atc gct gat acg ttc agt gat acc tac atc att tgg aat   787
Gln Glu Glu Ile Ala Asp Thr Phe Ser Asp Thr Tyr Ile Ile Trp Asn
    215                 220                 225

gag cag aaa gat ggc tca gca ttc ttc cag atg aaa ggc cct gag ctc   835
Glu Gln Lys Asp Gly Ser Ala Phe Phe Gln Met Lys Gly Pro Glu Leu
230                 235                 240                 245

gac ttc agc tat aaa gag agc gtg cct gaa aac gct gaa ctc tct gca   883
```

```
Asp Phe Ser Tyr Lys Glu Ser Val Pro Glu Asn Ala Glu Leu Ser Ala
                250                 255                 260

cgg gga gtc ccc aat att cag acc tct ttt cag tca cct taactggcat    932
Arg Gly Val Pro Asn Ile Gln Thr Ser Phe Gln Ser Pro
            265                 270

tggtttagtt tgg                                                   945


<210> 1768
<211> 274
<212> PRT
<213> Corynebacterium glutamicum

<400> 1768
Met Gln Thr Thr Thr Gly Glu Thr Ser Ile Ser Asn Glu Thr Ser Phe
  1               5                  10                  15

Asn Ala Ser Arg Glu Thr Ser Leu Thr Ala Leu Gly Phe Leu Asp Tyr
             20                  25                  30

Leu Asp Glu Glu Gln Arg Ala Ala Leu Leu Gly Glu Gly Leu Asp Ile
         35                  40                  45

Ser Thr Leu Thr Trp Ala Asn Gln Val Thr Ala Leu Arg Val Leu Glu
     50                  55                  60

Ser Leu Phe Asn Glu His Ala Tyr Glu Leu Val Ser Ala Val Ile Gln
 65                  70                  75                  80

His Val Ala Gln Glu Pro Gly Asp Asn Pro His His Phe Leu Lys Phe
                85                  90                  95

Ser Pro Glu Pro Ser Thr Glu Asn Ser Trp Glu Leu Thr Leu Asp Gly
            100                 105                 110

Pro Thr Val Gly Leu Lys Val Thr Phe Asp Pro Asp Gly Gln Ile Thr
        115                 120                 125

Phe Lys Asp Ala His Leu Gly Leu Ser Pro Ala Glu Val Val Ser Val
    130                 135                 140

Thr Glu Ala Leu Asp Thr Ser Tyr Ser Glu Ser Gln Ile Lys Lys Ala
145                 150                 155                 160

Ala Glu Gln Leu Val Gly Ser Leu Asn Pro Thr Gln Gln Ala Ala Leu
                165                 170                 175

Gln Gly Ser Gly Leu Arg Gly Ala Gln Leu Thr Glu Glu Gln Lys Thr
            180                 185                 190

Leu Phe Leu Lys Met Thr Ser Asn Trp Ile Asp Leu Ala Asn Gly Asp
        195                 200                 205

Ser Gly Ser Glu Gln Gln Glu Glu Ile Ala Asp Thr Phe Ser Asp Thr
    210                 215                 220

Tyr Ile Ile Trp Asn Glu Gln Lys Asp Gly Ser Ala Phe Phe Gln Met
225                 230                 235                 240
```

```
Lys Gly Pro Glu Leu Asp Phe Ser Tyr Lys Glu Ser Val Pro Glu Asn
                245                 250                 255

Ala Glu Leu Ser Ala Arg Gly Val Pro Asn Ile Gln Thr Ser Phe Gln
            260                 265                 270

Ser Pro
```

<210> 1769
<211> 942
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(919)
<223> RXA00468

<400> 1769

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ggcagaattt tgctcaagtt gcctaaatca agcacccgtt cgaataagtg tccacccttt 60

ggtttattct tgaactcact taagttttga atttttagtt gtg aaa gta gtt gat   115
                                          Val Lys Val Val Asp
                                            1               5

gca caa gtg gtt atg ggg cca acc cac gct atg agc ggt gca gcc gtg   163
Ala Gln Val Val Met Gly Pro Thr His Ala Met Ser Gly Ala Ala Val
                10                  15                  20

ggg ctt gct gtt gct caa att ctc cca gca gaa tgg ggt ggg gtt acc   211
Gly Leu Ala Val Ala Gln Ile Leu Pro Ala Glu Trp Gly Gly Val Thr
            25                  30                  35

acc gcc acg gag gct ttt att tat gcg ggt tta gcg gcg ggt gca gcg   259
Thr Ala Thr Glu Ala Phe Ile Tyr Ala Gly Leu Ala Ala Gly Ala Ala
        40                  45                  50

ctg ctc ccg gac ctt gat tca ccg cag gcc acg gtg tcg cgt tct ttt   307
Leu Leu Pro Asp Leu Asp Ser Pro Gln Ala Thr Val Ser Arg Ser Phe
    55                  60                  65

ggt ccg att acc caa gtg att tcg cgt ttt aca gag aat att tgc caa   355
Gly Pro Ile Thr Gln Val Ile Ser Arg Phe Thr Glu Asn Ile Cys Gln
70                  75                  80                  85

act ttc gtc aat gtc acc agg ggc agg aaa gac aaa cac tgc aac aac   403
Thr Phe Val Asn Val Thr Arg Gly Arg Lys Asp Lys His Cys Asn Asn
                90                  95                  100

ggg cac cgc acg ttg aca cat acg gtg tgg agc gct gct gcc aca ggc   451
Gly His Arg Thr Leu Thr His Thr Val Trp Ser Ala Ala Ala Thr Gly
            105                 110                 115

gct ggt gcc aca gcg cta att ggc gcc tat gga aaa cct gcg gtg att   499
Ala Gly Ala Thr Ala Leu Ile Gly Ala Tyr Gly Lys Pro Ala Val Ile
        120                 125                 130

ggt ttg ctg ttt ttc ttc ctc ggg ctc gcc att aga ggt ctc atg cct   547
Gly Leu Leu Phe Phe Phe Leu Gly Leu Ala Ile Arg Gly Leu Met Pro
```

```
    135                 140                 145

gaa tgg tca aag aac gca gat tgg ctt tta gtt act gga gct tcc gct   595
Glu Trp Ser Lys Asn Ala Asp Trp Leu Leu Val Thr Gly Ala Ser Ala
150                 155                 160                 165

gca tta gca gtg gga gta tgg aat tat gct ccc gaa agt tca ttc ggc   643
Ala Leu Ala Val Gly Val Trp Asn Tyr Ala Pro Glu Ser Ser Phe Gly
                170                 175                 180

att gtg tta ggc tcc gcc att aca gtt gga agc ctg acc cac ttg gct   691
Ile Val Leu Gly Ser Ala Ile Thr Val Gly Ser Leu Thr His Leu Ala
            185                 190                 195

ggc gat atg gcc act aag gcc ggt atc cca gca ttt gcc ccg gtc att   739
Gly Asp Met Ala Thr Lys Ala Gly Ile Pro Ala Phe Ala Pro Val Ile
        200                 205                 210

ccg ctg aag ggc aaa cgc tgg tgg aac ctc aaa ttg cct aag ttt tta   787
Pro Leu Lys Gly Lys Arg Trp Trp Asn Leu Lys Leu Pro Lys Phe Leu
    215                 220                 225

agc att cgt gcc aac ggt cct gcc gat aag ttc tta ctg ttc gta ttc   835
Ser Ile Arg Ala Asn Gly Pro Ala Asp Lys Phe Leu Leu Phe Val Phe
230                 235                 240                 245

tcg gtg gcg gtc atc att cag att ggt ttg gtc tca tcg gga aat atg   883
Ser Val Ala Val Ile Ile Gln Ile Gly Leu Val Ser Ser Gly Asn Met
                250                 255                 260

agc acc att atg atg aat ctg ctt agt cct gca ctg taattaatgg       929
Ser Thr Ile Met Met Asn Leu Leu Ser Pro Ala Leu
            265                 270

cagttgcgtt tcg                                                   942


<210> 1770
<211> 273
<212> PRT
<213> Corynebacterium glutamicum

<400> 1770
Val Lys Val Val Asp Ala Gln Val Val Met Gly Pro Thr His Ala Met
  1               5                  10                  15

Ser Gly Ala Ala Val Gly Leu Ala Val Ala Gln Ile Leu Pro Ala Glu
             20                  25                  30

Trp Gly Gly Val Thr Thr Ala Thr Glu Ala Phe Ile Tyr Ala Gly Leu
         35                  40                  45

Ala Ala Gly Ala Ala Leu Leu Pro Asp Leu Asp Ser Pro Gln Ala Thr
     50                  55                  60

Val Ser Arg Ser Phe Gly Pro Ile Thr Gln Val Ile Ser Arg Phe Thr
 65                  70                  75                  80

Glu Asn Ile Cys Gln Thr Phe Val Asn Val Thr Arg Gly Arg Lys Asp
                 85                  90                  95
```

```
Lys His Cys Asn Asn Gly His Arg Thr Leu Thr His Thr Val Trp Ser
            100                 105                 110

Ala Ala Ala Thr Gly Ala Gly Ala Thr Ala Leu Ile Gly Ala Tyr Gly
        115                 120                 125

Lys Pro Ala Val Ile Gly Leu Leu Phe Phe Phe Leu Gly Leu Ala Ile
    130                 135                 140

Arg Gly Leu Met Pro Glu Trp Ser Lys Asn Ala Asp Trp Leu Leu Val
145                 150                 155                 160

Thr Gly Ala Ser Ala Ala Leu Ala Val Gly Val Trp Asn Tyr Ala Pro
                165                 170                 175

Glu Ser Ser Phe Gly Ile Val Leu Gly Ser Ala Ile Thr Val Gly Ser
            180                 185                 190

Leu Thr His Leu Ala Gly Asp Met Ala Thr Lys Ala Gly Ile Pro Ala
        195                 200                 205

Phe Ala Pro Val Ile Pro Leu Lys Gly Lys Arg Trp Trp Asn Leu Lys
    210                 215                 220

Leu Pro Lys Phe Leu Ser Ile Arg Ala Asn Gly Pro Ala Asp Lys Phe
225                 230                 235                 240

Leu Leu Phe Val Phe Ser Val Ala Val Ile Ile Gln Ile Gly Leu Val
                245                 250                 255

Ser Ser Gly Asn Met Ser Thr Ile Met Met Asn Leu Leu Ser Pro Ala
            260                 265                 270

Leu
```

20240229-CN-NP-129CP-SEQLIST

<210> 1771
<211> 1299
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1276)
<223> RXA00469

<400> 1771

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tgcccctgcg acaccaaacc atcagggaag accctgaacg ccacctttc agggctttcc 60

cccattcact tatcagcctc aacactccac aatagagtct atg agt act ttt cag   115
                                            Met Ser Thr Phe Gln
                                              1               5

gag ccc cac cac aac cag gga ttc atc cct ttt gcc caa cct ggt tat   163
Glu Pro His His Asn Gln Gly Phe Ile Pro Phe Ala Gln Pro Gly Tyr
                  10                  15                  20

gaa gct cca aca cca cac ctt gca act ggt act ttt cag caa atg tgg   211
Glu Ala Pro Thr Pro His Leu Ala Thr Gly Thr Phe Gln Gln Met Trp
              25                  30                  35
```

```
cag acc cgc ccc gca cgc atc cct gcc aag caa ggt ggt cac gcc aaa   259
Gln Thr Arg Pro Ala Arg Ile Pro Ala Lys Gln Gly Gly His Ala Lys
         40                  45                  50

gta gct ggt gtc tgt gaa ggc att ggt gtg cgt tat caa atc gac ccg   307
Val Ala Gly Val Cys Glu Gly Ile Gly Val Arg Tyr Gln Ile Asp Pro
     55                  60                  65

gtg ctc att cgt cta ttt ttc gtg gtc act ggt gtc ttc ggc gcc ggt   355
Val Leu Ile Arg Leu Phe Phe Val Val Thr Gly Val Phe Gly Ala Gly
 70                  75                  80                  85

gtc gca gcc tat ctc att gca tgg ctg tgc atg ccc cgc tac tcc gtt   403
Val Ala Ala Tyr Leu Ile Ala Trp Leu Cys Met Pro Arg Tyr Ser Val
                 90                  95                 100

ccg gtc tcc ccc atc gaa gct ctc tgg acc ccg ggc cac acc aaa gac   451
Pro Val Ser Pro Ile Glu Ala Leu Trp Thr Pro Gly His Thr Lys Asp
            105                 110                 115

cgc aac cac ggc tgg tgg ctg gtc atc gcg ttc ttt atg ttc tca ggt   499
Arg Asn His Gly Trp Trp Leu Val Ile Ala Phe Phe Met Phe Ser Gly
        120                 125                 130

gtt tta tcc tcc ggc gct gga gga ata tcc ggc cca gca gca gcc att   547
Val Leu Ser Ser Gly Ala Gly Gly Ile Ser Gly Pro Ala Ala Ala Ile
    135                 140                 145

act tac ctt tgc ctt tta gcc atg tgg tgg gcg ttg cat aag aaa caa   595
Thr Tyr Leu Cys Leu Leu Ala Met Trp Trp Ala Leu His Lys Lys Gln
150                 155                 160                 165

cca ctt cca ccc cgc gga cta ctc acc act gaa ttc act gtt tct gag   643
Pro Leu Pro Pro Arg Gly Leu Leu Thr Thr Glu Phe Thr Val Ser Glu
                170                 175                 180

gat gcc acc atg aaa aac gaa gat ctc tac cca cga ccc caa cca gat   691
Asp Ala Thr Met Lys Asn Glu Asp Leu Tyr Pro Arg Pro Gln Pro Asp
            185                 190                 195

cta agc act atc acc ccc gtt gag ggc tac tat gca ccc ttc gcg caa   739
Leu Ser Thr Ile Thr Pro Val Glu Gly Tyr Tyr Ala Pro Phe Ala Gln
        200                 205                 210

caa acc ccc gaa gcg cct cat tgg gat cca ctt gcc caa aac caa tac   787
Gln Thr Pro Glu Ala Pro His Trp Asp Pro Leu Ala Gln Asn Gln Tyr
    215                 220                 225

aac acc tgg gat gta caa gtc cct cca caa aag cct cag aaa aag cgc   835
Asn Thr Trp Asp Val Gln Val Pro Pro Gln Lys Pro Gln Lys Lys Arg
230                 235                 240                 245

cat gtg tgg cca tgg att gtc ggc ggt gta gtt ggt acc gga gtt gtc   883
His Val Trp Pro Trp Ile Val Gly Gly Val Val Gly Thr Gly Val Val
                250                 255                 260

atg agc gcc ctc gca ggc ctg ttt att tca aat atc gat ccc atc tac   931
Met Ser Ala Leu Ala Gly Leu Phe Ile Ser Asn Ile Asp Pro Ile Tyr
            265                 270                 275
```

```
ttt gaa gac gac cct gga atc ggc gat gtc aat ctc atc ccc acc aac   979
Phe Glu Asp Asp Pro Gly Ile Gly Asp Val Asn Leu Ile Pro Thr Asn
        280                 285                 290

gat gaa ctc ctc agc agc tac acc tct ggt gtg ggc gaa atg aac cta   1027
Asp Glu Leu Leu Ser Ser Tyr Thr Ser Gly Val Gly Glu Met Asn Leu
    295                 300                 305

gat ttc agc aac ctc acc caa ctt gat cag gaa caa aac gtt caa atc   1075
Asp Phe Ser Asn Leu Thr Gln Leu Asp Gln Glu Gln Asn Val Gln Ile
310                 315                 320                 325

acc tca ggt atc ggt gaa gtc atg gtg acc ctg cct gat gac gtg cca   1123
Thr Ser Gly Ile Gly Glu Val Met Val Thr Leu Pro Asp Asp Val Pro
                330                 335                 340

gta agc ttg agt tgc tcc gcc ggt gtg ggc aca gcg cgc tgt gat gtt   1171
Val Ser Leu Ser Cys Ser Ala Gly Val Gly Thr Ala Arg Cys Asp Val
            345                 350                 355

gga gac ctc gcc gcc cac aat gct gat ttg gaa ggt ccg atg ttg aat   1219
Gly Asp Leu Ala Ala His Asn Ala Asp Leu Glu Gly Pro Met Leu Asn
        360                 365                 370

ctg gtt gta aat tct gga atc ggc gat gtg aag gtg gag ttc gct gat   1267
Leu Val Val Asn Ser Gly Ile Gly Asp Val Lys Val Glu Phe Ala Asp
    375                 380                 385

cag aat gac tagcccgacc ctatgtgagt agt                            1299
Gln Asn Asp
390
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<210> 1772
<211> 392
<212> PRT
<213> Corynebacterium glutamicum

<400> 1772

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Met Ser Thr Phe Gln Glu Pro His His Asn Gln Gly Phe Ile Pro Phe
  1               5                  10                  15

Ala Gln Pro Gly Tyr Glu Ala Pro Thr Pro His Leu Ala Thr Gly Thr
             20                  25                  30

Phe Gln Gln Met Trp Gln Thr Arg Pro Ala Arg Ile Pro Ala Lys Gln
         35                  40                  45

Gly Gly His Ala Lys Val Ala Gly Val Cys Glu Gly Ile Gly Val Arg
     50                  55                  60

Tyr Gln Ile Asp Pro Val Leu Ile Arg Leu Phe Phe Val Val Thr Gly
 65                  70                  75                  80

Val Phe Gly Ala Gly Val Ala Ala Tyr Leu Ile Ala Trp Leu Cys Met
                 85                  90                  95

Pro Arg Tyr Ser Val Pro Val Ser Pro Ile Glu Ala Leu Trp Thr Pro
            100                 105                 110

Gly His Thr Lys Asp Arg Asn His Gly Trp Trp Leu Val Ile Ala Phe
```

```
        115                 120                 125

Phe Met Phe Ser Gly Val Leu Ser Ser Gly Ala Gly Gly Ile Ser Gly
    130                 135                 140

Pro Ala Ala Ala Ile Thr Tyr Leu Cys Leu Leu Ala Met Trp Trp Ala
145                 150                 155                 160

Leu His Lys Lys Gln Pro Leu Pro Pro Arg Gly Leu Leu Thr Thr Glu
                165                 170                 175

Phe Thr Val Ser Glu Asp Ala Thr Met Lys Asn Glu Asp Leu Tyr Pro
            180                 185                 190

Arg Pro Gln Pro Asp Leu Ser Thr Ile Thr Pro Val Glu Gly Tyr Tyr
        195                 200                 205

Ala Pro Phe Ala Gln Gln Thr Pro Glu Ala Pro His Trp Asp Pro Leu
    210                 215                 220

Ala Gln Asn Gln Tyr Asn Thr Trp Asp Val Gln Val Pro Pro Gln Lys
225                 230                 235                 240

Pro Gln Lys Lys Arg His Val Trp Pro Trp Ile Val Gly Gly Val Val
                245                 250                 255

Gly Thr Gly Val Val Met Ser Ala Leu Ala Gly Leu Phe Ile Ser Asn
            260                 265                 270

Ile Asp Pro Ile Tyr Phe Glu Asp Asp Pro Gly Ile Gly Asp Val Asn
        275                 280                 285

Leu Ile Pro Thr Asn Asp Glu Leu Leu Ser Ser Tyr Thr Ser Gly Val
    290                 295                 300

Gly Glu Met Asn Leu Asp Phe Ser Asn Leu Thr Gln Leu Asp Gln Glu
305                 310                 315                 320

Gln Asn Val Gln Ile Thr Ser Gly Ile Gly Glu Val Met Val Thr Leu
                325                 330                 335

Pro Asp Asp Val Pro Val Ser Leu Ser Cys Ser Ala Gly Val Gly Thr
            340                 345                 350

Ala Arg Cys Asp Val Gly Asp Leu Ala Ala His Asn Ala Asp Leu Glu
        355                 360                 365

Gly Pro Met Leu Asn Leu Val Val Asn Ser Gly Ile Gly Asp Val Lys
    370                 375                 380

Val Glu Phe Ala Asp Gln Asn Asp
385                 390
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<210> 1773
<211> 984
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(961)
<223> RXA00472

<400> 1773
gtctaaacgc tcccgtgctt tcgccacagc attaatcgcc ttgggcctag ggctatcttc 60

ctgctctact acggaagata ccgctatatc ggagacgaca gtg tct agt gtt gca 115
Val Ser Ser Val Ala
1 5

acg aaa aca acc tcg act ctg cct gaa atg aac tcc gca gta tca gca 163
Thr Lys Thr Thr Ser Thr Leu Pro Glu Met Asn Ser Ala Val Ser Ala
10 15 20

gac ggc gtg acg atc act atc gat tct gcc ttc acg aca gac tct gta 211
Asp Gly Val Thr Ile Thr Ile Asp Ser Ala Phe Thr Thr Asp Ser Val
25 30 35

gaa atg gaa tcc cta gac aga cct tct ggc gac atc caa ccc gag atg 259
Glu Met Glu Ser Leu Asp Arg Pro Ser Gly Asp Ile Gln Pro Glu Met
40 45 50

tct aga gaa gac gga atc ttt gtc gta gtc gaa acc act ata aag aac 307
Ser Arg Glu Asp Gly Ile Phe Val Val Val Glu Thr Thr Ile Lys Asn
55 60 65

gag agt gga gca gat atg gac atc acc tgt gca tcc act ggt tca act 355
Glu Ser Gly Ala Asp Met Asp Ile Thr Cys Ala Ser Thr Gly Ser Thr
70 75 80 85

gtc tat gca gaa atc tcc act aat caa gag gcc gta tac caa cca ata 403
Val Tyr Ala Glu Ile Ser Thr Asn Gln Glu Ala Val Tyr Gln Pro Ile
90 95 100

cgc gat tta ttc ctc atc cca gga aac ccg gaa tgc aac cat aat cta 451
Arg Asp Leu Phe Leu Ile Pro Gly Asn Pro Glu Cys Asn His Asn Leu
105 110 115

gga tcc ggt ttc gac gca cca atg act tgg gta ttt caa atc cct aaa 499
Gly Ser Gly Phe Asp Ala Pro Met Thr Trp Val Phe Gln Ile Pro Lys
120 125 130

gat gcc act gcg gag cga ttt gga ttc aca cat agt gag ctc ggt gat 547
Asp Ala Thr Ala Glu Arg Phe Gly Phe Thr His Ser Glu Leu Gly Asp
135 140 145

ggg aaa cta act tgg att gca ctc aat gat ttg agt aat tcg gag cca 595
Gly Lys Leu Thr Trp Ile Ala Leu Asn Asp Leu Ser Asn Ser Glu Pro
150 155 160 165

gct act gaa tca act atg cga gac gaa gca gca atc gat ccg agc acc 643
Ala Thr Glu Ser Thr Met Arg Asp Glu Ala Ala Ile Asp Pro Ser Thr
170 175 180

cct cag caa act cca gta cag gaa act gtg atc tca caa aac acc att 691
Pro Gln Gln Thr Pro Val Gln Glu Thr Val Ile Ser Gln Asn Thr Ile
185 190 195

gaa act cct gta gcc cct gct cct gcg gta cct gct tat ggc gct tct 739
Glu Thr Pro Val Ala Pro Ala Pro Ala Val Pro Ala Tyr Gly Ala Ser
200 205 210

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tgc cct gtc tcg atg ctc cag cag cca agt caa gct gca gat ggt tca   787
Cys Pro Val Ser Met Leu Gln Gln Pro Ser Gln Ala Ala Asp Gly Ser
    215                 220                 225

gct ttg gtc tgc att tat gca gga acc ccc aac cca atc tgg gtc tac   835
Ala Leu Val Cys Ile Tyr Ala Gly Thr Pro Asn Pro Ile Trp Val Tyr
230                 235                 240                 245

ggc cca gaa cct ctc gga gtc ggg act gct aca ccg ggt ggg gca tgc   883
Gly Pro Glu Pro Leu Gly Val Gly Thr Ala Thr Pro Gly Gly Ala Cys
                250                 255                 260

gaa gga tac gag gcc ggt ggg caa gat gct tct gga aat ata atg atg   931
Glu Gly Tyr Glu Ala Gly Gly Gln Asp Ala Ser Gly Asn Ile Met Met
            265                 270                 275

tgc tca ggc gga caa tgg gtc tat ggg cca taaatctaaa atcaaagagt     981
Cys Ser Gly Gly Gln Trp Val Tyr Gly Pro
        280                 285

gca                                                               984


<210> 1774
<211> 287
<212> PRT
<213> Corynebacterium glutamicum

<400> 1774
Val Ser Ser Val Ala Thr Lys Thr Thr Ser Thr Leu Pro Glu Met Asn
  1               5                  10                  15

Ser Ala Val Ser Ala Asp Gly Val Thr Ile Thr Ile Asp Ser Ala Phe
             20                  25                  30

Thr Thr Asp Ser Val Glu Met Glu Ser Leu Asp Arg Pro Ser Gly Asp
         35                  40                  45

Ile Gln Pro Glu Met Ser Arg Glu Asp Gly Ile Phe Val Val Val Glu
     50                  55                  60

Thr Thr Ile Lys Asn Glu Ser Gly Ala Asp Met Asp Ile Thr Cys Ala
 65                  70                  75                  80

Ser Thr Gly Ser Thr Val Tyr Ala Glu Ile Ser Thr Asn Gln Glu Ala
                 85                  90                  95

Val Tyr Gln Pro Ile Arg Asp Leu Phe Leu Ile Pro Gly Asn Pro Glu
            100                 105                 110

Cys Asn His Asn Leu Gly Ser Gly Phe Asp Ala Pro Met Thr Trp Val
        115                 120                 125

Phe Gln Ile Pro Lys Asp Ala Thr Ala Glu Arg Phe Gly Phe Thr His
    130                 135                 140

Ser Glu Leu Gly Asp Gly Lys Leu Thr Trp Ile Ala Leu Asn Asp Leu
145                 150                 155                 160

Ser Asn Ser Glu Pro Ala Thr Glu Ser Thr Met Arg Asp Glu Ala Ala
```

```
                165                 170                 175

Ile Asp Pro Ser Thr Pro Gln Gln Thr Pro Val Gln Glu Thr Val Ile
            180                 185                 190

Ser Gln Asn Thr Ile Glu Thr Pro Val Ala Pro Ala Pro Ala Val Pro
        195                 200                 205

Ala Tyr Gly Ala Ser Cys Pro Val Ser Met Leu Gln Gln Pro Ser Gln
    210                 215                 220

Ala Ala Asp Gly Ser Ala Leu Val Cys Ile Tyr Ala Gly Thr Pro Asn
225                 230                 235                 240

Pro Ile Trp Val Tyr Gly Pro Glu Pro Leu Gly Val Gly Thr Ala Thr
                245                 250                 255

Pro Gly Gly Ala Cys Glu Gly Tyr Glu Ala Gly Gly Gln Asp Ala Ser
            260                 265                 270

Gly Asn Ile Met Met Cys Ser Gly Gly Gln Trp Val Tyr Gly Pro
        275                 280                 285



<210> 1775
<211> 1701
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1678)
<223> RXA00474

<400> 1775
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aacagccaac aacgttgcgg gcggtcccat gacgcgggtg atg gca ttg tgg ttt   115
                                              Met Ala Leu Trp Phe
                                                1               5

ccg gat tgg cct gtg cag gcg gtt cat ttg gat gaa gat gct ccc gcg   163
Pro Asp Trp Pro Val Gln Ala Val His Leu Asp Glu Asp Ala Pro Ala
                10                  15                  20

cac aat aaa cct gtg gcg att gct gcg cat tac cgc atc cag gtg tgt   211
His Asn Lys Pro Val Ala Ile Ala Ala His Tyr Arg Ile Gln Val Cys
            25                  30                  35

ggc gtg gct gcg cgc aag cgt ggg gtg cgt cgt ggg atg aag gtt cgg   259
Gly Val Ala Ala Arg Lys Arg Gly Val Arg Arg Gly Met Lys Val Arg
        40                  45                  50

cag gcg cag gct gtg tgc cct gag ctg gag gtt gtt gac gcg gat gca   307
Gln Ala Gln Ala Val Cys Pro Glu Leu Glu Val Val Asp Ala Asp Ala
    55                  60                  65

gat cgt gat gcc cgg atg ttt gag ggc atc gtg gca tcg ctc ggt gag   355
Asp Arg Asp Ala Arg Met Phe Glu Gly Ile Val Ala Ser Leu Gly Glu
70                  75                  80                  85
```

```
gtt gcc tcc agc gtc gag gtg ctt cgt ccg ggt ctg gtc gcg gtc gat   403
Val Ala Ser Ser Val Glu Val Leu Arg Pro Gly Leu Val Ala Val Asp
                 90                  95                 100

gcg gga gct gcc gcg cgc tat tac ggt tca gag gac atc gct gct cag   451
Ala Gly Ala Ala Ala Arg Tyr Tyr Gly Ser Glu Asp Ile Ala Ala Gln
            105                 110                 115

atg ctt atc gac gcc gcc ctg cgc caa ggc atc gac gtt ttc gcc ggg   499
Met Leu Ile Asp Ala Ala Leu Arg Gln Gly Ile Asp Val Phe Ala Gly
        120                 125                 130

gtt gcg gat gag atc acg acg gcc gtc atc gcg gcg agg gcg aat ggt   547
Val Ala Asp Glu Ile Thr Thr Ala Val Ile Ala Ala Arg Ala Asn Gly
    135                 140                 145

ggg act gtg gtg aag agg gag gcg tcg aga agc ttt tta cag cag caa   595
Gly Thr Val Val Lys Arg Glu Ala Ser Arg Ser Phe Leu Gln Gln Gln
150                 155                 160                 165

ccc ctg ggc gtg ctg gcg gcc gag gaa gcg ctg ggt tgt gag gcg gag   643
Pro Leu Gly Val Leu Ala Ala Glu Glu Ala Leu Gly Cys Glu Ala Glu
                170                 175                 180

gtg gtg cgc gcg ctg gcg gat ctg ggc atg cgc acg ctt ggt gag ctg   691
Val Val Arg Ala Leu Ala Asp Leu Gly Met Arg Thr Leu Gly Glu Leu
            185                 190                 195

gcg gaa ctg ccg gta gaa gcc gtg gcg acg cgt ttc ggc aac gct ggt   739
Ala Glu Leu Pro Val Glu Ala Val Ala Thr Arg Phe Gly Asn Ala Gly
        200                 205                 210

ctg cgg tgt cac aac att gcg cgt gcc agg cac gat cgt aag gtc gcg   787
Leu Arg Cys His Asn Ile Ala Arg Ala Arg His Asp Arg Lys Val Ala
    215                 220                 225

cca ccg atc acg cat gca gat tgg gag gtt tcg cat gtg ccg gag gag   835
Pro Pro Ile Thr His Ala Asp Trp Glu Val Ser His Val Pro Glu Glu
230                 235                 240                 245

cct att ttg cgt gtc gac gcc gcc tcg ttt gtt gcg cgc aac ctt gcc   883
Pro Ile Leu Arg Val Asp Ala Ala Ser Phe Val Ala Arg Asn Leu Ala
                250                 255                 260

tcg cgc ctg cat caa ctg ctg agc aaa ggt ggc gtg gtg tgc caa ttg   931
Ser Arg Leu His Gln Leu Leu Ser Lys Gly Gly Val Val Cys Gln Leu
            265                 270                 275

ctc aag gtc aca gcc gat ttc agt act ggt gat acg gtg agc aga att   979
Leu Lys Val Thr Ala Asp Phe Ser Thr Gly Asp Thr Val Ser Arg Ile
        280                 285                 290

tgg cgt acc ggt gaa cct tta acg gaa cag gca act gcg gat cgg gtg   1027
Trp Arg Thr Gly Glu Pro Leu Thr Glu Gln Ala Thr Ala Asp Arg Val
    295                 300                 305

cgt tgg cag ttg gat ggg tgg ttg act gcg cgc ggt gtg cat tcc gat   1075
Arg Trp Gln Leu Asp Gly Trp Leu Thr Ala Arg Gly Val His Ser Asp
310                 315                 320                 325

gat ccg aat gag cac gat ggg att acg gcg ttg tgg ctt att cct ttg   1123
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Asp Pro Asn Glu His Asp Gly Ile Thr Ala Leu Trp Leu Ile Pro Leu
                330                 335                 340

gaa tgt gtg cca ccg gat atg gcc agc ggc gga ttg tgg gat acc ggg   1171
Glu Cys Val Pro Pro Asp Met Ala Ser Gly Gly Leu Trp Asp Thr Gly
            345                 350                 355

cgc agc cag cag cat gtg gcc aga caa gtc att gag cgt gtg caa tca   1219
Arg Ser Gln Gln His Val Ala Arg Gln Val Ile Glu Arg Val Gln Ser
        360                 365                 370

agc ttg ggc gtg gat gcg gtg ctg cag cct gtt ccg gct ggt ggt cgg   1267
Ser Leu Gly Val Asp Ala Val Leu Gln Pro Val Pro Ala Gly Gly Arg
    375                 380                 385

gga gta gaa gaa cgc att cat ttt gtt ccc tat ggt gaa aaa cgt gat   1315
Gly Val Glu Glu Arg Ile His Phe Val Pro Tyr Gly Glu Lys Arg Asp
390                 395                 400                 405

gct atc cgc aat cca gcg ggg tcg tgg cca ggg aaa ata cca ggt ccg   1363
Ala Ile Arg Asn Pro Ala Gly Ser Trp Pro Gly Lys Ile Pro Gly Pro
                410                 415                 420

ctg cct gct cgg ttg ggc ggt ggg atc aac cac ccg gcc tcg caa gtg   1411
Leu Pro Ala Arg Leu Gly Gly Gly Ile Asn His Pro Ala Ser Gln Val
            425                 430                 435

acc atg att gat aca gaa ggg cag cgt att tac gtc acc gca gag gca   1459
Thr Met Ile Asp Thr Glu Gly Gln Arg Ile Tyr Val Thr Ala Glu Ala
        440                 445                 450

ttg ctc agc tcg tcg ccg tat gcc ttg tcc tgg ggg ccg gcc cgc tat   1507
Leu Leu Ser Ser Ser Pro Tyr Ala Leu Ser Trp Gly Pro Ala Arg Tyr
    455                 460                 465

ttg atc act ggc tgg gct ggg cca tgg ccg gtg gat gat cga tgg tgg   1555
Leu Ile Thr Gly Trp Ala Gly Pro Trp Pro Val Asp Asp Arg Trp Trp
470                 475                 480                 485

gag aaa aac ggc aca aaa tat gcc cgc ctc caa gtg gtg gga cgg gca   1603
Glu Lys Asn Gly Thr Lys Tyr Ala Arg Leu Gln Val Val Gly Arg Ala
                490                 495                 500

gta tct gaa gaa agg cag ctc aat gcg tgg ctg ttg atg tgg aaa gac   1651
Val Ser Glu Glu Arg Gln Leu Asn Ala Trp Leu Leu Met Trp Lys Asp
            505                 510                 515

aac aag tgg cgg att gag gcc aca tat taggaaacta ctgcgctaaa         1698
Asn Lys Trp Arg Ile Glu Ala Thr Tyr
        520                 525

aca                                                               1701
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<210> 1776
<211> 526
<212> PRT
<213> Corynebacterium glutamicum

<400> 1776
Met Ala Leu Trp Phe Pro Asp Trp Pro Val Gln Ala Val His Leu Asp

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  1               5                  10                  15

Glu Asp Ala Pro Ala His Asn Lys Pro Val Ala Ile Ala Ala His Tyr
            20                  25                  30

Arg Ile Gln Val Cys Gly Val Ala Ala Arg Lys Arg Gly Val Arg Arg
        35                  40                  45

Gly Met Lys Val Arg Gln Ala Gln Ala Val Cys Pro Glu Leu Glu Val
    50                  55                  60

Val Asp Ala Asp Ala Asp Arg Asp Ala Arg Met Phe Glu Gly Ile Val
65                  70                  75                  80

Ala Ser Leu Gly Glu Val Ala Ser Ser Val Glu Val Leu Arg Pro Gly
                85                  90                  95

Leu Val Ala Val Asp Ala Gly Ala Ala Ala Arg Tyr Tyr Gly Ser Glu
            100                 105                 110

Asp Ile Ala Ala Gln Met Leu Ile Asp Ala Ala Leu Arg Gln Gly Ile
        115                 120                 125

Asp Val Phe Ala Gly Val Ala Asp Glu Ile Thr Thr Ala Val Ile Ala
    130                 135                 140

Ala Arg Ala Asn Gly Gly Thr Val Val Lys Arg Glu Ala Ser Arg Ser
145                 150                 155                 160

Phe Leu Gln Gln Gln Pro Leu Gly Val Leu Ala Ala Glu Glu Ala Leu
                165                 170                 175

Gly Cys Glu Ala Glu Val Val Arg Ala Leu Ala Asp Leu Gly Met Arg
            180                 185                 190

Thr Leu Gly Glu Leu Ala Glu Leu Pro Val Glu Ala Val Ala Thr Arg
        195                 200                 205

Phe Gly Asn Ala Gly Leu Arg Cys His Asn Ile Ala Arg Ala Arg His
    210                 215                 220

Asp Arg Lys Val Ala Pro Pro Ile Thr His Ala Asp Trp Glu Val Ser
225                 230                 235                 240

His Val Pro Glu Glu Pro Ile Leu Arg Val Asp Ala Ala Ser Phe Val
                245                 250                 255

Ala Arg Asn Leu Ala Ser Arg Leu His Gln Leu Leu Ser Lys Gly Gly
            260                 265                 270

Val Val Cys Gln Leu Leu Lys Val Thr Ala Asp Phe Ser Thr Gly Asp
        275                 280                 285

Thr Val Ser Arg Ile Trp Arg Thr Gly Glu Pro Leu Thr Glu Gln Ala
    290                 295                 300

Thr Ala Asp Arg Val Arg Trp Gln Leu Asp Gly Trp Leu Thr Ala Arg
305                 310                 315                 320

Gly Val His Ser Asp Asp Pro Asn Glu His Asp Gly Ile Thr Ala Leu
                325                 330                 335
```

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Trp Leu Ile Pro Leu Glu Cys Val Pro Pro Asp Met Ala Ser Gly Gly
            340                 345                 350

Leu Trp Asp Thr Gly Arg Ser Gln Gln His Val Ala Arg Gln Val Ile
        355                 360                 365

Glu Arg Val Gln Ser Ser Leu Gly Val Asp Ala Val Leu Gln Pro Val
    370                 375                 380

Pro Ala Gly Gly Arg Gly Val Glu Glu Arg Ile His Phe Val Pro Tyr
385                 390                 395                 400

Gly Glu Lys Arg Asp Ala Ile Arg Asn Pro Ala Gly Ser Trp Pro Gly
                405                 410                 415

Lys Ile Pro Gly Pro Leu Pro Ala Arg Leu Gly Gly Gly Ile Asn His
            420                 425                 430

Pro Ala Ser Gln Val Thr Met Ile Asp Thr Glu Gly Gln Arg Ile Tyr
        435                 440                 445

Val Thr Ala Glu Ala Leu Leu Ser Ser Ser Pro Tyr Ala Leu Ser Trp
    450                 455                 460

Gly Pro Ala Arg Tyr Leu Ile Thr Gly Trp Ala Gly Pro Trp Pro Val
465                 470                 475                 480

Asp Asp Arg Trp Trp Glu Lys Asn Gly Thr Lys Tyr Ala Arg Leu Gln
                485                 490                 495

Val Val Gly Arg Ala Val Ser Glu Glu Arg Gln Leu Asn Ala Trp Leu
            500                 505                 510

Leu Met Trp Lys Asp Asn Lys Trp Arg Ile Glu Ala Thr Tyr
        515                 520                 525


<210> 1777
<211> 783
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(760)
<223> RXA00475

<400> 1777
ggggtgtctg taattttcac gtctcctggc gttttaaaga cgaattacaa caattcgttc 60

acgattgagc gaaattgggc gtcttgctta ggtttcgggg gtg acc cag ggt tac   115
                                              Val Thr Gln Gly Tyr
                                                1               5

ggt gtg tgc atg att gtg cag cca act tct cat tca aag cat cgt gcc   163
Gly Val Cys Met Ile Val Gln Pro Thr Ser His Ser Lys His Arg Ala
                10                  15                  20

cgc ctg aag act cta gcg att gtc ggc gct agc gcg ttg act ctt gcg   211
Arg Leu Lys Thr Leu Ala Ile Val Gly Ala Ser Ala Leu Thr Leu Ala
```

```
             25                  30                  35

ggt tgt gga acc tcc aat tcc acc acc aac gat gct tct tct gta acc   259
Gly Cys Gly Thr Ser Asn Ser Thr Thr Asn Asp Ala Ser Ser Val Thr
         40                  45                  50

caa act atg tcc gca act gcg gat ggc gca cag ttg tcc aac gaa gct   307
Gln Thr Met Ser Ala Thr Ala Asp Gly Ala Gln Leu Ser Asn Glu Ala
     55                  60                  65

tcc acc ggc cca acc gca ttg ggc gaa gcc gat gta gca atg aag act   355
Ser Thr Gly Pro Thr Ala Leu Gly Glu Ala Asp Val Ala Met Lys Thr
 70                  75                  80                  85

ctc cga cct gat gcg cct gca cag ctc atg gtc acc gat gtt cgg att   403
Leu Arg Pro Asp Ala Pro Ala Gln Leu Met Val Thr Asp Val Arg Ile
                 90                  95                 100

ggc tct cac agt ggc ttt gac cgc gtg gta ttt gat ctc act ggc acc   451
Gly Ser His Ser Gly Phe Asp Arg Val Val Phe Asp Leu Thr Gly Thr
            105                 110                 115

gga act cct ggt tgg ttc att gat tac acc tcc aat ccc acc cag cag   499
Gly Thr Pro Gly Trp Phe Ile Asp Tyr Thr Ser Asn Pro Thr Gln Gln
        120                 125                 130

ggc agc gga aac acc atc aac ttc acg ggc gat aca gcg ctg aac gta   547
Gly Ser Gly Asn Thr Ile Asn Phe Thr Gly Asp Thr Ala Leu Asn Val
    135                 140                 145

aat att gac ggt act gtt tat cct ttc gat ttg ggc ctt gag gat cca   595
Asn Ile Asp Gly Thr Val Tyr Pro Phe Asp Leu Gly Leu Glu Asp Pro
150                 155                 160                 165

gag atc ggc acc gtg gat ggc tcc ggc agc att gtc acc cag gtc gtc   643
Glu Ile Gly Thr Val Asp Gly Ser Gly Ser Ile Val Thr Gln Val Val
                170                 175                 180

agc gca ggt act ttt gag gga cgc tcc cag ttc gtc atc ggc ctc aac   691
Ser Ala Gly Thr Phe Glu Gly Arg Ser Gln Phe Val Ile Gly Leu Asn
            185                 190                 195

ggc aag cac cgc tac tcg gtc act gag ttg cag gat ccg cac cgt ctc   739
Gly Lys His Arg Tyr Ser Val Thr Glu Leu Gln Asp Pro His Arg Leu
        200                 205                 210

gtt gtg gat gtt tta gcg cag tagtttccta atatgtggcc tca             783
Val Val Asp Val Leu Ala Gln
    215                 220
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<210> 1778
<211> 220
<212> PRT
<213> Corynebacterium glutamicum

<400> 1778

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Val Thr Gln Gly Tyr Gly Val Cys Met Ile Val Gln Pro Thr Ser His
  1               5                  10                  15

Ser Lys His Arg Ala Arg Leu Lys Thr Leu Ala Ile Val Gly Ala Ser
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            20                  25                  30

Ala Leu Thr Leu Ala Gly Cys Gly Thr Ser Asn Ser Thr Thr Asn Asp
         35                  40                  45

Ala Ser Ser Val Thr Gln Thr Met Ser Ala Thr Ala Asp Gly Ala Gln
     50                  55                  60

Leu Ser Asn Glu Ala Ser Thr Gly Pro Thr Ala Leu Gly Glu Ala Asp
 65                  70                  75                  80

Val Ala Met Lys Thr Leu Arg Pro Asp Ala Pro Ala Gln Leu Met Val
                 85                  90                  95

Thr Asp Val Arg Ile Gly Ser His Ser Gly Phe Asp Arg Val Val Phe
            100                 105                 110

Asp Leu Thr Gly Thr Gly Thr Pro Gly Trp Phe Ile Asp Tyr Thr Ser
        115                 120                 125

Asn Pro Thr Gln Gln Gly Ser Gly Asn Thr Ile Asn Phe Thr Gly Asp
    130                 135                 140

Thr Ala Leu Asn Val Asn Ile Asp Gly Thr Val Tyr Pro Phe Asp Leu
145                 150                 155                 160

Gly Leu Glu Asp Pro Glu Ile Gly Thr Val Asp Gly Ser Gly Ser Ile
                165                 170                 175

Val Thr Gln Val Val Ser Ala Gly Thr Phe Glu Gly Arg Ser Gln Phe
            180                 185                 190

Val Ile Gly Leu Asn Gly Lys His Arg Tyr Ser Val Thr Glu Leu Gln
        195                 200                 205

Asp Pro His Arg Leu Val Val Asp Val Leu Ala Gln
    210                 215                 220


<210> 1779
<211> 984
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(961)
<223> RXA00476

<400> 1779
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ccagacatca gatggaggcg gcgatactag ggtagaggac atg act ctt cgc tgt   115
                                              Met Thr Leu Arg Cys
                                                1               5

tct gac gtc aat gtt gaa ccc ctg ccg gga acg gca aaa aca ggt tct   163
Ser Asp Val Asn Val Glu Pro Leu Pro Gly Thr Ala Lys Thr Gly Ser
            10                  15                  20

ggg ttt gtt ctc ctt gaa cat gct ggc tcg tgg agc cgt gat gtt tta   211
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```
Gly Phe Val Leu Leu Glu His Ala Gly Ser Trp Ser Arg Asp Val Leu
            25                  30                  35

gac ggc gga aca ttt gat cct gag ttg act gat caa ttg aag agg cac   259
Asp Gly Gly Thr Phe Asp Pro Glu Leu Thr Asp Gln Leu Lys Arg His
         40                  45                  50

ctg aaa gct tcc gga atg ggt ctg caa tta att agg aag ccg gga agg   307
Leu Lys Ala Ser Gly Met Gly Leu Gln Leu Ile Arg Lys Pro Gly Arg
     55                  60                  65

gag ggt cga aac gtc gaa aag cat aat ctt ttt ctc gtt ttt gct gag   355
Glu Gly Arg Asn Val Glu Lys His Asn Leu Phe Leu Val Phe Ala Glu
 70                  75                  80                  85

gcc tca att att gag cac ctg gtg gtg gac gcg ccg gct gat gtt ttg   403
Ala Ser Ile Ile Glu His Leu Val Val Asp Ala Pro Ala Asp Val Leu
                90                  95                 100

gat ctt gat tta agc ggg ccg ggc aaa aac aat gcg cag cgc atg gat   451
Asp Leu Asp Leu Ser Gly Pro Gly Lys Asn Asn Ala Gln Arg Met Asp
            105                 110                 115

gat ccg atg ctg ctg att tgt acg cat tcg aag cgc gat gtg tgc tgc   499
Asp Pro Met Leu Leu Ile Cys Thr His Ser Lys Arg Asp Val Cys Cys
        120                 125                 130

gcg atc aag ggg cgt ccg ctg gca gct gcc gtg gag cca caa ttt ggg   547
Ala Ile Lys Gly Arg Pro Leu Ala Ala Ala Val Glu Pro Gln Phe Gly
    135                 140                 145

ccg ctg cat gtg tgg gag gct tcg cac acc aag ggc cac cgt ttt gcg   595
Pro Leu His Val Trp Glu Ala Ser His Thr Lys Gly His Arg Phe Ala
150                 155                 160                 165

cca tcg atg ctg ctc atg ccg tgg aat tac tct tat ggc cta ctt gat   643
Pro Ser Met Leu Leu Met Pro Trp Asn Tyr Ser Tyr Gly Leu Leu Asp
                170                 175                 180

gag gcc gaa acc gtg cag ctt ttc caa ggc gcg ttg gac aac aaa ctc   691
Glu Ala Glu Thr Val Gln Leu Phe Gln Gly Ala Leu Asp Asn Lys Leu
            185                 190                 195

ttc ctg ccg ggc aac cgt ggc cga gga acc tta gat gct cgt ggc cag   739
Phe Leu Pro Gly Asn Arg Gly Arg Gly Thr Leu Asp Ala Arg Gly Gln
        200                 205                 210

gtt gca gaa att gcc gtg gcg gaa gct ttc ggc gag gcg gtt gct cct   787
Val Ala Glu Ile Ala Val Ala Glu Ala Phe Gly Glu Ala Val Ala Pro
    215                 220                 225

gcg agt ttg cag gtt gaa ttc gaa gat gat tct gtt ttg gtt act cat   835
Ala Ser Leu Gln Val Glu Phe Glu Asp Asp Ser Val Leu Val Thr His
230                 235                 240                 245

ccc gat ggg cgc acg tgg gtt gtg gag ctt gaa cgc atc gag gtc gac   883
Pro Asp Gly Arg Thr Trp Val Val Glu Leu Glu Arg Ile Glu Val Asp
                250                 255                 260

ggc gtg gtg tcc tcg tgt ggt gat cag ccg aaa act gga aaa gcg tgg   931
Gly Val Val Ser Ser Cys Gly Asp Gln Pro Lys Thr Gly Lys Ala Trp
```

```
            265                 270                 275

gtg gct agg caa gtt aca gaa ctg atc gga taaaagcaga gttatatctg     981
Val Ala Arg Gln Val Thr Glu Leu Ile Gly
        280                 285

atg                                                               984
```

<210> 1780
<211> 287
<212> PRT
<213> Corynebacterium glutamicum

<400> 1780

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Met Thr Leu Arg Cys Ser Asp Val Asn Val Glu Pro Leu Pro Gly Thr
  1               5                  10                  15

Ala Lys Thr Gly Ser Gly Phe Val Leu Leu Glu His Ala Gly Ser Trp
             20                  25                  30

Ser Arg Asp Val Leu Asp Gly Gly Thr Phe Asp Pro Glu Leu Thr Asp
         35                  40                  45

Gln Leu Lys Arg His Leu Lys Ala Ser Gly Met Gly Leu Gln Leu Ile
     50                  55                  60

Arg Lys Pro Gly Arg Glu Gly Arg Asn Val Glu Lys His Asn Leu Phe
 65                  70                  75                  80

Leu Val Phe Ala Glu Ala Ser Ile Ile Glu His Leu Val Val Asp Ala
                 85                  90                  95

Pro Ala Asp Val Leu Asp Leu Asp Leu Ser Gly Pro Gly Lys Asn Asn
            100                 105                 110

Ala Gln Arg Met Asp Asp Pro Met Leu Leu Ile Cys Thr His Ser Lys
        115                 120                 125

Arg Asp Val Cys Cys Ala Ile Lys Gly Arg Pro Leu Ala Ala Ala Val
    130                 135                 140

Glu Pro Gln Phe Gly Pro Leu His Val Trp Glu Ala Ser His Thr Lys
145                 150                 155                 160

Gly His Arg Phe Ala Pro Ser Met Leu Leu Met Pro Trp Asn Tyr Ser
                165                 170                 175

Tyr Gly Leu Leu Asp Glu Ala Glu Thr Val Gln Leu Phe Gln Gly Ala
            180                 185                 190

Leu Asp Asn Lys Leu Phe Leu Pro Gly Asn Arg Gly Arg Gly Thr Leu
        195                 200                 205

Asp Ala Arg Gly Gln Val Ala Glu Ile Ala Val Ala Glu Ala Phe Gly
    210                 215                 220

Glu Ala Val Ala Pro Ala Ser Leu Gln Val Glu Phe Glu Asp Asp Ser
225                 230                 235                 240

Val Leu Val Thr His Pro Asp Gly Arg Thr Trp Val Val Glu Leu Glu
```

```
                245                 250                 255

Arg Ile Glu Val Asp Gly Val Val Ser Ser Cys Gly Asp Gln Pro Lys
            260                 265                 270

Thr Gly Lys Ala Trp Val Ala Arg Gln Val Thr Glu Leu Ile Gly
        275                 280                 285


<210> 1781
<211> 708
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(685)
<223> RXA00481

<400> 1781
gtccataaaa ataatgtgcc tacaagaaat ttatagtatc ccatgagtta atatttttaa 60

aaataaactt tatctgactt tgtagaaaaa ggtgattact atg ctg aat atg cag   115
                                              Met Leu Asn Met Gln
                                                1               5

gaa cca gat aaa atc cat ccg gca gaa cct aca ctt cgt aat att tat   163
Glu Pro Asp Lys Ile His Pro Ala Glu Pro Thr Leu Arg Asn Ile Tyr
                10                  15                  20

gac gtt aaa act agt gat ccc aaa agt gaa tta gtt gat cgt tct ggc   211
Asp Val Lys Thr Ser Asp Pro Lys Ser Glu Leu Val Asp Arg Ser Gly
            25                  30                  35

atg tcg gaa gaa gac att gcg caa att ggg cgg cta atg aaa tcg ttg   259
Met Ser Glu Glu Asp Ile Ala Gln Ile Gly Arg Leu Met Lys Ser Leu
        40                  45                  50

gcc agt ctt cgc gat gtg gaa cgt agt att ggt gaa gcc tcg gca cgt   307
Ala Ser Leu Arg Asp Val Glu Arg Ser Ile Gly Glu Ala Ser Ala Arg
    55                  60                  65

tat atg gag cta agt gcc cct gat atg cga gct ttg cac tat ttg att   355
Tyr Met Glu Leu Ser Ala Pro Asp Met Arg Ala Leu His Tyr Leu Ile
70                  75                  80                  85

gtg gcg ggc aat gcg ggc gaa gtg gtg act cca gga atg ctt gga gct   403
Val Ala Gly Asn Ala Gly Glu Val Val Thr Pro Gly Met Leu Gly Ala
                90                  95                 100

cac ctt aag ctt tcc ccg gca tct gta aca aag acg ctt aat agg cta   451
His Leu Lys Leu Ser Pro Ala Ser Val Thr Lys Thr Leu Asn Arg Leu
            105                 110                 115

gaa aaa ggt ggg cat att gtt cgt aat gtg cac ccc gtc gac cgc agg   499
Glu Lys Gly Gly His Ile Val Arg Asn Val His Pro Val Asp Arg Arg
        120                 125                 130

gct ttc gcc ctc atg gtc act gat gcc act cgt gga gag gcg atg cgg   547
Ala Phe Ala Leu Met Val Thr Asp Ala Thr Arg Gly Glu Ala Met Arg
    135                 140                 145
```

```
acg ctt ggt aag cat cag gcg cgt cgt ttt gat gct gct aaa cga tta   595
Thr Leu Gly Lys His Gln Ala Arg Arg Phe Asp Ala Ala Lys Arg Leu
150                 155                 160                 165

act cca caa gag cgt gaa gtg gtt atc cga ttc ctt cag gat atg gca   643
Thr Pro Gln Glu Arg Glu Val Val Ile Arg Phe Leu Gln Asp Met Ala
                170                 175                 180

cag gag tta tcc ctt aat aat gca cca tgg ctc aac acg gag           685
Gln Glu Leu Ser Leu Asn Asn Ala Pro Trp Leu Asn Thr Glu
            185                 190                 195

tagatgacca tctacgttaa tta                                        708
```

<210> 1782
<211> 195
<212> PRT
<213> Corynebacterium glutamicum

<400> 1782

```
Met Leu Asn Met Gln Glu Pro Asp Lys Ile His Pro Ala Glu Pro Thr
  1               5                  10                  15

Leu Arg Asn Ile Tyr Asp Val Lys Thr Ser Asp Pro Lys Ser Glu Leu
             20                  25                  30

Val Asp Arg Ser Gly Met Ser Glu Glu Asp Ile Ala Gln Ile Gly Arg
         35                  40                  45

Leu Met Lys Ser Leu Ala Ser Leu Arg Asp Val Glu Arg Ser Ile Gly
     50                  55                  60

Glu Ala Ser Ala Arg Tyr Met Glu Leu Ser Ala Pro Asp Met Arg Ala
 65                  70                  75                  80

Leu His Tyr Leu Ile Val Ala Gly Asn Ala Gly Glu Val Val Thr Pro
                 85                  90                  95

Gly Met Leu Gly Ala His Leu Lys Leu Ser Pro Ala Ser Val Thr Lys
            100                 105                 110

Thr Leu Asn Arg Leu Glu Lys Gly Gly His Ile Val Arg Asn Val His
        115                 120                 125

Pro Val Asp Arg Arg Ala Phe Ala Leu Met Val Thr Asp Ala Thr Arg
    130                 135                 140

Gly Glu Ala Met Arg Thr Leu Gly Lys His Gln Ala Arg Arg Phe Asp
145                 150                 155                 160

Ala Ala Lys Arg Leu Thr Pro Gln Glu Arg Glu Val Val Ile Arg Phe
                165                 170                 175

Leu Gln Asp Met Ala Gln Glu Leu Ser Leu Asn Asn Ala Pro Trp Leu
            180                 185                 190

Asn Thr Glu
        195
```

<210> 1783
<211> 725
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(702)
<223> RXA00486

<400> 1783

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cat gcg atc atg gca gca gtc gac cat gcc cgc gca gcc gtt cta gat   48
His Ala Ile Met Ala Ala Val Asp His Ala Arg Ala Ala Val Leu Asp
  1               5                  10                  15

tcg ctg tct gaa gtg tcc gga acg ttg aaa gtc acc tcc ttc caa tcc   96
Ser Leu Ser Glu Val Ser Gly Thr Leu Lys Val Thr Ser Phe Gln Ser
             20                  25                  30

ctg ctg ttc acc ctt gcc ccg aaa gcc atc gcg cgc ctg acc gag aaa   144
Leu Leu Phe Thr Leu Ala Pro Lys Ala Ile Ala Arg Leu Thr Glu Lys
         35                  40                  45

tac cca cac ctg caa gta gaa atc tcc caa cta gaa gtc acc gca gcg   192
Tyr Pro His Leu Gln Val Glu Ile Ser Gln Leu Glu Val Thr Ala Ala
     50                  55                  60

ctc gaa gaa ctc cgc gcc cgc cgc gtc gac gtc gca ctc ggc gag gaa   240
Leu Glu Glu Leu Arg Ala Arg Arg Val Asp Val Ala Leu Gly Glu Glu
 65                  70                  75                  80

tac ccc gtg gaa gtc ccc ctt gtt gag gcc agc att cac cgc gaa gtc   288
Tyr Pro Val Glu Val Pro Leu Val Glu Ala Ser Ile His Arg Glu Val
                 85                  90                  95

ctc ttc gaa gac ccc atg ctg ctc gtc acc cca gca agc ggc cca tac   336
Leu Phe Glu Asp Pro Met Leu Leu Val Thr Pro Ala Ser Gly Pro Tyr
            100                 105                 110

tct ggc ctc acc ctg cca gaa ctc cgc gac atc ccc atc gcc atc gat   384
Ser Gly Leu Thr Leu Pro Glu Leu Arg Asp Ile Pro Ile Ala Ile Asp
        115                 120                 125

cca ccc gac ctt ccc gcg ggc gaa tgg gtc cat agg ctc tgc cgg cgc   432
Pro Pro Asp Leu Pro Ala Gly Glu Trp Val His Arg Leu Cys Arg Arg
    130                 135                 140

gcc ggg ttt gag ccc cgc gtg acc ttt gaa acc agc gat ccc atg ctc   480
Ala Gly Phe Glu Pro Arg Val Thr Phe Glu Thr Ser Asp Pro Met Leu
145                 150                 155                 160

caa gca cac ctc gtg cgt agc ggc ttg gcc gtg aca ttt tcc ccc aca   528
Gln Ala His Leu Val Arg Ser Gly Leu Ala Val Thr Phe Ser Pro Thr
                165                 170                 175

ctg ctc acc ccg atg ctg gaa agc gtg cac atc cag ccg ctg ccc ggc   576
Leu Leu Thr Pro Met Leu Glu Ser Val His Ile Gln Pro Leu Pro Gly
            180                 185                 190

aac ccc acg cgc acg ctc tac acc gcg gtc agg gaa ggg cgc cag ggg   624
```

```
Asn Pro Thr Arg Thr Leu Tyr Thr Ala Val Arg Glu Gly Arg Gln Gly
        195                 200                 205

cat cca gcc att aaa gct ttt cga cga gcc ctc gcc cat gtg gcc aaa   672
His Pro Ala Ile Lys Ala Phe Arg Arg Ala Leu Ala His Val Ala Lys
    210                 215                 220

gaa tct tat ttg gag gct cgt cta gta gag tgagttcttg tgagccttca     722
Glu Ser Tyr Leu Glu Ala Arg Leu Val Glu
225                 230

gac                                                               725
```

<210> 1784
<211> 234
<212> PRT
<213> Corynebacterium glutamicum

<400> 1784

```
His Ala Ile Met Ala Ala Val Asp His Ala Arg Ala Ala Val Leu Asp
  1               5                  10                  15

Ser Leu Ser Glu Val Ser Gly Thr Leu Lys Val Thr Ser Phe Gln Ser
             20                  25                  30

Leu Leu Phe Thr Leu Ala Pro Lys Ala Ile Ala Arg Leu Thr Glu Lys
         35                  40                  45

Tyr Pro His Leu Gln Val Glu Ile Ser Gln Leu Glu Val Thr Ala Ala
     50                  55                  60

Leu Glu Glu Leu Arg Ala Arg Arg Val Asp Val Ala Leu Gly Glu Glu
 65                  70                  75                  80

Tyr Pro Val Glu Val Pro Leu Val Glu Ala Ser Ile His Arg Glu Val
                 85                  90                  95

Leu Phe Glu Asp Pro Met Leu Leu Val Thr Pro Ala Ser Gly Pro Tyr
            100                 105                 110

Ser Gly Leu Thr Leu Pro Glu Leu Arg Asp Ile Pro Ile Ala Ile Asp
        115                 120                 125

Pro Pro Asp Leu Pro Ala Gly Glu Trp Val His Arg Leu Cys Arg Arg
    130                 135                 140

Ala Gly Phe Glu Pro Arg Val Thr Phe Glu Thr Ser Asp Pro Met Leu
145                 150                 155                 160

Gln Ala His Leu Val Arg Ser Gly Leu Ala Val Thr Phe Ser Pro Thr
                165                 170                 175

Leu Leu Thr Pro Met Leu Glu Ser Val His Ile Gln Pro Leu Pro Gly
            180                 185                 190

Asn Pro Thr Arg Thr Leu Tyr Thr Ala Val Arg Glu Gly Arg Gln Gly
        195                 200                 205

His Pro Ala Ile Lys Ala Phe Arg Arg Ala Leu Ala His Val Ala Lys
    210                 215                 220
```

```
Glu Ser Tyr Leu Glu Ala Arg Leu Val Glu
225                 230


<210> 1785
<211> 1026
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1003)
<223> RXA00490

<400> 1785
gattgagcac gacacctcca aaattgttca gtattactta actatagttg gctgtttttc 60

gatctagtcc ttaaaggttt ctttggcaat aatcaagggc atg aat aaa cag tcc   115
                                            Met Asn Lys Gln Ser
                                              1               5

gct gca gtg ttg atg gtg atg ggt tcc gcc cta tcc ctg caa ttt ggt   163
Ala Ala Val Leu Met Val Met Gly Ser Ala Leu Ser Leu Gln Phe Gly
                 10                  15                  20

gct gcc att gga acg cag ctt ttc ccc ctc aac ggc ccc tgg gct gtc   211
Ala Ala Ile Gly Thr Gln Leu Phe Pro Leu Asn Gly Pro Trp Ala Val
             25                  30                  35

acc tct tta agg ctg ttc atc gca ggc ttg atc atg tgc ctg gtg atc   259
Thr Ser Leu Arg Leu Phe Ile Ala Gly Leu Ile Met Cys Leu Val Ile
         40                  45                  50

cgc ccg cga ctt cgt tcc tgg act aaa aaa caa tgg atc gcc gtg ctg   307
Arg Pro Arg Leu Arg Ser Trp Thr Lys Lys Gln Trp Ile Ala Val Leu
     55                  60                  65

ctg ttg gga tta tct ctt ggc gga atg aac agc ctg ttt tac gca tcc   355
Leu Leu Gly Leu Ser Leu Gly Gly Met Asn Ser Leu Phe Tyr Ala Ser
 70                  75                  80                  85

atc gaa ctc atc ccg ctg ggt acc gcc gtg acc att gag ttc ctc ggc   403
Ile Glu Leu Ile Pro Leu Gly Thr Ala Val Thr Ile Glu Phe Leu Gly
                 90                  95                 100

ccc ctg att ttc tcc gcg gtg tta gcc cgc acg ctg aaa aac gga ttg   451
Pro Leu Ile Phe Ser Ala Val Leu Ala Arg Thr Leu Lys Asn Gly Leu
            105                 110                 115

tgc gtg gct tta gcg ttt ctc ggc atg gca cta ctg ggt atc gat tcc   499
Cys Val Ala Leu Ala Phe Leu Gly Met Ala Leu Leu Gly Ile Asp Ser
        120                 125                 130

ctc agc ggc gaa acc ctt gac cca ctc ggc gtc att ttc gca gcc gtc   547
Leu Ser Gly Glu Thr Leu Asp Pro Leu Gly Val Ile Phe Ala Ala Val
    135                 140                 145

gca gga atc ttc tgg gtg tgc tac atc ctg gca tca aag aaa atc ggc   595
Ala Gly Ile Phe Trp Val Cys Tyr Ile Leu Ala Ser Lys Lys Ile Gly
150                 155                 160                 165
```

```
caa ctc atc ccc gga aca agc ggc ctg gcc gtc gca ctg att atc ggc   643
Gln Leu Ile Pro Gly Thr Ser Gly Leu Ala Val Ala Leu Ile Ile Gly
                170                 175                 180

gca gtg gca gta ttt cca ctg ggt gct aca cac atg ggc ccg att ttc   691
Ala Val Ala Val Phe Pro Leu Gly Ala Thr His Met Gly Pro Ile Phe
            185                 190                 195

cag acc cca acc cta ctc atc ctg gcg ctt ggc aca gca ctt ctc ggg   739
Gln Thr Pro Thr Leu Leu Ile Leu Ala Leu Gly Thr Ala Leu Leu Gly
        200                 205                 210

tcg ctt atc ccc tat tcg ctg gaa tta tcg gca ctg cgc cga ctc ccc   787
Ser Leu Ile Pro Tyr Ser Leu Glu Leu Ser Ala Leu Arg Arg Leu Pro
    215                 220                 225

gcc ccc att ttc agt att ctg ctc agc ctc gaa ccg gca ttc gcc gcc   835
Ala Pro Ile Phe Ser Ile Leu Leu Ser Leu Glu Pro Ala Phe Ala Ala
230                 235                 240                 245

gcc gtc ggc tgg atc ctg ctt gat caa acc ccc acc gcg ctc aag tgg   883
Ala Val Gly Trp Ile Leu Leu Asp Gln Thr Pro Thr Ala Leu Lys Trp
                250                 255                 260

gcc gcg atc atc ctt gtc atc gcg gcc agc atc ggc gtc acg tgg gag   931
Ala Ala Ile Ile Leu Val Ile Ala Ala Ser Ile Gly Val Thr Trp Glu
            265                 270                 275

cct aaa aag atg ctt gtc gac gcg ccc ctc cac tca aaa tgc aac gcg   979
Pro Lys Lys Met Leu Val Asp Ala Pro Leu His Ser Lys Cys Asn Ala
        280                 285                 290

aag agg cga gta cac aca cct agt taacgtgcag gcttaccttt tgg        1026
Lys Arg Arg Val His Thr Pro Ser
    295                 300
```

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<210> 1786
<211> 301
<212> PRT
<213> Corynebacterium glutamicum

<400> 1786

```
Met Asn Lys Gln Ser Ala Ala Val Leu Met Val Met Gly Ser Ala Leu
  1               5                  10                  15

Ser Leu Gln Phe Gly Ala Ala Ile Gly Thr Gln Leu Phe Pro Leu Asn
             20                  25                  30

Gly Pro Trp Ala Val Thr Ser Leu Arg Leu Phe Ile Ala Gly Leu Ile
         35                  40                  45

Met Cys Leu Val Ile Arg Pro Arg Leu Arg Ser Trp Thr Lys Lys Gln
     50                  55                  60

Trp Ile Ala Val Leu Leu Leu Gly Leu Ser Leu Gly Gly Met Asn Ser
 65                  70                  75                  80

Leu Phe Tyr Ala Ser Ile Glu Leu Ile Pro Leu Gly Thr Ala Val Thr
                 85                  90                  95
```

```
Ile Glu Phe Leu Gly Pro Leu Ile Phe Ser Ala Val Leu Ala Arg Thr
            100                 105                 110

Leu Lys Asn Gly Leu Cys Val Ala Leu Ala Phe Leu Gly Met Ala Leu
        115                 120                 125

Leu Gly Ile Asp Ser Leu Ser Gly Glu Thr Leu Asp Pro Leu Gly Val
    130                 135                 140

Ile Phe Ala Ala Val Ala Gly Ile Phe Trp Val Cys Tyr Ile Leu Ala
145                 150                 155                 160

Ser Lys Lys Ile Gly Gln Leu Ile Pro Gly Thr Ser Gly Leu Ala Val
                165                 170                 175

Ala Leu Ile Ile Gly Ala Val Ala Val Phe Pro Leu Gly Ala Thr His
            180                 185                 190

Met Gly Pro Ile Phe Gln Thr Pro Thr Leu Leu Ile Leu Ala Leu Gly
        195                 200                 205

Thr Ala Leu Leu Gly Ser Leu Ile Pro Tyr Ser Leu Glu Leu Ser Ala
    210                 215                 220

Leu Arg Arg Leu Pro Ala Pro Ile Phe Ser Ile Leu Leu Ser Leu Glu
225                 230                 235                 240

Pro Ala Phe Ala Ala Ala Val Gly Trp Ile Leu Leu Asp Gln Thr Pro
                245                 250                 255

Thr Ala Leu Lys Trp Ala Ala Ile Ile Leu Val Ile Ala Ala Ser Ile
            260                 265                 270

Gly Val Thr Trp Glu Pro Lys Lys Met Leu Val Asp Ala Pro Leu His
        275                 280                 285

Ser Lys Cys Asn Ala Lys Arg Arg Val His Thr Pro Ser
    290                 295                 300
```

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<210> 1787
<211> 543
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(520)
<223> RXA00491

<400> 1787

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tcctcatagt gtgtccacaa ttatctaaac tttagtagct tgtccttaaa tcggataacc 60

gctgcagctc acacgctatt ccacaaccgg aaatctggca gtg tat tgg gtt tta   115
                                              Val Tyr Trp Val Leu
                                                1               5

gca acc tct gcc aat agg gtg gaa gat gtg aac ttt gat gcg atg atg   163
Ala Thr Ser Ala Asn Arg Val Glu Asp Val Asn Phe Asp Ala Met Met
                10                  15                  20
```

```
ccc cgc gac ccg ttt gcc gat gat ccc aat gac ccg gca tcg ttt att   211
Pro Arg Asp Pro Phe Ala Asp Asp Pro Asn Asp Pro Ala Ser Phe Ile
            25                  30                  35

acc gac gat gac cct tat gat cat ccc gaa ccg ctt tct gaa gaa gag   259
Thr Asp Asp Asp Pro Tyr Asp His Pro Glu Pro Leu Ser Glu Glu Glu
        40                  45                  50

cga atc cac gtg agc caa gac ctt cgc ctc gtg atg gaa ttt aaa aaa   307
Arg Ile His Val Ser Gln Asp Leu Arg Leu Val Met Glu Phe Lys Lys
    55                  60                  65

gtt tta ggt ccc cga gga atc gaa ggc gtg ttc ttc atg tgc gaa gac   355
Val Leu Gly Pro Arg Gly Ile Glu Gly Val Phe Phe Met Cys Glu Asp
70                  75                  80                  85

tgc gaa gag ttc cac tac tac gac tgg gac atc atg gca gca aac atg   403
Cys Glu Glu Phe His Tyr Tyr Asp Trp Asp Ile Met Ala Ala Asn Met
                90                  95                  100

cgc gcc acc ttg gct ggg gaa ctc agc ccc gtg cat gaa cca agt gcg   451
Arg Ala Thr Leu Ala Gly Glu Leu Ser Pro Val His Glu Pro Ser Ala
            105                 110                 115

caa ccc aat att gat gcc tat gtg ccg tgg gac tac tgc att ggt tac   499
Gln Pro Asn Ile Asp Ala Tyr Val Pro Trp Asp Tyr Cys Ile Gly Tyr
        120                 125                 130

cta gac gga ctt gaa gcc aaa taaaaactgc tagcaactaa aga             543
Leu Asp Gly Leu Glu Ala Lys
    135                 140
```

Sequence Listing.ST25.txt

<210> 1788
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

<400> 1788

```
Val Tyr Trp Val Leu Ala Thr Ser Ala Asn Arg Val Glu Asp Val Asn
  1               5                  10                  15

Phe Asp Ala Met Met Pro Arg Asp Pro Phe Ala Asp Asp Pro Asn Asp
            20                  25                  30

Pro Ala Ser Phe Ile Thr Asp Asp Asp Pro Tyr Asp His Pro Glu Pro
        35                  40                  45

Leu Ser Glu Glu Glu Arg Ile His Val Ser Gln Asp Leu Arg Leu Val
    50                  55                  60

Met Glu Phe Lys Lys Val Leu Gly Pro Arg Gly Ile Glu Gly Val Phe
65                  70                  75                  80

Phe Met Cys Glu Asp Cys Glu Glu Phe His Tyr Tyr Asp Trp Asp Ile
                85                  90                  95

Met Ala Ala Asn Met Arg Ala Thr Leu Ala Gly Glu Leu Ser Pro Val
            100                 105                 110
```

```
His Glu Pro Ser Ala Gln Pro Asn Ile Asp Ala Tyr Val Pro Trp Asp
        115                 120                 125

Tyr Cys Ile Gly Tyr Leu Asp Gly Leu Glu Ala Lys
    130                 135                 140


<210> 1789
<211> 347
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(324)
<223> RXA00493

<400> 1789
ttc gaa ggc gac cag aag gtc ggc gtt cgc gca ctg gct act gct ttg   48
Phe Glu Gly Asp Gln Lys Val Gly Val Arg Ala Leu Ala Thr Ala Leu
  1               5                  10                  15

ggc aag cca gcg tac tgg atc gcc tcc aac gca ggt ctt gac ggc tct   96
Gly Lys Pro Ala Tyr Trp Ile Ala Ser Asn Ala Gly Leu Asp Gly Ser
             20                  25                  30

gtt gtt gtt gca cgc act gct gct ctg cca aac ggc gag ggc ttc aac   144
Val Val Val Ala Arg Thr Ala Ala Leu Pro Asn Gly Glu Gly Phe Asn
         35                  40                  45

gct gca act ttg gaa tac gga aac ctg atc aac gac ggt gtc atc gac   192
Ala Ala Thr Leu Glu Tyr Gly Asn Leu Ile Asn Asp Gly Val Ile Asp
     50                  55                  60

cca gtc aag gtc acc cat tcc gca gta gtg aat gca acc tct gtt gca   240
Pro Val Lys Val Thr His Ser Ala Val Val Asn Ala Thr Ser Val Ala
 65                  70                  75                  80

cgc atg gtt ctg acc act gag gct tct gtt gtt gag aag cct gca gaa   288
Arg Met Val Leu Thr Thr Glu Ala Ser Val Val Glu Lys Pro Ala Glu
                85                  90                  95

gaa gca gcc gat gca cat gca gga cat cat cac cac taaagttctg        334
Glu Ala Ala Asp Ala His Ala Gly His His His His
            100                 105

tgaaaaacac cgt                                                   347


<210> 1790
<211> 108
<212> PRT
<213> Corynebacterium glutamicum

<400> 1790
Phe Glu Gly Asp Gln Lys Val Gly Val Arg Ala Leu Ala Thr Ala Leu
  1               5                  10                  15

Gly Lys Pro Ala Tyr Trp Ile Ala Ser Asn Ala Gly Leu Asp Gly Ser
             20                  25                  30
```

```
Val Val Val Ala Arg Thr Ala Ala Leu Pro Asn Gly Glu Gly Phe Asn
         35                  40                  45

Ala Ala Thr Leu Glu Tyr Gly Asn Leu Ile Asn Asp Gly Val Ile Asp
     50                  55                  60

Pro Val Lys Val Thr His Ser Ala Val Val Asn Ala Thr Ser Val Ala
 65                  70                  75                  80

Arg Met Val Leu Thr Thr Glu Ala Ser Val Val Glu Lys Pro Ala Glu
                 85                  90                  95

Glu Ala Ala Asp Ala His Ala Gly His His His His
            100                 105


<210> 1791
<211> 536
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(513)
<223> RXA00519

<400> 1791
atg gct ggc ggc gga ctg ttc gag acc ggt gct ggt gga tct gct cct   48
Met Ala Gly Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser Ala Pro
  1               5                  10                  15

aag cac gtc cag cag gtt cag gaa gaa aac cac ctg cgt tgg gat tcc   96
Lys His Val Gln Gln Val Gln Glu Glu Asn His Leu Arg Trp Asp Ser
             20                  25                  30

ctc ggt gag ttc ctc gca ctg gct gag tcc ttc cgc cac gag ctc aac   144
Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu Leu Asn
         35                  40                  45

aac aac ggc aac acc aag gcc ggc gtt ctg gct gac gct ctg gac aag   192
Asn Asn Gly Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu Asp Lys
     50                  55                  60

gca act gag aag ctg ctg aac gaa gag aag tcc cca tcc cgc aag gtt   240
Ala Thr Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg Lys Val
 65                  70                  75                  80

ggc gag atc gac aac cgt ggc tcc cac ttc tgg ctg acc aag ttc tgg   288
Gly Glu Ile Asp Asn Arg Gly Ser His Phe Trp Leu Thr Lys Phe Trp
                 85                  90                  95

gct gac gag ctc gct gct cag acc gag gac gca gat ctg gct gct acc   336
Ala Asp Glu Leu Ala Ala Gln Thr Glu Asp Ala Asp Leu Ala Ala Thr
            100                 105                 110

ttc gca cca gtc gca gaa gca ctg aac aca ggc gct gca gac atc gat   384
Phe Ala Pro Val Ala Glu Ala Leu Asn Thr Gly Ala Ala Asp Ile Asp
        115                 120                 125

gct gca ctg ctc gca gtt cag ggt gga gca act gac ctt ggt ggc tac   432
Ala Ala Leu Leu Ala Val Gln Gly Gly Ala Thr Asp Leu Gly Gly Tyr
```

```
    130                 135                 140

tac tcc cct aac gag gag aag ctc acc aac atc atg cgc cca gtc gca   480
Tyr Ser Pro Asn Glu Glu Lys Leu Thr Asn Ile Met Arg Pro Val Ala
145                 150                 155                 160

cag ttc aac gag atc gtt gac gca ctg aag aag taaagtctct tcacaaaaag 533
Gln Phe Asn Glu Ile Val Asp Ala Leu Lys Lys
                165                 170

cgc                                                               536


<210> 1792
<211> 171
<212> PRT
<213> Corynebacterium glutamicum

<400> 1792
Met Ala Gly Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser Ala Pro
  1               5                  10                  15

Lys His Val Gln Gln Val Gln Glu Glu Asn His Leu Arg Trp Asp Ser
             20                  25                  30

Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu Leu Asn
         35                  40                  45

Asn Asn Gly Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu Asp Lys
     50                  55                  60

Ala Thr Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg Lys Val
 65                  70                  75                  80

Gly Glu Ile Asp Asn Arg Gly Ser His Phe Trp Leu Thr Lys Phe Trp
                 85                  90                  95

Ala Asp Glu Leu Ala Ala Gln Thr Glu Asp Ala Asp Leu Ala Ala Thr
            100                 105                 110

Phe Ala Pro Val Ala Glu Ala Leu Asn Thr Gly Ala Ala Asp Ile Asp
        115                 120                 125

Ala Ala Leu Leu Ala Val Gln Gly Gly Ala Thr Asp Leu Gly Gly Tyr
    130                 135                 140

Tyr Ser Pro Asn Glu Glu Lys Leu Thr Asn Ile Met Arg Pro Val Ala
145                 150                 155                 160

Gln Phe Asn Glu Ile Val Asp Ala Leu Lys Lys
                165                 170


<210> 1793
<211> 1212
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1189)
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<223> RXA00528

<400> 1793

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ttctgctggg aatccccaca ttttggaacg tagcgtcgat aagcgtgcgg cgaagctttt 60

tcggtcgcgg ccgttatctt tttaagagga gaaattttag atg agc acg tcc acc   115
                                            Met Ser Thr Ser Thr
                                              1               5

atc agg gtt gcc att gcc gga gtc gga aac tgc gcg acc tcc ctc att   163
Ile Arg Val Ala Ile Ala Gly Val Gly Asn Cys Ala Thr Ser Leu Ile
                 10                  15                  20

cag ggt gtg gaa tat tac cga aat gcg gat cct tcc gaa act gtc ccg   211
Gln Gly Val Glu Tyr Tyr Arg Asn Ala Asp Pro Ser Glu Thr Val Pro
             25                  30                  35

ggt ttg atg cac gtc aaa ttc ggt gat tac cac gtt ggc gac att gaa   259
Gly Leu Met His Val Lys Phe Gly Asp Tyr His Val Gly Asp Ile Glu
         40                  45                  50

ttc gtg gcc gcg ttc gac gtc gac gcc gaa aaa gta ggc atc gat ctt   307
Phe Val Ala Ala Phe Asp Val Asp Ala Glu Lys Val Gly Ile Asp Leu
     55                  60                  65

gcc gac gcc acc gag gct tca caa aac tgc act atc aaa atc gcc gat   355
Ala Asp Ala Thr Glu Ala Ser Gln Asn Cys Thr Ile Lys Ile Ala Asp
 70                  75                  80                  85

gtc cca cag acc ggc atc aac gtg ctg cgt ggc ccg act ctc gac ggc   403
Val Pro Gln Thr Gly Ile Asn Val Leu Arg Gly Pro Thr Leu Asp Gly
                 90                  95                 100

ctg ggc gat cat tac cgc gcg acc atc gac gag tcc acc gcc gag cca   451
Leu Gly Asp His Tyr Arg Ala Thr Ile Asp Glu Ser Thr Ala Glu Pro
            105                 110                 115

gtc gac gtt gtc cag gcg ctt atc gac gca aaa gcc gat gtt ttg gtg   499
Val Asp Val Val Gln Ala Leu Ile Asp Ala Lys Ala Asp Val Leu Val
        120                 125                 130

tcc tac ctc cca gtg ggc tcc gaa gaa gcc gac aaa ttc tac gca caa   547
Ser Tyr Leu Pro Val Gly Ser Glu Glu Ala Asp Lys Phe Tyr Ala Gln
    135                 140                 145

gcc gcc atc gat gca ggc tgc gcc ttt gtc aac gct ctc cca gta ttc   595
Ala Ala Ile Asp Ala Gly Cys Ala Phe Val Asn Ala Leu Pro Val Phe
150                 155                 160                 165

atc gcc tcc gac cct gag tgg gct aag aag ttc act gac gct ggc atc   643
Ile Ala Ser Asp Pro Glu Trp Ala Lys Lys Phe Thr Asp Ala Gly Ile
                170                 175                 180

cca att gtt ggc gat gac atc aaa tcc cag atc ggt gca acc atc acc   691
Pro Ile Val Gly Asp Asp Ile Lys Ser Gln Ile Gly Ala Thr Ile Thr
            185                 190                 195

cac cgt gtc ctc gca cgc ctt ttt gaa gaa cgt ggc gtt cgc gta gat   739
His Arg Val Leu Ala Arg Leu Phe Glu Glu Arg Gly Val Arg Val Asp
        200                 205                 210
```

```
cgc acc atg cag ctc aac gtc ggc ggc aac atg gac ttc aaa aac atg   787
Arg Thr Met Gln Leu Asn Val Gly Gly Asn Met Asp Phe Lys Asn Met
    215                 220                 225

ctt gac cgc aat cgc ttg gaa tcc aag aag gtc tcc aaa acc caa gca   835
Leu Asp Arg Asn Arg Leu Glu Ser Lys Lys Val Ser Lys Thr Gln Ala
230                 235                 240                 245

gtg acc tcc aac att cca gat ggt cca ctg tct gga aag gtg gaa gac   883
Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser Gly Lys Val Glu Asp
                250                 255                 260

cgc aac gtc cac atc gga cca tcc gac cac gtc caa tgg ctc gat gac   931
Arg Asn Val His Ile Gly Pro Ser Asp His Val Gln Trp Leu Asp Asp
            265                 270                 275

cgc aag tgg gct tat gtc cgc ctc gaa ggc acc gca ttc ggt gga gtt   979
Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr Ala Phe Gly Gly Val
        280                 285                 290

ccc ctc aac ctt gag tac aaa ctc gag gtg tgg gat tca ccc aac tct   1027
Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp Asp Ser Pro Asn Ser
    295                 300                 305

gcc ggc atc atc atc gac gct gtt cgc gcc gcc aag atc gcc ctc gat   1075
Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Ala Lys Ile Ala Leu Asp
310                 315                 320                 325

cgc ggt atc ggc gga ccg atc atg cca gca agc tcc tac ctg atg aag   1123
Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser Ser Tyr Leu Met Lys
                330                 335                 340

tcc cca cct gag cag ctt cca gac gat gtt gct tgt gaa cgc cta gag   1171
Ser Pro Pro Glu Gln Leu Pro Asp Asp Val Ala Cys Glu Arg Leu Glu
            345                 350                 355

gca ttc atc atc gag gcg taaaattagg ctaaaaattt ggg                1212
Ala Phe Ile Ile Glu Ala
        360
```

<210> 1794
<211> 363
<212> PRT
<213> Corynebacterium glutamicum

<400> 1794

```
Met Ser Thr Ser Thr Ile Arg Val Ala Ile Ala Gly Val Gly Asn Cys
  1               5                  10                  15

Ala Thr Ser Leu Ile Gln Gly Val Glu Tyr Tyr Arg Asn Ala Asp Pro
             20                  25                  30

Ser Glu Thr Val Pro Gly Leu Met His Val Lys Phe Gly Asp Tyr His
         35                  40                  45

Val Gly Asp Ile Glu Phe Val Ala Ala Phe Asp Val Asp Ala Glu Lys
     50                  55                  60

Val Gly Ile Asp Leu Ala Asp Ala Thr Glu Ala Ser Gln Asn Cys Thr
 65                  70                  75                  80
```

```
Ile Lys Ile Ala Asp Val Pro Gln Thr Gly Ile Asn Val Leu Arg Gly
                 85                  90                  95

Pro Thr Leu Asp Gly Leu Gly Asp His Tyr Arg Ala Thr Ile Asp Glu
            100                 105                 110

Ser Thr Ala Glu Pro Val Asp Val Val Gln Ala Leu Ile Asp Ala Lys
        115                 120                 125

Ala Asp Val Leu Val Ser Tyr Leu Pro Val Gly Ser Glu Glu Ala Asp
    130                 135                 140

Lys Phe Tyr Ala Gln Ala Ala Ile Asp Ala Gly Cys Ala Phe Val Asn
145                 150                 155                 160

Ala Leu Pro Val Phe Ile Ala Ser Asp Pro Glu Trp Ala Lys Lys Phe
                165                 170                 175

Thr Asp Ala Gly Ile Pro Ile Val Gly Asp Asp Ile Lys Ser Gln Ile
            180                 185                 190

Gly Ala Thr Ile Thr His Arg Val Leu Ala Arg Leu Phe Glu Glu Arg
        195                 200                 205

Gly Val Arg Val Asp Arg Thr Met Gln Leu Asn Val Gly Gly Asn Met
    210                 215                 220

Asp Phe Lys Asn Met Leu Asp Arg Asn Arg Leu Glu Ser Lys Lys Val
225                 230                 235                 240

Ser Lys Thr Gln Ala Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser
                245                 250                 255

Gly Lys Val Glu Asp Arg Asn Val His Ile Gly Pro Ser Asp His Val
            260                 265                 270

Gln Trp Leu Asp Asp Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr
        275                 280                 285

Ala Phe Gly Gly Val Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp
    290                 295                 300

Asp Ser Pro Asn Ser Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Ala
305                 310                 315                 320

Lys Ile Ala Leu Asp Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser
                325                 330                 335

Ser Tyr Leu Met Lys Ser Pro Pro Glu Gln Leu Pro Asp Asp Val Ala
            340                 345                 350

Cys Glu Arg Leu Glu Ala Phe Ile Ile Glu Ala
        355                 360
```

<210> 1795
<211> 666
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(643)
<223> RXA00529

<400> 1795
gcaaagcttt gtaccggaag cgttaaggca ctggattttg tcgagcagtt tcaggctgtt 60

tagcgggcga gttcttatag agatgtataa ggtgaagctc atg aag ttg aag tgg 115
Met Lys Leu Lys Trp
1 5

att gca cca att ctt ccg gtt ttg gcc ctt gca ggc tgc gga aac tac 163
Ile Ala Pro Ile Leu Pro Val Leu Ala Leu Ala Gly Cys Gly Asn Tyr
10 15 20

gtc aac gta gag tcg caa ggg aaa tct gga att tcc cat gat gag gac 211
Val Asn Val Glu Ser Gln Gly Lys Ser Gly Ile Ser His Asp Glu Asp
25 30 35

gga aat ata agc gtt cac atg tac atc tgt ggt gat aat gcg gtg gat 259
Gly Asn Ile Ser Val His Met Tyr Ile Cys Gly Asp Asn Ala Val Asp
40 45 50

gaa ctg ata ctt agc ggt ggt ttt tac gat ggc cca cct ggg aca aac 307
Glu Leu Ile Leu Ser Gly Gly Phe Tyr Asp Gly Pro Pro Gly Thr Asn
55 60 65

aac cca gcc ctt ggg atg ttg aaa act tcc aac cct gag tcg ggt tat 355
Asn Pro Ala Leu Gly Met Leu Lys Thr Ser Asn Pro Glu Ser Gly Tyr
70 75 80 85

gtt gta gtc aac atc gct gat cca gca ccg tgg gaa gtt gtt gag cca 403
Val Val Val Asn Ile Ala Asp Pro Ala Pro Trp Glu Val Val Glu Pro
90 95 100

atc aat ttg ccc acg gaa cag gga aag tac att att gcc aat ccg agg 451
Ile Asn Leu Pro Thr Glu Gln Gly Lys Tyr Ile Ile Ala Asn Pro Arg
105 110 115

ttg gta gat aaa ggt tgg ccg att cct ttc gca aaa gaa aag tat atg 499
Leu Val Asp Lys Gly Trp Pro Ile Pro Phe Ala Lys Glu Lys Tyr Met
120 125 130

ccg agt gtt tcc aca tca gta gga atg ctt gaa gga ata gat cca ggt 547
Pro Ser Val Ser Thr Ser Val Gly Met Leu Glu Gly Ile Asp Pro Gly
135 140 145

cta gtc atg cgg gat atg tat acc gag tcg act cat gtg ttc ggt act 595
Leu Val Met Arg Asp Met Tyr Thr Glu Ser Thr His Val Phe Gly Thr
150 155 160 165

gcc gaa gac ttt gtt gaa gcc ggt caa cag tgg tgc gag gat tat ttc 643
Ala Glu Asp Phe Val Glu Ala Gly Gln Gln Trp Cys Glu Asp Tyr Phe
170 175 180

taaaacgtga atctggcaaa aga 666

<210> 1796
<211> 181

<212> PRT
<213> Corynebacterium glutamicum

<400> 1796
Met Lys Leu Lys Trp Ile Ala Pro Ile Leu Pro Val Leu Ala Leu Ala
1 5 10 15

Gly Cys Gly Asn Tyr Val Asn Val Glu Ser Gln Gly Lys Ser Gly Ile
20 25 30

Ser His Asp Glu Asp Gly Asn Ile Ser Val His Met Tyr Ile Cys Gly
35 40 45

Asp Asn Ala Val Asp Glu Leu Ile Leu Ser Gly Gly Phe Tyr Asp Gly
50 55 60

Pro Pro Gly Thr Asn Asn Pro Ala Leu Gly Met Leu Lys Thr Ser Asn
65 70 75 80

Pro Glu Ser Gly Tyr Val Val Val Asn Ile Ala Asp Pro Ala Pro Trp
85 90 95

Glu Val Val Glu Pro Ile Asn Leu Pro Thr Glu Gln Gly Lys Tyr Ile
100 105 110

Ile Ala Asn Pro Arg Leu Val Asp Lys Gly Trp Pro Ile Pro Phe Ala
115 120 125

Lys Glu Lys Tyr Met Pro Ser Val Ser Thr Ser Val Gly Met Leu Glu
130 135 140

Gly Ile Asp Pro Gly Leu Val Met Arg Asp Met Tyr Thr Glu Ser Thr
145 150 155 160

His Val Phe Gly Thr Ala Glu Asp Phe Val Glu Ala Gly Gln Gln Trp
165 170 175

Cys Glu Asp Tyr Phe
180

<210> 1797
<211> 1404
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1381)
<223> RXA00530

<400> 1797
ggcgataagc ctcctccctg gggccttgcc catttcatag ggtgtccagg taatgtttca 60

ggggttagat ttcagctgaa gcaactgggg agttggcgct atg agc atc gga ttc 115
Met Ser Ile Gly Phe
1 5

gac cgc gac ctt tat att aag atg cag tcg cag cac atc aat gag cgc 163
Asp Arg Asp Leu Tyr Ile Lys Met Gln Ser Gln His Ile Asn Glu Arg
10 15 20

```
cgc gag cag atc ggc ggc aag ctg tat ctg gaa atg ggc ggc aag ctt   211
Arg Glu Gln Ile Gly Gly Lys Leu Tyr Leu Glu Met Gly Gly Lys Leu
             25                  30                  35

ttc gac gac atg cac gct tcc cgt gtg ctg cca ggt ttc acg cct gac   259
Phe Asp Asp Met His Ala Ser Arg Val Leu Pro Gly Phe Thr Pro Asp
         40                  45                  50

aac aag atc gct atg ctc act gag ctt aaa gat gag ctg gaa atc ctc   307
Asn Lys Ile Ala Met Leu Thr Glu Leu Lys Asp Glu Leu Glu Ile Leu
     55                  60                  65

gtc gca atc aat gcg aag gat ctg gag cgc aag aaa acc cgc gcc gac   355
Val Ala Ile Asn Ala Lys Asp Leu Glu Arg Lys Lys Thr Arg Ala Asp
 70                  75                  80                  85

ctc gac att tct tat gag gaa gat gtt tta cgc ctc att gat gtg ttc   403
Leu Asp Ile Ser Tyr Glu Glu Asp Val Leu Arg Leu Ile Asp Val Phe
                 90                  95                 100

cgt gag ctg ggc ttt ttg gcg gag cat gtg gtg ctc aca cag ttg gag   451
Arg Glu Leu Gly Phe Leu Ala Glu His Val Val Leu Thr Gln Leu Glu
            105                 110                 115

gat gac aac tat cag gca ctc gcg ttc aag cag cgc cta gag cgc ctt   499
Asp Asp Asn Tyr Gln Ala Leu Ala Phe Lys Gln Arg Leu Glu Arg Leu
        120                 125                 130

ggc ctg aag gtt gct gtt cac cgc gtg att cca ggt tac cca act gat   547
Gly Leu Lys Val Ala Val His Arg Val Ile Pro Gly Tyr Pro Thr Asp
    135                 140                 145

gct cgc cgc att gtt agc gag gaa ggt ttc ggc atc aac gag tat gtg   595
Ala Arg Arg Ile Val Ser Glu Glu Gly Phe Gly Ile Asn Glu Tyr Val
150                 155                 160                 165

gaa acc acc cgc aat ttg gtt gtt gtg acc gca ccg ggc cca ggt tct   643
Glu Thr Thr Arg Asn Leu Val Val Val Thr Ala Pro Gly Pro Gly Ser
                170                 175                 180

gga aag ctc gct acc tgc ttg agc cag att tat ggc gat cac cag cgc   691
Gly Lys Leu Ala Thr Cys Leu Ser Gln Ile Tyr Gly Asp His Gln Arg
            185                 190                 195

gga atc aag tcc ggc tac gca aag ttt gaa act ttc ccc att tgg aac   739
Gly Ile Lys Ser Gly Tyr Ala Lys Phe Glu Thr Phe Pro Ile Trp Asn
        200                 205                 210

ctg cct ctt gag cac cca gtt aac ttg gct tat gag gct gcc acg gca   787
Leu Pro Leu Glu His Pro Val Asn Leu Ala Tyr Glu Ala Ala Thr Ala
    215                 220                 225

gat ctc gat gac atc aac atc atc gat cct ttc cac ctc gcc gcc tat   835
Asp Leu Asp Asp Ile Asn Ile Ile Asp Pro Phe His Leu Ala Ala Tyr
230                 235                 240                 245

gac acc aaa gcc acc agc tac aac cgc gac gtg gaa gtc ttc ccg ctg   883
Asp Thr Lys Ala Thr Ser Tyr Asn Arg Asp Val Glu Val Phe Pro Leu
                250                 255                 260
```

```
ctg aaa acc atg ctg gaa atg ctg tcg ggc tca tcg ccg tac aaa tcc   931
Leu Lys Thr Met Leu Glu Met Leu Ser Gly Ser Ser Pro Tyr Lys Ser
            265                 270                 275

ccc acc gac atg ggt gtc aac atg gtc gga agc gca att atc gac gac   979
Pro Thr Asp Met Gly Val Asn Met Val Gly Ser Ala Ile Ile Asp Asp
        280                 285                 290

gcc gcg tgc cag gaa gcc gcc cgc caa gaa att gtt cgg cgt tac ttc   1027
Ala Ala Cys Gln Glu Ala Ala Arg Gln Glu Ile Val Arg Arg Tyr Phe
    295                 300                 305

aag gcg ctt gtc gac gag cgt cgc gag gag cag gac gat acc att tca   1075
Lys Ala Leu Val Asp Glu Arg Arg Glu Glu Gln Asp Asp Thr Ile Ser
310                 315                 320                 325

gcg cgc atc gcc att gtc atg agc aag gcc ggt tgc acc gtt gaa gac   1123
Ala Arg Ile Ala Ile Val Met Ser Lys Ala Gly Cys Thr Val Glu Asp
                330                 335                 340

cgc cgc gtg gtt gcc cga gca ctt gat gtt gaa gaa tcc acc ggc gcg   1171
Arg Arg Val Val Ala Arg Ala Leu Asp Val Glu Glu Ser Thr Gly Ala
            345                 350                 355

ccg ggt tgt gcc att gaa ctt aac gat ggt cga ctc gtc acc ggc aag   1219
Pro Gly Cys Ala Ile Glu Leu Asn Asp Gly Arg Leu Val Thr Gly Lys
        360                 365                 370

act tca gaa ctt ctc gga tgc tcc gca gcg atg gtg ctt aat gca ctg   1267
Thr Ser Glu Leu Leu Gly Cys Ser Ala Ala Met Val Leu Asn Ala Leu
    375                 380                 385

aag gaa ctc gct ggc att gat cgc agc gtg gat ctc ctc tcc cct gaa   1315
Lys Glu Leu Ala Gly Ile Asp Arg Ser Val Asp Leu Leu Ser Pro Glu
390                 395                 400                 405

tcc atc gag cca atc caa tcg ctg aag acc cag cac ctg gga tcc cgc   1363
Ser Ile Glu Pro Ile Gln Ser Leu Lys Thr Gln His Leu Gly Ser Arg
                410                 415                 420

aac ccc tcg cct gca cac tgatgaagtg cttattgctt tgt                 1404
Asn Pro Ser Pro Ala His
            425
```

<210> 1798
<211> 427
<212> PRT
<213> Corynebacterium glutamicum

<400> 1798

```
Met Ser Ile Gly Phe Asp Arg Asp Leu Tyr Ile Lys Met Gln Ser Gln
  1               5                  10                  15

His Ile Asn Glu Arg Arg Glu Gln Ile Gly Gly Lys Leu Tyr Leu Glu
             20                  25                  30

Met Gly Gly Lys Leu Phe Asp Asp Met His Ala Ser Arg Val Leu Pro
         35                  40                  45

Gly Phe Thr Pro Asp Asn Lys Ile Ala Met Leu Thr Glu Leu Lys Asp
```

```
     50                  55                  60

Glu Leu Glu Ile Leu Val Ala Ile Asn Ala Lys Asp Leu Glu Arg Lys
 65                  70                  75                  80

Lys Thr Arg Ala Asp Leu Asp Ile Ser Tyr Glu Glu Asp Val Leu Arg
                85                  90                  95

Leu Ile Asp Val Phe Arg Glu Leu Gly Phe Leu Ala Glu His Val Val
            100                 105                 110

Leu Thr Gln Leu Glu Asp Asp Asn Tyr Gln Ala Leu Ala Phe Lys Gln
        115                 120                 125

Arg Leu Glu Arg Leu Gly Leu Lys Val Ala Val His Arg Val Ile Pro
    130                 135                 140

Gly Tyr Pro Thr Asp Ala Arg Arg Ile Val Ser Glu Glu Gly Phe Gly
145                 150                 155                 160

Ile Asn Glu Tyr Val Glu Thr Thr Arg Asn Leu Val Val Val Thr Ala
                165                 170                 175

Pro Gly Pro Gly Ser Gly Lys Leu Ala Thr Cys Leu Ser Gln Ile Tyr
            180                 185                 190

Gly Asp His Gln Arg Gly Ile Lys Ser Gly Tyr Ala Lys Phe Glu Thr
        195                 200                 205

Phe Pro Ile Trp Asn Leu Pro Leu Glu His Pro Val Asn Leu Ala Tyr
    210                 215                 220

Glu Ala Ala Thr Ala Asp Leu Asp Asp Ile Asn Ile Ile Asp Pro Phe
225                 230                 235                 240

His Leu Ala Ala Tyr Asp Thr Lys Ala Thr Ser Tyr Asn Arg Asp Val
                245                 250                 255

Glu Val Phe Pro Leu Leu Lys Thr Met Leu Glu Met Leu Ser Gly Ser
            260                 265                 270

Ser Pro Tyr Lys Ser Pro Thr Asp Met Gly Val Asn Met Val Gly Ser
        275                 280                 285

Ala Ile Ile Asp Asp Ala Ala Cys Gln Glu Ala Ala Arg Gln Glu Ile
    290                 295                 300

Val Arg Arg Tyr Phe Lys Ala Leu Val Asp Glu Arg Arg Glu Glu Gln
305                 310                 315                 320

Asp Asp Thr Ile Ser Ala Arg Ile Ala Ile Val Met Ser Lys Ala Gly
                325                 330                 335

Cys Thr Val Glu Asp Arg Arg Val Val Ala Arg Ala Leu Asp Val Glu
            340                 345                 350

Glu Ser Thr Gly Ala Pro Gly Cys Ala Ile Glu Leu Asn Asp Gly Arg
        355                 360                 365

Leu Val Thr Gly Lys Thr Ser Glu Leu Leu Gly Cys Ser Ala Ala Met
    370                 375                 380
```

```
Val Leu Asn Ala Leu Lys Glu Leu Ala Gly Ile Asp Arg Ser Val Asp
385                 390                 395                 400

Leu Leu Ser Pro Glu Ser Ile Glu Pro Ile Gln Ser Leu Lys Thr Gln
                405                 410                 415

His Leu Gly Ser Arg Asn Pro Ser Pro Ala His
            420                 425


<210> 1799
<211> 840
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(817)
<223> RXA00535

<400> 1799
aatcgcatgg ggcaccgtgg tcagacaccg gatcgcgctc cgcaccccaa aagatggctc 60

cctaaggagc tcacctttac tcaatgctct gatgacaccg atg tgg tgg gca ggc   115
                                            Met Trp Trp Ala Gly
                                              1               5

atg agt acc gcg atg ctg gca tat ttc tta caa aca gta gca ctt ggt   163
Met Ser Thr Ala Met Leu Ala Tyr Phe Leu Gln Thr Val Ala Leu Gly
                10                  15                  20

ttc ggc acc ctc ttg gta gtg caa cca gtg ctt gtc ctg tcg ctg atg   211
Phe Gly Thr Leu Leu Val Val Gln Pro Val Leu Val Leu Ser Leu Met
            25                  30                  35

ttc acg ctg ccg ctc tca gca cga ttc aat ggc tac cga cta cgc cga   259
Phe Thr Leu Pro Leu Ser Ala Arg Phe Asn Gly Tyr Arg Leu Arg Arg
        40                  45                  50

act gaa atc ttc tgg gct acc ctc ctc acc gta gcc gtg ggc atc atg   307
Thr Glu Ile Phe Trp Ala Thr Leu Leu Thr Val Ala Val Gly Ile Met
    55                  60                  65

atc gtt ttg gga cgc ccc ctt ccc gga aac ccc cac ccc cca ctc gat   355
Ile Val Leu Gly Arg Pro Leu Pro Gly Asn Pro His Pro Pro Leu Asp
70                  75                  80                  85

cga tgg att cca gta ctt tta gtc ggc gtt gca gta atg ggt gga atg   403
Arg Trp Ile Pro Val Leu Leu Val Gly Val Ala Val Met Gly Gly Met
                90                  95                  100

tgg ctg ctt gcg gaa tac gta tta aag aag gac aaa gcc ctc atc ctt   451
Trp Leu Leu Ala Glu Tyr Val Leu Lys Lys Asp Lys Ala Leu Ile Leu
            105                 110                 115

ggt ctt gtg acg ggt gca ttg ttt ggc tac gta gca gtg atg tcc aaa   499
Gly Leu Val Thr Gly Ala Leu Phe Gly Tyr Val Ala Val Met Ser Lys
        120                 125                 130

gcc gcg gtg gat ctt ttt gtc cat caa ggc ata acg gga ctc atc ttg   547
```

```
Ala Ala Val Asp Leu Phe Val His Gln Gly Ile Thr Gly Leu Ile Leu
    135                 140                 145

aac tgg gaa ggc tac ggc cta atc ctc acc gca tta ctt gga aca atc   595
Asn Trp Glu Gly Tyr Gly Leu Ile Leu Thr Ala Leu Leu Gly Thr Ile
150                 155                 160                 165

gtg cag cag tat tcc ttt aac gct ggc gaa cta caa aaa tcg cta ccc   643
Val Gln Gln Tyr Ser Phe Asn Ala Gly Glu Leu Gln Lys Ser Leu Pro
                170                 175                 180

gcc atg acc att gcc gaa cca att gtt gcc ttc agt ttg ggc tac ttg   691
Ala Met Thr Ile Ala Glu Pro Ile Val Ala Phe Ser Leu Gly Tyr Leu
            185                 190                 195

gtt ctg ggc gaa aaa ttc caa gtc gtg gac tgg gaa tgg atc gcc atg   739
Val Leu Gly Glu Lys Phe Gln Val Val Asp Trp Glu Trp Ile Ala Met
        200                 205                 210

ggc atc gca cta ctg gtg atg att gtt tcc acc att gca ctg tct cgt   787
Gly Ile Ala Leu Leu Val Met Ile Val Ser Thr Ile Ala Leu Ser Arg
    215                 220                 225

aca agc aca atg ccg gcc gga tcg aaa agg taaaactcca aagttccccc     837
Thr Ser Thr Met Pro Ala Gly Ser Lys Arg
230                 235

cga                                                               840


<210> 1800
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

<400> 1800
Met Trp Trp Ala Gly Met Ser Thr Ala Met Leu Ala Tyr Phe Leu Gln
  1               5                  10                  15

Thr Val Ala Leu Gly Phe Gly Thr Leu Leu Val Val Gln Pro Val Leu
             20                  25                  30

Val Leu Ser Leu Met Phe Thr Leu Pro Leu Ser Ala Arg Phe Asn Gly
         35                  40                  45

Tyr Arg Leu Arg Arg Thr Glu Ile Phe Trp Ala Thr Leu Leu Thr Val
     50                  55                  60

Ala Val Gly Ile Met Ile Val Leu Gly Arg Pro Leu Pro Gly Asn Pro
 65                  70                  75                  80

His Pro Pro Leu Asp Arg Trp Ile Pro Val Leu Leu Val Gly Val Ala
                 85                  90                  95

Val Met Gly Gly Met Trp Leu Leu Ala Glu Tyr Val Leu Lys Lys Asp
            100                 105                 110

Lys Ala Leu Ile Leu Gly Leu Val Thr Gly Ala Leu Phe Gly Tyr Val
        115                 120                 125

Ala Val Met Ser Lys Ala Ala Val Asp Leu Phe Val His Gln Gly Ile
```

```
    130                 135                 140

Thr Gly Leu Ile Leu Asn Trp Glu Gly Tyr Gly Leu Ile Leu Thr Ala
145                 150                 155                 160

Leu Leu Gly Thr Ile Val Gln Gln Tyr Ser Phe Asn Ala Gly Glu Leu
                165                 170                 175

Gln Lys Ser Leu Pro Ala Met Thr Ile Ala Glu Pro Ile Val Ala Phe
            180                 185                 190

Ser Leu Gly Tyr Leu Val Leu Gly Glu Lys Phe Gln Val Val Asp Trp
        195                 200                 205

Glu Trp Ile Ala Met Gly Ile Ala Leu Leu Val Met Ile Val Ser Thr
    210                 215                 220

Ile Ala Leu Ser Arg Thr Ser Thr Met Pro Ala Gly Ser Lys Arg
225                 230                 235
```

<210> 1801
<211> 366
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(343)
<223> RXA00540

<400> 1801

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tctccctatc taagggctgg ctaggtttga ccagtggcaa cagttacact tgtgctcgta 60

aaacattgtc ctccccattt cttgagtaag ggaaaatacc gtg gcc cgt gta gtt   115
                                            Val Ala Arg Val Val
                                              1               5

gtc aat gtc atg cct aag gct gag att ctg gat ccc cag ggg cag gcg   163
Val Asn Val Met Pro Lys Ala Glu Ile Leu Asp Pro Gln Gly Gln Ala
                10                  15                  20

gta cac cgc gcc ctc gga cgt atc gga gtt tct ggc gtt tcc gat gtc   211
Val His Arg Ala Leu Gly Arg Ile Gly Val Ser Gly Val Ser Asp Val
            25                  30                  35

cgt cag gga aag cgc ttc gag ctt gag gta gat gat tcc gtc acc gaa   259
Arg Gln Gly Lys Arg Phe Glu Leu Glu Val Asp Asp Ser Val Thr Glu
        40                  45                  50

gct gac cta aag aaa att gct gaa acc ctc ctc gca aac acc gtc atc   307
Ala Asp Leu Lys Lys Ile Ala Glu Thr Leu Leu Ala Asn Thr Val Ile
    55                  60                  65

gaa gac ttc gat gtg gtg gga gtt gag gtc gcg aag tgagcgccaa        353
Glu Asp Phe Asp Val Val Gly Val Glu Val Ala Lys
70                  75                  80

aatcggtgtc att                                                   366
```

<210> 1802
<211> 81
<212> PRT
<213> Corynebacterium glutamicum

<400> 1802
Val Ala Arg Val Val Val Asn Val Met Pro Lys Ala Glu Ile Leu Asp
1 5 10 15

Pro Gln Gly Gln Ala Val His Arg Ala Leu Gly Arg Ile Gly Val Ser
20 25 30

Gly Val Ser Asp Val Arg Gln Gly Lys Arg Phe Glu Leu Glu Val Asp
35 40 45

Asp Ser Val Thr Glu Ala Asp Leu Lys Lys Ile Ala Glu Thr Leu Leu
50 55 60

Ala Asn Thr Val Ile Glu Asp Phe Asp Val Val Gly Val Glu Val Ala
65 70 75 80

Lys

<210> 1803
<211> 519
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(496)
<223> RXA00549

<400> 1803
attcgtttgc agcaggatct ggaaaatggt tcacaggata ctgcggacat ggcgcatgct 60

ttgggtatcg cgaagtcttt gccaactatc cctgagacac ttg act gaa aac gga 115
Leu Thr Glu Asn Gly
1 5

gag acc cct tat gag ggc atc atc ttg ggt cag tat gag tcc cgc cca 163
Glu Thr Pro Tyr Glu Gly Ile Ile Leu Gly Gln Tyr Glu Ser Arg Pro
10 15 20

ctt gat atg gct tct gcg atg gca act atc gct aat gaa ggt gtc tgg 211
Leu Asp Met Ala Ser Ala Met Ala Thr Ile Ala Asn Glu Gly Val Trp
25 30 35

cac cgc ccg cac ttc gtg tcc aag gtg gag act gtc agc ggt gag gtt 259
His Arg Pro His Phe Val Ser Lys Val Glu Thr Val Ser Gly Glu Val
40 45 50

ctc tac gag ttc gag gat ggc gac ggc gag cgt cgt gtt tct gaa aag 307
Leu Tyr Glu Phe Glu Asp Gly Asp Gly Glu Arg Arg Val Ser Glu Lys
55 60 65

gtt gca ctg aat ctg ctc aag gcc atg ggg cca atc gct gca tac tcc 355
Val Ala Leu Asn Leu Leu Lys Ala Met Gly Pro Ile Ala Ala Tyr Ser
70 75 80 85

```
aac gga aac gct ctg gct gat ggc cag gtt tct gca tcc aag act ggt   403
Asn Gly Asn Ala Leu Ala Asp Gly Gln Val Ser Ala Ser Lys Thr Gly
                 90                  95                 100

acc act cag ctt ggt gat acc ggt gca aac aag gat gcg tgg atg ttg   451
Thr Thr Gln Leu Gly Asp Thr Gly Ala Asn Lys Asp Ala Trp Met Leu
            105                 110                 115

ggt gcg gca cct cag cta gct act gcg gtg tgg gtc gga act gct       496
Gly Ala Ala Pro Gln Leu Ala Thr Ala Val Trp Val Gly Thr Ala
        120                 125                 130

tgataacact gcattgtata aca                                        519
```

<210> 1804
<211> 132
<212> PRT
<213> Corynebacterium glutamicum

<400> 1804

```
Leu Thr Glu Asn Gly Glu Thr Pro Tyr Glu Gly Ile Ile Leu Gly Gln
  1               5                  10                  15

Tyr Glu Ser Arg Pro Leu Asp Met Ala Ser Ala Met Ala Thr Ile Ala
             20                  25                  30

Asn Glu Gly Val Trp His Arg Pro His Phe Val Ser Lys Val Glu Thr
         35                  40                  45

Val Ser Gly Glu Val Leu Tyr Glu Phe Glu Asp Gly Asp Gly Glu Arg
     50                  55                  60

Arg Val Ser Glu Lys Val Ala Leu Asn Leu Leu Lys Ala Met Gly Pro
 65                  70                  75                  80

Ile Ala Ala Tyr Ser Asn Gly Asn Ala Leu Ala Asp Gly Gln Val Ser
                 85                  90                  95

Ala Ser Lys Thr Gly Thr Thr Gln Leu Gly Asp Thr Gly Ala Asn Lys
            100                 105                 110

Asp Ala Trp Met Leu Gly Ala Ala Pro Gln Leu Ala Thr Ala Val Trp
        115                 120                 125

Val Gly Thr Ala
    130
```

<210> 1805
<211> 444
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(421)
<223> RXA00550

<400> 1805

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aaggatgcgt ggatgttggg tgcggcacct cagctagcta ctgcggtgtg ggtcggaact 60

gcttgataac actgcattgt ataacacctg gggtggcagt atg tat ggt tct aac   115
                                            Met Tyr Gly Ser Asn
                                              1               5

tcc cct gcc acg atc tgg aag cag acc atg gat aac gcc ctc gag aac   163
Ser Pro Ala Thr Ile Trp Lys Gln Thr Met Asp Asn Ala Leu Glu Asn
                 10                  15                  20

tcc cct ctc gaa act tgg gat atc gct cca gca ttg ggg tac ggt aac   211
Ser Pro Leu Glu Thr Trp Asp Ile Ala Pro Ala Leu Gly Tyr Gly Asn
             25                  30                  35

cca cca gtt ccg gaa tat gtg tgg act cca agt cca aac atc gcg act   259
Pro Pro Val Pro Glu Tyr Val Trp Thr Pro Ser Pro Asn Ile Ala Thr
         40                  45                  50

aat gat cca gaa gga gca acc gag gaa gct cca gtg gag gat cca aat   307
Asn Asp Pro Glu Gly Ala Thr Glu Glu Ala Pro Val Glu Asp Pro Asn
     55                  60                  65

gca gta atc gat acc cct gct gta gat ccc act gca cct gca gag gag   355
Ala Val Ile Asp Thr Pro Ala Val Asp Pro Thr Ala Pro Ala Glu Glu
 70                  75                  80                  85

acc ggt aac ggt cag gta gaa atc ctg ccg ggg ctg act atc ccg gga   403
Thr Gly Asn Gly Gln Val Glu Ile Leu Pro Gly Leu Thr Ile Pro Gly
                 90                  95                 100

gat ctc tta ggg atc ggc taaaatccgg tcgtagccta aac                 444
Asp Leu Leu Gly Ile Gly
            105


<210> 1806
<211> 107
<212> PRT
<213> Corynebacterium glutamicum

<400> 1806
Met Tyr Gly Ser Asn Ser Pro Ala Thr Ile Trp Lys Gln Thr Met Asp
  1               5                  10                  15

Asn Ala Leu Glu Asn Ser Pro Leu Glu Thr Trp Asp Ile Ala Pro Ala
             20                  25                  30

Leu Gly Tyr Gly Asn Pro Pro Val Pro Glu Tyr Val Trp Thr Pro Ser
         35                  40                  45

Pro Asn Ile Ala Thr Asn Asp Pro Glu Gly Ala Thr Glu Glu Ala Pro
     50                  55                  60

Val Glu Asp Pro Asn Ala Val Ile Asp Thr Pro Ala Val Asp Pro Thr
 65                  70                  75                  80

Ala Pro Ala Glu Glu Thr Gly Asn Gly Gln Val Glu Ile Leu Pro Gly
                 85                  90                  95

Leu Thr Ile Pro Gly Asp Leu Leu Gly Ile Gly
            100                 105
```

<210> 1807
<211> 444
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(421)
<223> RXA00553

<400> 1807
gtcattgcaa gcgcgaacgc tgtgcagcaa ttgctgcgga tttcgctgag caaggaattg 60

atccgctcgt tacttcttaa aaagggtatg gtggctgggt atg agc atc gtt aag 115
Met Ser Ile Val Lys
1 5

atc aac gca att tcc gta ccc gaa ggc gct ggt gaa gag ctt gag aag 163
Ile Asn Ala Ile Ser Val Pro Glu Gly Ala Gly Glu Glu Leu Glu Lys
10 15 20

cgc ttc gca gcc cgc caa aat gcc gtg gat tcc gct ccg gga ttt gag 211
Arg Phe Ala Ala Arg Gln Asn Ala Val Asp Ser Ala Pro Gly Phe Glu
25 30 35

ggc ttt caa ctg tta cgc cct gtt tcc ggt gaa gac cgc tac ttt gta 259
Gly Phe Gln Leu Leu Arg Pro Val Ser Gly Glu Asp Arg Tyr Phe Val
40 45 50

gtc acc cag tgg gct gat gaa gac agc tat aac gcg tgg cgt gat gcc 307
Val Thr Gln Trp Ala Asp Glu Asp Ser Tyr Asn Ala Trp Arg Asp Ala
55 60 65

gaa aag gcc aag ggc ggt cat ggc cag gga gcc cac ggc tca gat aag 355
Glu Lys Ala Lys Gly Gly His Gly Gln Gly Ala His Gly Ser Asp Lys
70 75 80 85

aag cct gtc gct tcc ggc gct tcc ctg ctg gag ttc gaa gta gtc cta 403
Lys Pro Val Ala Ser Gly Ala Ser Leu Leu Glu Phe Glu Val Val Leu
90 95 100

gga tct acc ggc gct aag tagggaaaga gaaaagtcgg aac 444
Gly Ser Thr Gly Ala Lys
105

<210> 1808
<211> 107
<212> PRT
<213> Corynebacterium glutamicum

<400> 1808
Met Ser Ile Val Lys Ile Asn Ala Ile Ser Val Pro Glu Gly Ala Gly
1 5 10 15

Glu Glu Leu Glu Lys Arg Phe Ala Ala Arg Gln Asn Ala Val Asp Ser
20 25 30

Ala Pro Gly Phe Glu Gly Phe Gln Leu Leu Arg Pro Val Ser Gly Glu

```
         35                  40                  45

Asp Arg Tyr Phe Val Val Thr Gln Trp Ala Asp Glu Asp Ser Tyr Asn
     50                  55                  60

Ala Trp Arg Asp Ala Glu Lys Ala Lys Gly Gly His Gly Gln Gly Ala
 65                  70                  75                  80

His Gly Ser Asp Lys Lys Pro Val Ala Ser Gly Ala Ser Leu Leu Glu
                 85                  90                  95

Phe Glu Val Val Leu Gly Ser Thr Gly Ala Lys
            100                 105


<210> 1809
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(571)
<223> RXA00554

<400> 1809
atccgaaact ctcctgtacc gaccatcatt tatcccggtc tttaggctct ccaacagcag 60

aggactagac ttaagtatgc ctgcaaagga ggacaacttc atg aac acc caa cca   115
                                           Met Asn Thr Gln Pro
                                             1               5

gag cat cca gaa aat gat cta gtc gac gaa gcc gat ttt tct aac cgg   163
Glu His Pro Glu Asn Asp Leu Val Asp Glu Ala Asp Phe Ser Asn Arg
                10                  15                  20

ccc agg atc tac tcg gac gat cct gat tcc ttg gct gat gcg cca gac   211
Pro Arg Ile Tyr Ser Asp Asp Pro Asp Ser Leu Ala Asp Ala Pro Asp
            25                  30                  35

cca gcg ctg gag cat gag aag aac aag aaa tct tca cgc caa gca ctc   259
Pro Ala Leu Glu His Glu Lys Asn Lys Lys Ser Ser Arg Gln Ala Leu
        40                  45                  50

att tat ctg ttg cag gtt cca cta gtt aca ttc gtt tct gca tac gta   307
Ile Tyr Leu Leu Gln Val Pro Leu Val Thr Phe Val Ser Ala Tyr Val
    55                  60                  65

ttg gcc tgg gtg tca cga ctc cag ggc ggt ccc atc tgt gac gcc ggt   355
Leu Ala Trp Val Ser Arg Leu Gln Gly Gly Pro Ile Cys Asp Ala Gly
70                  75                  80                  85

gag gct gtg tgg att tgt tcc cgt gct gca gaa ctg tgg tgg cca att   403
Glu Ala Val Trp Ile Cys Ser Arg Ala Ala Glu Leu Trp Trp Pro Ile
                90                  95                  100

acc act agc gtc atc gca ttt ggt ggc atg ctt gga tct gca tgg atc   451
Thr Thr Ser Val Ile Ala Phe Gly Gly Met Leu Gly Ser Ala Trp Ile
            105                 110                 115

ctc tat gac aaa tac cga aat tac cta cgc tgg cgt cct tgg atg ggc   499
```

```
Leu Tyr Asp Lys Tyr Arg Asn Tyr Leu Arg Trp Arg Pro Trp Met Gly
        120                 125                 130

gtg ttg tgg att ttg att cca ttc agc atg ctg tgg gga acc tcg gtg   547
Val Leu Trp Ile Leu Ile Pro Phe Ser Met Leu Trp Gly Thr Ser Val
    135                 140                 145

ctc acc ttg tcc atc ttg ggg cac taaaaacttc acataaatga caa         594
Leu Thr Leu Ser Ile Leu Gly His
150                 155


<210> 1810
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 1810
Met Asn Thr Gln Pro Glu His Pro Glu Asn Asp Leu Val Asp Glu Ala
  1               5                  10                  15

Asp Phe Ser Asn Arg Pro Arg Ile Tyr Ser Asp Asp Pro Asp Ser Leu
             20                  25                  30

Ala Asp Ala Pro Asp Pro Ala Leu Glu His Glu Lys Asn Lys Lys Ser
         35                  40                  45

Ser Arg Gln Ala Leu Ile Tyr Leu Leu Gln Val Pro Leu Val Thr Phe
     50                  55                  60

Val Ser Ala Tyr Val Leu Ala Trp Val Ser Arg Leu Gln Gly Gly Pro
 65                  70                  75                  80

Ile Cys Asp Ala Gly Glu Ala Val Trp Ile Cys Ser Arg Ala Ala Glu
                 85                  90                  95

Leu Trp Trp Pro Ile Thr Thr Ser Val Ile Ala Phe Gly Gly Met Leu
            100                 105                 110

Gly Ser Ala Trp Ile Leu Tyr Asp Lys Tyr Arg Asn Tyr Leu Arg Trp
        115                 120                 125

Arg Pro Trp Met Gly Val Leu Trp Ile Leu Ile Pro Phe Ser Met Leu
    130                 135                 140

Trp Gly Thr Ser Val Leu Thr Leu Ser Ile Leu Gly His
145                 150                 155


<210> 1811
<211> 2762
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(2739)
<223> RXA00563

<400> 1811
ttc tac aag gat ctc tac gca cgt tcc gca cgc ggc acg gca gca ctg   48
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Phe Tyr Lys Asp Leu Tyr Ala Arg Ser Ala Arg Gly Thr Ala Ala Leu
  1               5                  10                  15

tgg atc gtg gcg gct aac ttg agc tcc tac tca gac atc gac gcc atc   96
Trp Ile Val Ala Ala Asn Leu Ser Ser Tyr Ser Asp Ile Asp Ala Ile
            20                  25                  30

atc aac tgg gtc gga tcc gag cag acc acc acc gtc aac ggc gca tcc   144
Ile Asn Trp Val Gly Ser Glu Gln Thr Thr Thr Val Asn Gly Ala Ser
        35                  40                  45

aag ctg gtc aag cca gct ttg gtc cct acc ttg ctg ttc cca ttc gcg   192
Lys Leu Val Lys Pro Ala Leu Val Pro Thr Leu Leu Phe Pro Phe Ala
    50                  55                  60

gca cct cgc gtg tcc gga tcc atg gca gat gca ggc cca cag gca gaa   240
Ala Pro Arg Val Ser Gly Ser Met Ala Asp Ala Gly Pro Gln Ala Glu
65                  70                  75                  80

tcc cag atg cga ctt ctg ctc tgg tct gtt gag cgc ctc atc gca ggt   288
Ser Gln Met Arg Leu Leu Leu Trp Ser Val Glu Arg Leu Ile Ala Gly
                85                  90                  95

ctt gcg cca ttg ggc tcc tcc atc aac gtg ggt cac cgc ctg cac gtg   336
Leu Ala Pro Leu Gly Ser Ser Ile Asn Val Gly His Arg Leu His Val
            100                 105                 110

gtc atc cca ggt tca cca aac cgt gga cgc ttc ggt ggc gat ggt gca   384
Val Ile Pro Gly Ser Pro Asn Arg Gly Arg Phe Gly Gly Asp Gly Ala
        115                 120                 125

tac ggt gaa tcc aag gca gct ctc gac gcc gtg gtt acc cgt tgg aac   432
Tyr Gly Glu Ser Lys Ala Ala Leu Asp Ala Val Val Thr Arg Trp Asn
    130                 135                 140

gca gag caa gct gca tgg gga gca cac acc tcc ctc gtg cac gct cac   480
Ala Glu Gln Ala Ala Trp Gly Ala His Thr Ser Leu Val His Ala His
145                 150                 155                 160

atc ggt tgg gtt cgc ggc acc ggc ctc atg ggc ggc aac gat cct ttg   528
Ile Gly Trp Val Arg Gly Thr Gly Leu Met Gly Gly Asn Asp Pro Leu
                165                 170                 175

gtc aag gca gct gaa gaa gca ggc gtg gaa acc tac tcc acc caa gaa   576
Val Lys Ala Ala Glu Glu Ala Gly Val Glu Thr Tyr Ser Thr Gln Glu
            180                 185                 190

att gca gag aaa ctg ctg tcc cag gca act tcc act gtt cgc gag cag   624
Ile Ala Glu Lys Leu Leu Ser Gln Ala Thr Ser Thr Val Arg Glu Gln
        195                 200                 205

gca gca tcc gcg cca atc acc gtc gac ttc act ggc gga ctt ggt gaa   672
Ala Ala Ser Ala Pro Ile Thr Val Asp Phe Thr Gly Gly Leu Gly Glu
    210                 215                 220

tct gat ctg aac ctg gcg gaa atg gca cgt gca gaa gca gct aag gca   720
Ser Asp Leu Asn Leu Ala Glu Met Ala Arg Ala Glu Ala Ala Lys Ala
225                 230                 235                 240

gct aac gca cca gtg gtt gag gct cca cgc aca gtg gca gca ctg cca   768
Ala Asn Ala Pro Val Val Glu Ala Pro Arg Thr Val Ala Ala Leu Pro
```

```
                245                 250                 255

act cct tac cga cca gtg gtt caa acc acc cct gat ttc gca ggt caa   816
Thr Pro Tyr Arg Pro Val Val Gln Thr Thr Pro Asp Phe Ala Gly Gln
            260                 265                 270

gtc acc caa aac ctt gac gag atg gtc gtc atc gtt ggc gcc ggc gag   864
Val Thr Gln Asn Leu Asp Glu Met Val Val Ile Val Gly Ala Gly Glu
        275                 280                 285

ctc ggc cca ctg ggt tct gca cgt acg cgt ttc gac gcc gaa ctc aac   912
Leu Gly Pro Leu Gly Ser Ala Arg Thr Arg Phe Asp Ala Glu Leu Asn
    290                 295                 300

ggt tcc ctc tcc gcc gcg ggt gtc atc gaa ctt gca tgg acg atg gga   960
Gly Ser Leu Ser Ala Ala Gly Val Ile Glu Leu Ala Trp Thr Met Gly
305                 310                 315                 320

ctt atc cac tgg gat gaa gat cca aag cca ggc tgg tac gac gac tcc  1008
Leu Ile His Trp Asp Glu Asp Pro Lys Pro Gly Trp Tyr Asp Asp Ser
                325                 330                 335

gac gac gca gtg gcc gaa gaa gac atc ttc gac cgc tac cac gac gaa  1056
Asp Asp Ala Val Ala Glu Glu Asp Ile Phe Asp Arg Tyr His Asp Glu
            340                 345                 350

gtc atg gca cgc gtt ggt gtc cgc aag tac aat gac atg cct gag tac  1104
Val Met Ala Arg Val Gly Val Arg Lys Tyr Asn Asp Met Pro Glu Tyr
        355                 360                 365

ggc atg atc gac aac ttt gca cca gag ctg acc acc gtc tac ctc gac  1152
Gly Met Ile Asp Asn Phe Ala Pro Glu Leu Thr Thr Val Tyr Leu Asp
    370                 375                 380

cag gac ctc acc ttc aac gtg gga tcc cgc gaa gag gca ctg acc tac  1200
Gln Asp Leu Thr Phe Asn Val Gly Ser Arg Glu Glu Ala Leu Thr Tyr
385                 390                 395                 400

gtc gac tcc gag cca gaa ctc acc ttt gct tct ttc gac gaa gca gca  1248
Val Asp Ser Glu Pro Glu Leu Thr Phe Ala Ser Phe Asp Glu Ala Ala
                405                 410                 415

ggg gag tgg aag gtc act cgc aag gca ggc tcc gca atc cgc gta cct  1296
Gly Glu Trp Lys Val Thr Arg Lys Ala Gly Ser Ala Ile Arg Val Pro
            420                 425                 430

cgc cgc atg gcg atg acc cgc ttc gtt ggt gga cag gtt cct aag gac  1344
Arg Arg Met Ala Met Thr Arg Phe Val Gly Gly Gln Val Pro Lys Asp
        435                 440                 445

ttc gac cca gct gtg tgg ggc att cca gct gac atg gtg gac aac ctg  1392
Phe Asp Pro Ala Val Trp Gly Ile Pro Ala Asp Met Val Asp Asn Leu
    450                 455                 460

gac acc gtc gcg ctg tgg aac att gtc tgt act gtc gac gcc ttc ctg  1440
Asp Thr Val Ala Leu Trp Asn Ile Val Cys Thr Val Asp Ala Phe Leu
465                 470                 475                 480

tcc gct gga ttc acc cca gca gag ctg ctt gct tcc gtt cac cca gca  1488
Ser Ala Gly Phe Thr Pro Ala Glu Leu Leu Ala Ser Val His Pro Ala
                485                 490                 495
```

```
cgc gtg tcc tct acc caa ggc acc ggc atg ggc ggc atg gaa tcc ctc   1536
Arg Val Ser Ser Thr Gln Gly Thr Gly Met Gly Gly Met Glu Ser Leu
            500                 505                 510

cgt ggc atc tac gtc gac cgc att ctg gca gag cca cgc gcc aac gac   1584
Arg Gly Ile Tyr Val Asp Arg Ile Leu Ala Glu Pro Arg Ala Asn Asp
        515                 520                 525

gtt ctg cag gaa gca ctg ccc aac gtt gtt gca gct cac gtc atg cag   1632
Val Leu Gln Glu Ala Leu Pro Asn Val Val Ala Ala His Val Met Gln
    530                 535                 540

tcc tac gtc ggt ggc tac gga cag atg atc cac cca gtc gca gct tgt   1680
Ser Tyr Val Gly Gly Tyr Gly Gln Met Ile His Pro Val Ala Ala Cys
545                 550                 555                 560

gca acc gca gct gtt tct gtg gaa gaa gca ctg gac aag atc cgc atc   1728
Ala Thr Ala Ala Val Ser Val Glu Glu Ala Leu Asp Lys Ile Arg Ile
                565                 570                 575

ggc aag tcc gac ttc gtt gtc gca ggt ggc ttc gat gcc ctg tcc gtt   1776
Gly Lys Ser Asp Phe Val Val Ala Gly Gly Phe Asp Ala Leu Ser Val
            580                 585                 590

gaa ggc atc acc ggc ttc ggc gac atg gca gca acc gcc gac tcc gca   1824
Glu Gly Ile Thr Gly Phe Gly Asp Met Ala Ala Thr Ala Asp Ser Ala
        595                 600                 605

gag atg gaa ggc aag gga att gag cac cgc ttc ttc tcc cgc gcc aac   1872
Glu Met Glu Gly Lys Gly Ile Glu His Arg Phe Phe Ser Arg Ala Asn
    610                 615                 620

gac cgg cgc cgc ggt gga ttc atc gaa tcc gaa ggt ggc gga acc gtc   1920
Asp Arg Arg Arg Gly Gly Phe Ile Glu Ser Glu Gly Gly Gly Thr Val
625                 630                 635                 640

ctt ctg gca cgc gga tca ctc gca gct gac ctg ggc ctt cca gta ctc   1968
Leu Leu Ala Arg Gly Ser Leu Ala Ala Asp Leu Gly Leu Pro Val Leu
                645                 650                 655

ggt gtc atc gga ttc gca gag tcc ttt gca gat ggt gcc cac acc tcc   2016
Gly Val Ile Gly Phe Ala Glu Ser Phe Ala Asp Gly Ala His Thr Ser
            660                 665                 670

atc cca gcc cca ggc ctc ggt gcc ctt ggt gct gct cgc gat ggt gtg   2064
Ile Pro Ala Pro Gly Leu Gly Ala Leu Gly Ala Ala Arg Asp Gly Val
        675                 680                 685

gaa tct cgc ctt gca gta gca ctg cgt tcc gtc ggt gtc tct gct gat   2112
Glu Ser Arg Leu Ala Val Ala Leu Arg Ser Val Gly Val Ser Ala Asp
    690                 695                 700

gag atc tcc att atc tcc aag cac gac acc tcc acc aac gcg aat gat   2160
Glu Ile Ser Ile Ile Ser Lys His Asp Thr Ser Thr Asn Ala Asn Asp
705                 710                 715                 720

cca aac gag tcc gac ctg cac gag cgc atc gca tcc gct atc ggt cgt   2208
Pro Asn Glu Ser Asp Leu His Glu Arg Ile Ala Ser Ala Ile Gly Arg
                725                 730                 735
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gca gac ggc aac ccg atg tac gtg att tcc cag aag tca ctc acc gga   2256
Ala Asp Gly Asn Pro Met Tyr Val Ile Ser Gln Lys Ser Leu Thr Gly
            740                 745                 750

cac gcc aag ggt ggt gca gca gca ttc cag atg atc ggt ctc acc cag   2304
His Ala Lys Gly Gly Ala Ala Ala Phe Gln Met Ile Gly Leu Thr Gln
        755                 760                 765

gtc ctc cga tcc gga ctg gtg cca gcc aac cgc gca ctc gac tgc gtt   2352
Val Leu Arg Ser Gly Leu Val Pro Ala Asn Arg Ala Leu Asp Cys Val
    770                 775                 780

gac cca gta ctg tcc aag cat tcc cac ctc gtc tgg ctg cgc aag cca   2400
Asp Pro Val Leu Ser Lys His Ser His Leu Val Trp Leu Arg Lys Pro
785                 790                 795                 800

cta gac ctt cgt gcg aag gca cca aag gca ggt ctt gtt acc tcc ctt   2448
Leu Asp Leu Arg Ala Lys Ala Pro Lys Ala Gly Leu Val Thr Ser Leu
                805                 810                 815

ggc ttc gga cac gtc tcc gct ctg gtt gcg att gtt cac cca gac gcc   2496
Gly Phe Gly His Val Ser Ala Leu Val Ala Ile Val His Pro Asp Ala
            820                 825                 830

ttc tat gag gca gtt cgt gtg gca cgt ggt gct gag gca gct gac gta   2544
Phe Tyr Glu Ala Val Arg Val Ala Arg Gly Ala Glu Ala Ala Asp Val
        835                 840                 845

tgg cgc gca tcc gcg atc gct cgc gaa gaa gca ggc ctt cgt acc atc   2592
Trp Arg Ala Ser Ala Ile Ala Arg Glu Glu Ala Gly Leu Arg Thr Ile
    850                 855                 860

gtc gcc ggt atg cac ggt ggc gta ctg tac gaa cgc cca gtc gag cgc   2640
Val Ala Gly Met His Gly Gly Val Leu Tyr Glu Arg Pro Val Glu Arg
865                 870                 875                 880

aac ctc ggt gtc cac gga gac gca gct aag gaa gtt gaa gct gca gtc   2688
Asn Leu Gly Val His Gly Asp Ala Ala Lys Glu Val Glu Ala Ala Val
                885                 890                 895

ctc ctg gat tcc cgc gcc cgc cta gtt gac ggt gtc ctc cgc gcc gaa   2736
Leu Leu Asp Ser Arg Ala Arg Leu Val Asp Gly Val Leu Arg Ala Glu
            900                 905                 910

ggc tagttggtta ttgcgttgag ccc                                    2762
Gly
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<210> 1812
<211> 913
<212> PRT
<213> Corynebacterium glutamicum

<400> 1812

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Phe Tyr Lys Asp Leu Tyr Ala Arg Ser Ala Arg Gly Thr Ala Ala Leu
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Trp Ile Val Ala Ala Asn Leu Ser Ser Tyr Ser Asp Ile Asp Ala Ile
             20                  25                  30
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Ile Asn Trp Val Gly Ser Glu Gln Thr Thr Thr Val Asn Gly Ala Ser
         35                  40                  45

Lys Leu Val Lys Pro Ala Leu Val Pro Thr Leu Leu Phe Pro Phe Ala
     50                  55                  60

Ala Pro Arg Val Ser Gly Ser Met Ala Asp Ala Gly Pro Gln Ala Glu
 65                  70                  75                  80

Ser Gln Met Arg Leu Leu Leu Trp Ser Val Glu Arg Leu Ile Ala Gly
                 85                  90                  95

Leu Ala Pro Leu Gly Ser Ser Ile Asn Val Gly His Arg Leu His Val
            100                 105                 110

Val Ile Pro Gly Ser Pro Asn Arg Gly Arg Phe Gly Gly Asp Gly Ala
        115                 120                 125

Tyr Gly Glu Ser Lys Ala Ala Leu Asp Ala Val Val Thr Arg Trp Asn
    130                 135                 140

Ala Glu Gln Ala Ala Trp Gly Ala His Thr Ser Leu Val His Ala His
145                 150                 155                 160

Ile Gly Trp Val Arg Gly Thr Gly Leu Met Gly Gly Asn Asp Pro Leu
                165                 170                 175

Val Lys Ala Ala Glu Glu Ala Gly Val Glu Thr Tyr Ser Thr Gln Glu
            180                 185                 190

Ile Ala Glu Lys Leu Leu Ser Gln Ala Thr Ser Thr Val Arg Glu Gln
        195                 200                 205

Ala Ala Ser Ala Pro Ile Thr Val Asp Phe Thr Gly Gly Leu Gly Glu
    210                 215                 220

Ser Asp Leu Asn Leu Ala Glu Met Ala Arg Ala Glu Ala Ala Lys Ala
225                 230                 235                 240

Ala Asn Ala Pro Val Val Glu Ala Pro Arg Thr Val Ala Ala Leu Pro
                245                 250                 255

Thr Pro Tyr Arg Pro Val Val Gln Thr Thr Pro Asp Phe Ala Gly Gln
            260                 265                 270

Val Thr Gln Asn Leu Asp Glu Met Val Val Ile Val Gly Ala Gly Glu
        275                 280                 285

Leu Gly Pro Leu Gly Ser Ala Arg Thr Arg Phe Asp Ala Glu Leu Asn
    290                 295                 300

Gly Ser Leu Ser Ala Ala Gly Val Ile Glu Leu Ala Trp Thr Met Gly
305                 310                 315                 320

Leu Ile His Trp Asp Glu Asp Pro Lys Pro Gly Trp Tyr Asp Asp Ser
                325                 330                 335

Asp Asp Ala Val Ala Glu Glu Asp Ile Phe Asp Arg Tyr His Asp Glu
            340                 345                 350

Val Met Ala Arg Val Gly Val Arg Lys Tyr Asn Asp Met Pro Glu Tyr
```

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        355                 360                 365

Gly Met Ile Asp Asn Phe Ala Pro Glu Leu Thr Thr Val Tyr Leu Asp
    370                 375                 380

Gln Asp Leu Thr Phe Asn Val Gly Ser Arg Glu Glu Ala Leu Thr Tyr
385                 390                 395                 400

Val Asp Ser Glu Pro Glu Leu Thr Phe Ala Ser Phe Asp Glu Ala Ala
                405                 410                 415

Gly Glu Trp Lys Val Thr Arg Lys Ala Gly Ser Ala Ile Arg Val Pro
            420                 425                 430

Arg Arg Met Ala Met Thr Arg Phe Val Gly Gly Gln Val Pro Lys Asp
        435                 440                 445

Phe Asp Pro Ala Val Trp Gly Ile Pro Ala Asp Met Val Asp Asn Leu
    450                 455                 460

Asp Thr Val Ala Leu Trp Asn Ile Val Cys Thr Val Asp Ala Phe Leu
465                 470                 475                 480

Ser Ala Gly Phe Thr Pro Ala Glu Leu Leu Ala Ser Val His Pro Ala
                485                 490                 495

Arg Val Ser Ser Thr Gln Gly Thr Gly Met Gly Gly Met Glu Ser Leu
            500                 505                 510

Arg Gly Ile Tyr Val Asp Arg Ile Leu Ala Glu Pro Arg Ala Asn Asp
        515                 520                 525

Val Leu Gln Glu Ala Leu Pro Asn Val Val Ala Ala His Val Met Gln
    530                 535                 540

Ser Tyr Val Gly Gly Tyr Gly Gln Met Ile His Pro Val Ala Ala Cys
545                 550                 555                 560

Ala Thr Ala Ala Val Ser Val Glu Glu Ala Leu Asp Lys Ile Arg Ile
                565                 570                 575

Gly Lys Ser Asp Phe Val Val Ala Gly Gly Phe Asp Ala Leu Ser Val
            580                 585                 590

Glu Gly Ile Thr Gly Phe Gly Asp Met Ala Ala Thr Ala Asp Ser Ala
        595                 600                 605

Glu Met Glu Gly Lys Gly Ile Glu His Arg Phe Phe Ser Arg Ala Asn
    610                 615                 620

Asp Arg Arg Arg Gly Gly Phe Ile Glu Ser Glu Gly Gly Gly Thr Val
625                 630                 635                 640

Leu Leu Ala Arg Gly Ser Leu Ala Ala Asp Leu Gly Leu Pro Val Leu
                645                 650                 655

Gly Val Ile Gly Phe Ala Glu Ser Phe Ala Asp Gly Ala His Thr Ser
            660                 665                 670

Ile Pro Ala Pro Gly Leu Gly Ala Leu Gly Ala Ala Arg Asp Gly Val
        675                 680                 685
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Glu Ser Arg Leu Ala Val Ala Leu Arg Ser Val Gly Val Ser Ala Asp
    690                 695                 700

Glu Ile Ser Ile Ile Ser Lys His Asp Thr Ser Thr Asn Ala Asn Asp
705                 710                 715                 720

Pro Asn Glu Ser Asp Leu His Glu Arg Ile Ala Ser Ala Ile Gly Arg
                725                 730                 735

Ala Asp Gly Asn Pro Met Tyr Val Ile Ser Gln Lys Ser Leu Thr Gly
            740                 745                 750

His Ala Lys Gly Gly Ala Ala Ala Phe Gln Met Ile Gly Leu Thr Gln
        755                 760                 765

Val Leu Arg Ser Gly Leu Val Pro Ala Asn Arg Ala Leu Asp Cys Val
    770                 775                 780

Asp Pro Val Leu Ser Lys His Ser His Leu Val Trp Leu Arg Lys Pro
785                 790                 795                 800

Leu Asp Leu Arg Ala Lys Ala Pro Lys Ala Gly Leu Val Thr Ser Leu
                805                 810                 815

Gly Phe Gly His Val Ser Ala Leu Val Ala Ile Val His Pro Asp Ala
            820                 825                 830

Phe Tyr Glu Ala Val Arg Val Ala Arg Gly Ala Glu Ala Ala Asp Val
        835                 840                 845

Trp Arg Ala Ser Ala Ile Ala Arg Glu Glu Ala Gly Leu Arg Thr Ile
    850                 855                 860

Val Ala Gly Met His Gly Gly Val Leu Tyr Glu Arg Pro Val Glu Arg
865                 870                 875                 880

Asn Leu Gly Val His Gly Asp Ala Ala Lys Glu Val Glu Ala Ala Val
                885                 890                 895

Leu Leu Asp Ser Arg Ala Arg Leu Val Asp Gly Val Leu Arg Ala Glu
            900                 905                 910

Gly
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<210> 1813
<211> 528
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(505)
<223> RXA00564

<400> 1813
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aaaaacggat ggaaccagta ttgggaaaag gatggttgcg atg aaa tac aac gtc 115

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                                                    Met Lys Tyr Asn Val
                                                      1               5

gat gtc tct cgt gaa agc gag gac tgg ctc gcc acc gtc acc aat ctc   163
Asp Val Ser Arg Glu Ser Glu Asp Trp Leu Ala Thr Val Thr Asn Leu
                 10                  15                  20

gaa ggc gta tcc acg tgg gcg aca acc ttc gcc aac ctt gat cgc aac   211
Glu Gly Val Ser Thr Trp Ala Thr Thr Phe Ala Asn Leu Asp Arg Asn
             25                  30                  35

ggc cgg gaa gcc att gct cta gct gaa gat ctc ccc gaa ggt gcg gaa   259
Gly Arg Glu Ala Ile Ala Leu Ala Glu Asp Leu Pro Glu Gly Ala Glu
         40                  45                  50

agc tca ctg acc atc tct tgg tcg gtt cct aca gat tcc cac ccc gaa   307
Ser Ser Leu Thr Ile Ser Trp Ser Val Pro Thr Asp Ser His Pro Glu
     55                  60                  65

ctg gac act gca att caa att gct caa cag cgt cgc tat cta gtg caa   355
Leu Asp Thr Ala Ile Gln Ile Ala Gln Gln Arg Arg Tyr Leu Val Gln
 70                  75                  80                  85

gcc caa caa gac tta gag ccc aaa gtt cga tcc gct att tcc gct ctc   403
Ala Gln Gln Asp Leu Glu Pro Lys Val Arg Ser Ala Ile Ser Ala Leu
                 90                  95                 100

acc caa gct gcg ctg cta ggt atg act gca ggt cga gta tcc cca act   451
Thr Gln Ala Ala Leu Leu Gly Met Thr Ala Gly Arg Val Ser Pro Thr
             105                 110                 115

cac aac ccg ggt agc aga gct atc tca ttg gat cag gtg tca gga gtt   499
His Asn Pro Gly Ser Arg Ala Ile Ser Leu Asp Gln Val Ser Gly Val
         120                 125                 130

tta aac tagcgtgcgc aattcccgtg tga                                 528
Leu Asn
    135
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<210> 1814
<211> 135
<212> PRT
<213> Corynebacterium glutamicum

<400> 1814

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Met Lys Tyr Asn Val Asp Val Ser Arg Glu Ser Glu Asp Trp Leu Ala
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Thr Val Thr Asn Leu Glu Gly Val Ser Thr Trp Ala Thr Thr Phe Ala
             20                  25                  30

Asn Leu Asp Arg Asn Gly Arg Glu Ala Ile Ala Leu Ala Glu Asp Leu
         35                  40                  45

Pro Glu Gly Ala Glu Ser Ser Leu Thr Ile Ser Trp Ser Val Pro Thr
     50                  55                  60

Asp Ser His Pro Glu Leu Asp Thr Ala Ile Gln Ile Ala Gln Gln Arg
 65                  70                  75                  80
```

```
Arg Tyr Leu Val Gln Ala Gln Gln Asp Leu Glu Pro Lys Val Arg Ser
                85                  90                  95

Ala Ile Ser Ala Leu Thr Gln Ala Ala Leu Leu Gly Met Thr Ala Gly
            100                 105                 110

Arg Val Ser Pro Thr His Asn Pro Gly Ser Arg Ala Ile Ser Leu Asp
        115                 120                 125

Gln Val Ser Gly Val Leu Asn
    130                 135


<210> 1815
<211> 774
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(751)
<223> RXA00573

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atcgtgacca cccttgcagc tcatgaggtt caggtttccc atg ctc gtt agg cca   115
                                            Met Leu Val Arg Pro
                                              1               5

tgt ggt gag caa gca gtc atc atc gat ttg ctt gct gaa gat gcc gaa   163
Cys Gly Glu Gln Ala Val Ile Ile Asp Leu Leu Ala Glu Asp Ala Glu
                10                  15                  20

gcc gtc caa ggc agc atc ttg gat gct gtt ctt gca ctc aac cgc tct   211
Ala Val Gln Gly Ser Ile Leu Asp Ala Val Leu Ala Leu Asn Arg Ser
            25                  30                  35

ttg gtg ggc atg cag gtc cct gga atc atc gat act att ccc gct gcg   259
Leu Val Gly Met Gln Val Pro Gly Ile Ile Asp Thr Ile Pro Ala Ala
        40                  45                  50

caa aca ctg tta gtg acg ttt gac acc aag cag atc acc ccg aat cgt   307
Gln Thr Leu Leu Val Thr Phe Asp Thr Lys Gln Ile Thr Pro Asn Arg
    55                  60                  65

ttc gca gag atc gtt gat tca att gcg ctg acc cca gcc gca aag ggc   355
Phe Ala Glu Ile Val Asp Ser Ile Ala Leu Thr Pro Ala Ala Lys Gly
70                  75                  80                  85

gca gca gag ctt acc gac acc att gag att ccc gtg gtc tac gac ggc   403
Ala Ala Glu Leu Thr Asp Thr Ile Glu Ile Pro Val Val Tyr Asp Gly
                90                  95                 100

cct gat cta gaa acc gta gct caa cac aca ggt ctg agc gtg gag gaa   451
Pro Asp Leu Glu Thr Val Ala Gln His Thr Gly Leu Ser Val Glu Glu
            105                 110                 115

gtt atc gcc acg cat tct ggc acc gtg tgg act gct gct ttc ggt gga   499
Val Ile Ala Thr His Ser Gly Thr Val Trp Thr Ala Ala Phe Gly Gly
        120                 125                 130
```

```
ttt gca cca ggt ttt tac tat ctg atc ccc cag act ccc ctg tgg gat   547
Phe Ala Pro Gly Phe Tyr Tyr Leu Ile Pro Gln Thr Pro Leu Trp Asp
    135                 140                 145

att ccc cgc ttg gaa tcg cca cgc acc aag att cct gca ggt tct gtc   595
Ile Pro Arg Leu Glu Ser Pro Arg Thr Lys Ile Pro Ala Gly Ser Val
150                 155                 160                 165

gca gtg gcc ggt gaa ttc agc gct gtg tac ccg cag cag tcc cct ggt   643
Ala Val Ala Gly Glu Phe Ser Ala Val Tyr Pro Gln Gln Ser Pro Gly
                170                 175                 180

ggt tgg caa ctg ctg ggc act act gag att ccc atg tgg gat gtg gac   691
Gly Trp Gln Leu Leu Gly Thr Thr Glu Ile Pro Met Trp Asp Val Asp
            185                 190                 195

cgg tgg caa cca tcg ctt ctc aag ccc ggt gat tca gtt cga ttt gtg   739
Arg Trp Gln Pro Ser Leu Leu Lys Pro Gly Asp Ser Val Arg Phe Val
        200                 205                 210

cag gtg aag aaa tgagcttcaa agtaatttcc act                         774
Gln Val Lys Lys
    215
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<210> 1816
<211> 217
<212> PRT
<213> Corynebacterium glutamicum

<400> 1816

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Met Leu Val Arg Pro Cys Gly Glu Gln Ala Val Ile Ile Asp Leu Leu
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Ala Glu Asp Ala Glu Ala Val Gln Gly Ser Ile Leu Asp Ala Val Leu
             20                  25                  30

Ala Leu Asn Arg Ser Leu Val Gly Met Gln Val Pro Gly Ile Ile Asp
         35                  40                  45

Thr Ile Pro Ala Ala Gln Thr Leu Leu Val Thr Phe Asp Thr Lys Gln
     50                  55                  60

Ile Thr Pro Asn Arg Phe Ala Glu Ile Val Asp Ser Ile Ala Leu Thr
 65                  70                  75                  80

Pro Ala Ala Lys Gly Ala Ala Glu Leu Thr Asp Thr Ile Glu Ile Pro
                 85                  90                  95

Val Val Tyr Asp Gly Pro Asp Leu Glu Thr Val Ala Gln His Thr Gly
            100                 105                 110

Leu Ser Val Glu Glu Val Ile Ala Thr His Ser Gly Thr Val Trp Thr
        115                 120                 125

Ala Ala Phe Gly Gly Phe Ala Pro Gly Phe Tyr Tyr Leu Ile Pro Gln
    130                 135                 140

Thr Pro Leu Trp Asp Ile Pro Arg Leu Glu Ser Pro Arg Thr Lys Ile
145                 150                 155                 160
```

```
Pro Ala Gly Ser Val Ala Val Ala Gly Glu Phe Ser Ala Val Tyr Pro
               165                 170                 175

Gln Gln Ser Pro Gly Gly Trp Gln Leu Leu Gly Thr Thr Glu Ile Pro
            180                 185                 190

Met Trp Asp Val Asp Arg Trp Gln Pro Ser Leu Leu Lys Pro Gly Asp
        195                 200                 205

Ser Val Arg Phe Val Gln Val Lys Lys
    210                 215


<210> 1817
<211> 795
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(772)
<223> RXA00576

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acagtccgag cttcttagcg gcggtctgtg gcttcatagc cctgcccgat ggctggcgta 60

cagattcttc gttcacgccc acaacggtag cattgttttc atg ctg acc tta agt   115
                                            Met Leu Thr Leu Ser
                                              1               5

ttc atc act ggc acg gag cca gga aag tgg ttt acc cga ttc cga gat   163
Phe Ile Thr Gly Thr Glu Pro Gly Lys Trp Phe Thr Arg Phe Arg Asp
                10                  15                  20

cgg act cat cac ggt gga ctt gag acc ctt gat tcg gac gac gcc cta   211
Arg Thr His His Gly Gly Leu Glu Thr Leu Asp Ser Asp Asp Ala Leu
             25                  30                  35

ggc ctc atg ctc gct ggc cag gca caa ctc gcc tta acc agg ctt cca   259
Gly Leu Met Leu Ala Gly Gln Ala Gln Leu Ala Leu Thr Arg Leu Pro
         40                  45                  50

gat gcg cgt atc gac gcc tcc ctc cac gtg gtc act ctt tat cag gaa   307
Asp Ala Arg Ile Asp Ala Ser Leu His Val Val Thr Leu Tyr Gln Glu
     55                  60                  65

caa ccc gga gtc gct ttt cca aaa gac ttt ttc ctc agt gcc gaa gaa   355
Gln Pro Gly Val Ala Phe Pro Lys Asp Phe Phe Leu Ser Ala Glu Glu
 70                  75                  80                  85

ggc gcg gtg gac ctt gcg gac tta gat ggg gag atc atc aac tgg tcc   403
Gly Ala Val Asp Leu Ala Asp Leu Asp Gly Glu Ile Ile Asn Trp Ser
                90                  95                 100

atg ccc gat agt ggg gaa gtc gat gcc gct gct gtt cgc gat gct ctg   451
Met Pro Asp Ser Gly Glu Val Asp Ala Ala Ala Val Arg Asp Ala Leu
            105                 110                 115

caa atc gtg gca gcg aac gtc ggt gtg gtg atc gcc ccc agg cca ctt   499
Gln Ile Val Ala Ala Asn Val Gly Val Val Ile Ala Pro Arg Pro Leu
```

```
        120                 125                 130

ctc aag gtg ttg agc aag aaa ttg gtg gag cac cgg gac atc aag ggt   547
Leu Lys Val Leu Ser Lys Lys Leu Val Glu His Arg Asp Ile Lys Gly
    135                 140                 145

gga act gaa aca tct atc gcc ctg gta tgg aag aaa gat gag gat tct   595
Gly Thr Glu Thr Ser Ile Ala Leu Val Trp Lys Lys Asp Glu Asp Ser
150                 155                 160                 165

gaa gag att caa gac ttc gtc ggt att gct cgc ggt cga acg cgg aat   643
Glu Glu Ile Gln Asp Phe Val Gly Ile Ala Arg Gly Arg Thr Arg Asn
                170                 175                 180

tcc agc agg cag caa acg gta aag ctc agt gct cgt gaa aaa aca ctg   691
Ser Ser Arg Gln Gln Thr Val Lys Leu Ser Ala Arg Glu Lys Thr Leu
            185                 190                 195

gca aaa caa gcc cgc agg cag ggg gag aaa cca aaa act ccg aag cgt   739
Ala Lys Gln Ala Arg Arg Gln Gly Glu Lys Pro Lys Thr Pro Lys Arg
        200                 205                 210

ccg cag gca aga aaa cgt ccc gga aaa cgg cga taggggtcac ccgcgcatgt 792
Pro Gln Ala Arg Lys Arg Pro Gly Lys Arg Arg
    215                 220

ccg                                                               795


<210> 1818
<211> 224
<212> PRT
<213> Corynebacterium glutamicum

<400> 1818
Met Leu Thr Leu Ser Phe Ile Thr Gly Thr Glu Pro Gly Lys Trp Phe
  1               5                  10                  15

Thr Arg Phe Arg Asp Arg Thr His His Gly Gly Leu Glu Thr Leu Asp
             20                  25                  30

Ser Asp Asp Ala Leu Gly Leu Met Leu Ala Gly Gln Ala Gln Leu Ala
         35                  40                  45

Leu Thr Arg Leu Pro Asp Ala Arg Ile Asp Ala Ser Leu His Val Val
     50                  55                  60

Thr Leu Tyr Gln Glu Gln Pro Gly Val Ala Phe Pro Lys Asp Phe Phe
 65                  70                  75                  80

Leu Ser Ala Glu Glu Gly Ala Val Asp Leu Ala Asp Leu Asp Gly Glu
                 85                  90                  95

Ile Ile Asn Trp Ser Met Pro Asp Ser Gly Glu Val Asp Ala Ala Ala
            100                 105                 110

Val Arg Asp Ala Leu Gln Ile Val Ala Ala Asn Val Gly Val Val Ile
        115                 120                 125

Ala Pro Arg Pro Leu Leu Lys Val Leu Ser Lys Lys Leu Val Glu His
    130                 135                 140
```

```
Arg Asp Ile Lys Gly Gly Thr Glu Thr Ser Ile Ala Leu Val Trp Lys
145                 150                 155                 160

Lys Asp Glu Asp Ser Glu Glu Ile Gln Asp Phe Val Gly Ile Ala Arg
                165                 170                 175

Gly Arg Thr Arg Asn Ser Ser Arg Gln Gln Thr Val Lys Leu Ser Ala
            180                 185                 190

Arg Glu Lys Thr Leu Ala Lys Gln Ala Arg Arg Gln Gly Glu Lys Pro
        195                 200                 205

Lys Thr Pro Lys Arg Pro Gln Ala Arg Lys Arg Pro Gly Lys Arg Arg
    210                 215                 220
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<210> 1819
<211> 471
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(448)
<223> RXA00577

<400> 1819
ctggctccgt gccagtgatg aaacttaagg tcagcatgaa aacaatgcta ccgttgtggg 60

cgtgaacgaa gaatctgtac gccagccatc gggcagggct atg aag cca cag acc 115
                                              Met Lys Pro Gln Thr
                                                1   5

gcc gct aag aag ctc gga ctg ttt ttg ccc gcc acg cca gag gag ttc 163
Ala Ala Lys Lys Leu Gly Leu Phe Leu Pro Ala Thr Pro Glu Glu Phe
                10   15   20

caa aca ggt gca ttg act cac caa gag ttc aag aac ctg cag gaa aac 211
Gln Thr Gly Ala Leu Thr His Gln Glu Phe Lys Asn Leu Gln Glu Asn
            25   30   35

cca ccg gag tgg ctc caa acc cta cgc cgc gag ggc cca cac cct cgt 259
Pro Pro Glu Trp Leu Gln Thr Leu Arg Arg Glu Gly Pro His Pro Arg
        40   45   50

cca gtg gtc gcc caa aaa ttg ggc atc acc atc gcg gct ctg aaa aag 307
Pro Val Val Ala Gln Lys Leu Gly Ile Thr Ile Ala Ala Leu Lys Lys
    55   60   65

aac gac atg gac aaa cca ctg acc acc gcc gag atc aag gca ctt ctg 355
Asn Asp Met Asp Lys Pro Leu Thr Thr Ala Glu Ile Lys Ala Leu Leu
70   75   80   85

gaa aac cag cca gaa tgg ttg cgc acc gca cgc aca cag ctt gct gaa 403
Glu Asn Gln Pro Glu Trp Leu Arg Thr Ala Arg Thr Gln Leu Ala Glu
                90   95   100
```
```

```
ggt cgc gaa acc gca aag aaa gaa act gaa gaa act acc gaa gac       448
Gly Arg Glu Thr Ala Lys Lys Glu Thr Glu Glu Thr Thr Glu Asp
            105                 110                 115

taaatcttca caaagactgc gct                                       471


<210> 1820
<211> 116
<212> PRT
<213> Corynebacterium glutamicum

<400> 1820
Met Lys Pro Gln Thr Ala Ala Lys Lys Leu Gly Leu Phe Leu Pro Ala
  1               5                  10                  15

Thr Pro Glu Glu Phe Gln Thr Gly Ala Leu Thr His Gln Glu Phe Lys
             20                  25                  30

Asn Leu Gln Glu Asn Pro Pro Glu Trp Leu Gln Thr Leu Arg Arg Glu
         35                  40                  45

Gly Pro His Pro Arg Pro Val Val Ala Gln Lys Leu Gly Ile Thr Ile
     50                  55                  60

Ala Ala Leu Lys Lys Asn Asp Met Asp Lys Pro Leu Thr Thr Ala Glu
 65                  70                  75                  80

Ile Lys Ala Leu Leu Glu Asn Gln Pro Glu Trp Leu Arg Thr Ala Arg
                 85                  90                  95

Thr Gln Leu Ala Glu Gly Arg Glu Thr Ala Lys Lys Glu Thr Glu Glu
            100                 105                 110

Thr Thr Glu Asp
        115


<210> 1821
<211> 846
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(823)
<223> RXA00578

<400> 1821
tgggcggtgc acttcttgct ctgtctgatc cggaggctga gtgggaggaa atccgcgtta 60

aatcacggcc tctgctgaat ttgtttgggg ttgaattccc atg acg tac ctc gtg   115
                                              Met Thr Tyr Leu Val
                                                1               5

tgg gac ggt gca aca ctc gta gaa ggc gcg ctg gaa tca aca ccc aca   163
Trp Asp Gly Ala Thr Leu Val Glu Gly Ala Leu Glu Ser Thr Pro Thr
                10                  15                  20

gtt gtt gat tcc tac cta gcc aaa gac cac cgc gtg gtg cgc tgg gat   211
Val Val Asp Ser Tyr Leu Ala Lys Asp His Arg Val Val Arg Trp Asp
```

```
            25                  30                  35

ctt cat gaa cag cgc ttc gcc act agc gtg gac gtg gac ccg tgg gat   259
Leu His Glu Gln Arg Phe Ala Thr Ser Val Asp Val Asp Pro Trp Asp
         40                  45                  50

ttt ctc cac gca gta agg gaa gca att cca cgc cag ggc tca tgg ttt   307
Phe Leu His Ala Val Arg Glu Ala Ile Pro Arg Gln Gly Ser Trp Phe
     55                  60                  65

ccc aaa gtt gaa tgg cat ggc gat gat ctt ttc gca gtc aat att cgc   355
Pro Lys Val Glu Trp His Gly Asp Asp Leu Phe Ala Val Asn Ile Arg
 70                  75                  80                  85

ccg gca cca aca ctg cga aag gcc aca tca ttg tgg ctt tcc gaa gac   403
Pro Ala Pro Thr Leu Arg Lys Ala Thr Ser Leu Trp Leu Ser Glu Asp
                 90                  95                 100

cca gat cca cgc aca cag cca acc att aaa ggc cca gac cta gat gtg   451
Pro Asp Pro Arg Thr Gln Pro Thr Ile Lys Gly Pro Asp Leu Asp Val
            105                 110                 115

ctt gct cac ctt cgc agt cgc gcc aac gat aac ggc tgc gat gat gcg   499
Leu Ala His Leu Arg Ser Arg Ala Asn Asp Asn Gly Cys Asp Asp Ala
        120                 125                 130

ctg ttg atc agc gcg gat ggg ttc att ctg gaa gct gcc aac gcc acc   547
Leu Leu Ile Ser Ala Asp Gly Phe Ile Leu Glu Ala Ala Asn Ala Thr
    135                 140                 145

gtg gtg ttt tgg gcg gat cca cag acg gtc atc gtg ccc agg gga gat   595
Val Val Phe Trp Ala Asp Pro Gln Thr Val Ile Val Pro Arg Gly Asp
150                 155                 160                 165

gtg ctc cca tcg gtg aca ctc gcc gca acc att ccg ctg tgg gaa aaa   643
Val Leu Pro Ser Val Thr Leu Ala Ala Thr Ile Pro Leu Trp Glu Lys
                170                 175                 180

gcc gga atc aca ttg cgc tat caa aac att cgg cac att ggt ttt ccc   691
Ala Gly Ile Thr Leu Arg Tyr Gln Asn Ile Arg His Ile Gly Phe Pro
            185                 190                 195

gcg tgg tgc ggt agt tcg ctg cat ggt tgg aca cct gtg gtc agt tgg   739
Ala Trp Cys Gly Ser Ser Leu His Gly Trp Thr Pro Val Val Ser Trp
        200                 205                 210

ggc agg gga ttg ggc aaa att gca gca gcg aaa gct cca tcg gtg aag   787
Gly Arg Gly Leu Gly Lys Ile Ala Ala Ala Lys Ala Pro Ser Val Lys
    215                 220                 225

ccc tgg aat gaa aaa ttg cgc cca acc att ttt ctg tgaggaaaag       833
Pro Trp Asn Glu Lys Leu Arg Pro Thr Ile Phe Leu
230                 235                 240

gttgagcgca gtc                                                  846
```

<210> 1822
<211> 241
<212> PRT
<213> Corynebacterium glutamicum

<400> 1822
Met Thr Tyr Leu Val Trp Asp Gly Ala Thr Leu Val Glu Gly Ala Leu
1 5 10 15

Glu Ser Thr Pro Thr Val Val Asp Ser Tyr Leu Ala Lys Asp His Arg
20 25 30

Val Val Arg Trp Asp Leu His Glu Gln Arg Phe Ala Thr Ser Val Asp
35 40 45

Val Asp Pro Trp Asp Phe Leu His Ala Val Arg Glu Ala Ile Pro Arg
50 55 60

Gln Gly Ser Trp Phe Pro Lys Val Glu Trp His Gly Asp Asp Leu Phe
65 70 75 80

Ala Val Asn Ile Arg Pro Ala Pro Thr Leu Arg Lys Ala Thr Ser Leu
85 90 95

Trp Leu Ser Glu Asp Pro Asp Pro Arg Thr Gln Pro Thr Ile Lys Gly
100 105 110

Pro Asp Leu Asp Val Leu Ala His Leu Arg Ser Arg Ala Asn Asp Asn
115 120 125

Gly Cys Asp Asp Ala Leu Leu Ile Ser Ala Asp Gly Phe Ile Leu Glu
130 135 140

Ala Ala Asn Ala Thr Val Val Phe Trp Ala Asp Pro Gln Thr Val Ile
145 150 155 160

Val Pro Arg Gly Asp Val Leu Pro Ser Val Thr Leu Ala Ala Thr Ile
165 170 175

Pro Leu Trp Glu Lys Ala Gly Ile Thr Leu Arg Tyr Gln Asn Ile Arg
180 185 190

His Ile Gly Phe Pro Ala Trp Cys Gly Ser Ser Leu His Gly Trp Thr
195 200 205

Pro Val Val Ser Trp Gly Arg Gly Leu Gly Lys Ile Ala Ala Ala Lys
210 215 220

Ala Pro Ser Val Lys Pro Trp Asn Glu Lys Leu Arg Pro Thr Ile Phe
225 230 235 240

Leu

<210> 1823
<211> 642
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(619)
<223> RXA00582

<400> 1823
actggccagc cttccgacgc atcgacttcc tccgcgccat tcgcgactac tcgcagcgca 60

gcagaagatt cggtaaataa cttattctcc aaggagagac atg tct gac tac atc 115
Met Ser Asp Tyr Ile
1 5

gtc gca ttt gaa tcc gca tac ggc tct acc aag cag tac gca gaa tct 163
Val Ala Phe Glu Ser Ala Tyr Gly Ser Thr Lys Gln Tyr Ala Glu Ser
10 15 20

ctg gcg caa cgc ctc ggc gta gat gcc tta aat ttt gaa caa gcg tgt 211
Leu Ala Gln Arg Leu Gly Val Asp Ala Leu Asn Phe Glu Gln Ala Cys
25 30 35

gcg gaa ctc gcg gcg aac ccg acc gca gca atc gtg gtt ttg agc ttt 259
Ala Glu Leu Ala Ala Asn Pro Thr Ala Ala Ile Val Val Leu Ser Phe
40 45 50

gtt cac ggc cca tcc cat cca ggt gcg aaa ttc att acc gat acc gat 307
Val His Gly Pro Ser His Pro Gly Ala Lys Phe Ile Thr Asp Thr Asp
55 60 65

ctc tcc ggc cac cgc gtc gca ctg tgc acc gtc ggc atg acg ctt gat 355
Leu Ser Gly His Arg Val Ala Leu Cys Thr Val Gly Met Thr Leu Asp
70 75 80 85

gat gtc gtg caa aag aag gac ggc gca gct cga tca ctg gga aac aag 403
Asp Val Val Gln Lys Lys Asp Gly Ala Ala Arg Ser Leu Gly Asn Lys
90 95 100

gca gac gat gtc acc cgt ttc tac ctt ccg gga cgc ctt aat tac tca 451
Ala Asp Asp Val Thr Arg Phe Tyr Leu Pro Gly Arg Leu Asn Tyr Ser
105 110 115

gag ctc tcg acc gcg cac cgc acc acc atg tgg acg atc gtc aac atg 499
Glu Leu Ser Thr Ala His Arg Thr Thr Met Trp Thr Ile Val Asn Met
120 125 130

ctg aaa gcg aag ccg ttg aag aat gac aac gac aaa atg atg atc aac 547
Leu Lys Ala Lys Pro Leu Lys Asn Asp Asn Asp Lys Met Met Ile Asn
135 140 145

act ttt gat acc gat gtt gac cgc gtc gat gag tcc cgc ctg gac gca 595
Thr Phe Asp Thr Asp Val Asp Arg Val Asp Glu Ser Arg Leu Asp Ala
150 155 160 165

gtg gag gag tgg gcg agg ggc ctc tagagtgggc gttgcaaaaa ctc 642
Val Glu Glu Trp Ala Arg Gly Leu
170

<210> 1824
<211> 173
<212> PRT
<213> Corynebacterium glutamicum

<400> 1824
Met Ser Asp Tyr Ile Val Ala Phe Glu Ser Ala Tyr Gly Ser Thr Lys
1 5 10 15

Gln Tyr Ala Glu Ser Leu Ala Gln Arg Leu Gly Val Asp Ala Leu Asn
20 25 30

Phe Glu Gln Ala Cys Ala Glu Leu Ala Ala Asn Pro Thr Ala Ala Ile
35 40 45

Val Val Leu Ser Phe Val His Gly Pro Ser His Pro Gly Ala Lys Phe
50 55 60

Ile Thr Asp Thr Asp Leu Ser Gly His Arg Val Ala Leu Cys Thr Val
65 70 75 80

Gly Met Thr Leu Asp Asp Val Val Gln Lys Lys Asp Gly Ala Ala Arg
85 90 95

Ser Leu Gly Asn Lys Ala Asp Asp Val Thr Arg Phe Tyr Leu Pro Gly
100 105 110

Arg Leu Asn Tyr Ser Glu Leu Ser Thr Ala His Arg Thr Thr Met Trp
115 120 125

Thr Ile Val Asn Met Leu Lys Ala Lys Pro Leu Lys Asn Asp Asn Asp
130 135 140

Lys Met Met Ile Asn Thr Phe Asp Thr Asp Val Asp Arg Val Asp Glu
145 150 155 160

Ser Arg Leu Asp Ala Val Glu Glu Trp Ala Arg Gly Leu
165 170

<210> 1825
<211> 441
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(418)
<223> RXA00585

<400> 1825
tgtgaagacg tcgatcccag aagatgacct gtttgccgga atcacacccg atgcagaata 60

atgcagttag accacatcct ttaggaagga ccttttcggc gtg att gac ctc agc 115
Val Ile Asp Leu Ser
1 5

cct gta ttc aat aca gct gcc ggc gta tac aac gac acc aac gca atc 163
Pro Val Phe Asn Thr Ala Ala Gly Val Tyr Asn Asp Thr Asn Ala Ile
10 15 20

atc ttg gct cag cag cag caa ggt gga cca ctt gga cct gag ttt gga 211
Ile Leu Ala Gln Gln Gln Gln Gly Gly Pro Leu Gly Pro Glu Phe Gly
25 30 35

aag gcc tcg ccg gtt ggt ttg cta ctg atc gtc gcg atg ctc gtt gcc 259
Lys Ala Ser Pro Val Gly Leu Leu Leu Ile Val Ala Met Leu Val Ala
40 45 50

att ctt gtt ctc ggc tgg gcg ttc cac cga cgc tgg tca cgg atg aat 307

```
Ile Leu Val Leu Gly Trp Ala Phe His Arg Arg Trp Ser Arg Met Asn
     55                  60                  65

cgt cgt cgt att ttc gca gag cgc aac ggc ctt gat ccc ttc gat att   355
Arg Arg Arg Ile Phe Ala Glu Arg Asn Gly Leu Asp Pro Phe Asp Ile
 70                  75                  80                  85

gag ggt gtt cgc aag gca atg gct gag gcc ggc ttg aat gaa aag tcc   403
Glu Gly Val Arg Lys Ala Met Ala Glu Ala Gly Leu Asn Glu Lys Ser
                 90                  95                 100

aaa aag ggc ttc ctt taaaaagaaa gtgtgttaag gtt                    441
Lys Lys Gly Phe Leu
            105


<210> 1826
<211> 106
<212> PRT
<213> Corynebacterium glutamicum

<400> 1826
Val Ile Asp Leu Ser Pro Val Phe Asn Thr Ala Ala Gly Val Tyr Asn
  1               5                  10                  15

Asp Thr Asn Ala Ile Ile Leu Ala Gln Gln Gln Gln Gly Gly Pro Leu
             20                  25                  30

Gly Pro Glu Phe Gly Lys Ala Ser Pro Val Gly Leu Leu Leu Ile Val
         35                  40                  45

Ala Met Leu Val Ala Ile Leu Val Leu Gly Trp Ala Phe His Arg Arg
     50                  55                  60

Trp Ser Arg Met Asn Arg Arg Arg Ile Phe Ala Glu Arg Asn Gly Leu
 65                  70                  75                  80

Asp Pro Phe Asp Ile Glu Gly Val Arg Lys Ala Met Ala Glu Ala Gly
                 85                  90                  95

Leu Asn Glu Lys Ser Lys Lys Gly Phe Leu
            100                 105


<210> 1827
<211> 1005
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(982)
<223> RXA00586

<400> 1827
tcatccaagg ggtaaatagg tatgacggcg gaaacgacta tcatgaatgc aatacacatc 60

aactaaaccc tgcggaagca tataaagctt caaggaaagg atg aaa cac gtg agt   115
                                               Met Lys His Val Ser
                                                 1               5
```

```
ggt cta cgc cta atg gcg atc cac gcc cac cct gac gac gag tca agc   163
Gly Leu Arg Leu Met Ala Ile His Ala His Pro Asp Asp Glu Ser Ser
                10                  15                  20

aag ggc gca gca acc atg gcg cgc tat gca gct gag ggc aat caa gta   211
Lys Gly Ala Ala Thr Met Ala Arg Tyr Ala Ala Glu Gly Asn Gln Val
            25                  30                  35

atg gtt gtt acc tgc act ggt ggt gag cgt gga gac att ctc aac cct   259
Met Val Val Thr Cys Thr Gly Gly Glu Arg Gly Asp Ile Leu Asn Pro
        40                  45                  50

gct atg gat aag cca gga atc ctg gac aat att ttt gct gtg cgt cag   307
Ala Met Asp Lys Pro Gly Ile Leu Asp Asn Ile Phe Ala Val Arg Gln
    55                  60                  65

gaa gag atg gcg aag gcc atg gaa att ctt ggc act gag cac aga tgg   355
Glu Glu Met Ala Lys Ala Met Glu Ile Leu Gly Thr Glu His Arg Trp
70                  75                  80                  85

cta ggt tat gag gac tct ggg ctg ccc caa ggt gat cct ttg cct cct   403
Leu Gly Tyr Glu Asp Ser Gly Leu Pro Gln Gly Asp Pro Leu Pro Pro
                90                  95                  100

ctg cct gag ggc tgt ttt gct tta gaa gac tcg gat aaa gtc acc caa   451
Leu Pro Glu Gly Cys Phe Ala Leu Glu Asp Ser Asp Lys Val Thr Gln
            105                 110                 115

gat tta gtg aag att ctg cgc gag ttc cgc cca cac gtc atc att acc   499
Asp Leu Val Lys Ile Leu Arg Glu Phe Arg Pro His Val Ile Ile Thr
        120                 125                 130

tat gat gag aac ggc ggt tac cca cac ccg gat cac ctc aag gtt cat   547
Tyr Asp Glu Asn Gly Gly Tyr Pro His Pro Asp His Leu Lys Val His
    135                 140                 145

gag gtg tcg atg ctt gca tgg gag aag tcc ggc gat gca gcg tat gca   595
Glu Val Ser Met Leu Ala Trp Glu Lys Ser Gly Asp Ala Ala Tyr Ala
150                 155                 160                 165

cct gag ttg ggc gca ccg tgg gag cca ctg aag ctt tat tac acc cac   643
Pro Glu Leu Gly Ala Pro Trp Glu Pro Leu Lys Leu Tyr Tyr Thr His
                170                 175                 180

ggc ttt atc cgt cag cgc atg gaa atg ttc cat gat ctg ctc att gaa   691
Gly Phe Ile Arg Gln Arg Met Glu Met Phe His Asp Leu Leu Ile Glu
            185                 190                 195

cag ggc aag ccc agc cca tac acc ccg atg ctt gag cgt tgg aag gca   739
Gln Gly Lys Pro Ser Pro Tyr Thr Pro Met Leu Glu Arg Trp Lys Ala
        200                 205                 210

aat gag gct gat gtg atg gct cga gtt acc act cag gtt cct tgt gag   787
Asn Glu Ala Asp Val Met Ala Arg Val Thr Thr Gln Val Pro Cys Glu
    215                 220                 225

cgc ttc ttt gat cag cgt gat gac gcc ctg cgt gcg cac gca act cag   835
Arg Phe Phe Asp Gln Arg Asp Asp Ala Leu Arg Ala His Ala Thr Gln
230                 235                 240                 245

att gat cct gcg ggt gct ttc ttt gga act ccc gtt gag gtg cag cgt   883
```

```
Ile Asp Pro Ala Gly Ala Phe Phe Gly Thr Pro Val Glu Val Gln Arg
                250                 255                 260

cgc ctg tgg ccg act gaa gag ttc gaa tta gct aaa act cgt gtg aag   931
Arg Leu Trp Pro Thr Glu Glu Phe Glu Leu Ala Lys Thr Arg Val Lys
            265                 270                 275

acg tcg atc cca gaa gat gac ctg ttt gcc gga atc aca ccc gat gca   979
Thr Ser Ile Pro Glu Asp Asp Leu Phe Ala Gly Ile Thr Pro Asp Ala
        280                 285                 290

gaa taatgcagtt agaccacatc ctt                                    1005
Glu
```

<210> 1828
<211> 294
<212> PRT
<213> Corynebacterium glutamicum

<400> 1828

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Met Lys His Val Ser Gly Leu Arg Leu Met Ala Ile His Ala His Pro
  1               5                  10                  15

Asp Asp Glu Ser Ser Lys Gly Ala Ala Thr Met Ala Arg Tyr Ala Ala
             20                  25                  30

Glu Gly Asn Gln Val Met Val Val Thr Cys Thr Gly Gly Glu Arg Gly
         35                  40                  45

Asp Ile Leu Asn Pro Ala Met Asp Lys Pro Gly Ile Leu Asp Asn Ile
     50                  55                  60

Phe Ala Val Arg Gln Glu Glu Met Ala Lys Ala Met Glu Ile Leu Gly
 65                  70                  75                  80

Thr Glu His Arg Trp Leu Gly Tyr Glu Asp Ser Gly Leu Pro Gln Gly
                 85                  90                  95

Asp Pro Leu Pro Pro Leu Pro Glu Gly Cys Phe Ala Leu Glu Asp Ser
            100                 105                 110

Asp Lys Val Thr Gln Asp Leu Val Lys Ile Leu Arg Glu Phe Arg Pro
        115                 120                 125

His Val Ile Ile Thr Tyr Asp Glu Asn Gly Gly Tyr Pro His Pro Asp
    130                 135                 140

His Leu Lys Val His Glu Val Ser Met Leu Ala Trp Glu Lys Ser Gly
145                 150                 155                 160

Asp Ala Ala Tyr Ala Pro Glu Leu Gly Ala Pro Trp Glu Pro Leu Lys
                165                 170                 175

Leu Tyr Tyr Thr His Gly Phe Ile Arg Gln Arg Met Glu Met Phe His
            180                 185                 190

Asp Leu Leu Ile Glu Gln Gly Lys Pro Ser Pro Tyr Thr Pro Met Leu
        195                 200                 205
```

```
Glu Arg Trp Lys Ala Asn Glu Ala Asp Val Met Ala Arg Val Thr Thr
    210                 215                 220

Gln Val Pro Cys Glu Arg Phe Phe Asp Gln Arg Asp Asp Ala Leu Arg
225                 230                 235                 240

Ala His Ala Thr Gln Ile Asp Pro Ala Gly Ala Phe Phe Gly Thr Pro
                245                 250                 255

Val Glu Val Gln Arg Arg Leu Trp Pro Thr Glu Glu Phe Glu Leu Ala
            260                 265                 270

Lys Thr Arg Val Lys Thr Ser Ile Pro Glu Asp Asp Leu Phe Ala Gly
        275                 280                 285

Ile Thr Pro Asp Ala Glu
    290


<210> 1829
<211> 606
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(583)
<223> RXA00587

<400> 1829
cccttggatg acctcggtta acagtttttc ctgaggtgac taagatgtat aggtgaccaa 60

ctcgattcgg ctttgaagag gatgcagaca gacttccatc atg agt aca aat tcc   115
                                           Met Ser Thr Asn Ser
                                             1               5

aac tct cca tcc aac gca tca ggc gct tcg aac att cca aac acc caa   163
Asn Ser Pro Ser Asn Ala Ser Gly Ala Ser Asn Ile Pro Asn Thr Gln
                10                  15                  20

cgt ccg gct agc cga tac aat tcg cct cgc ccg gaa gct gct gca ggc   211
Arg Pro Ala Ser Arg Tyr Asn Ser Pro Arg Pro Glu Ala Ala Ala Gly
            25                  30                  35

agg aac atc agc gga aaa atc atc gca gtc att ggc gtg ctg ctg gtg   259
Arg Asn Ile Ser Gly Lys Ile Ile Ala Val Ile Gly Val Leu Leu Val
        40                  45                  50

atc gcc att gtg att gtt ggc gca aac ttc ctc aaa aac cgc gat gca   307
Ile Ala Ile Val Ile Val Gly Ala Asn Phe Leu Lys Asn Arg Asp Ala
    55                  60                  65

caa aca gtg tcc ggc caa atg ggt tca ttt gaa cgc atc gac gac gac   355
Gln Thr Val Ser Gly Gln Met Gly Ser Phe Glu Arg Ile Asp Asp Asp
70                  75                  80                  85

acc ttc cgc ttt gaa gtt gac gtc acc cgc gat gac cca agc caa gtc   403
Thr Phe Arg Phe Glu Val Asp Val Thr Arg Asp Asp Pro Ser Gln Val
                90                  95                  100

gcc tac tgc atc gtg acc gca aag gac tac tcg cac gca gaa gtc ggg   451
```

```
Ala Tyr Cys Ile Val Thr Ala Lys Asp Tyr Ser His Ala Glu Val Gly
            105                 110                 115

cgt cga gaa gtg ctt gtg gag ccc agc gac cac tca acg gtg cgt atc   499
Arg Arg Glu Val Leu Val Glu Pro Ser Asp His Ser Thr Val Arg Ile
        120                 125                 130

tcc acg ctg atc ccc acc cgc gaa cca gca gtt tcc ggt ggt gtt tac   547
Ser Thr Leu Ile Pro Thr Arg Glu Pro Ala Val Ser Gly Gly Val Tyr
    135                 140                 145

ggt tgt tca acc gtg atc cca tca cat atg aac ctg taaaactaga        593
Gly Cys Ser Thr Val Ile Pro Ser His Met Asn Leu
150                 155                 160

aaattttgct gtg                                                   606


<210> 1830
<211> 161
<212> PRT
<213> Corynebacterium glutamicum

<400> 1830
Met Ser Thr Asn Ser Asn Ser Pro Ser Asn Ala Ser Gly Ala Ser Asn
  1               5                  10                  15

Ile Pro Asn Thr Gln Arg Pro Ala Ser Arg Tyr Asn Ser Pro Arg Pro
             20                  25                  30

Glu Ala Ala Ala Gly Arg Asn Ile Ser Gly Lys Ile Ile Ala Val Ile
         35                  40                  45

Gly Val Leu Leu Val Ile Ala Ile Val Ile Val Gly Ala Asn Phe Leu
     50                  55                  60

Lys Asn Arg Asp Ala Gln Thr Val Ser Gly Gln Met Gly Ser Phe Glu
 65                  70                  75                  80

Arg Ile Asp Asp Asp Thr Phe Arg Phe Glu Val Asp Val Thr Arg Asp
                 85                  90                  95

Asp Pro Ser Gln Val Ala Tyr Cys Ile Val Thr Ala Lys Asp Tyr Ser
            100                 105                 110

His Ala Glu Val Gly Arg Arg Glu Val Leu Val Glu Pro Ser Asp His
        115                 120                 125

Ser Thr Val Arg Ile Ser Thr Leu Ile Pro Thr Arg Glu Pro Ala Val
    130                 135                 140

Ser Gly Gly Val Tyr Gly Cys Ser Thr Val Ile Pro Ser His Met Asn
145                 150                 155                 160

Leu


<210> 1831
<211> 353
<212> DNA
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<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(330)
<223> RXA00595

<400> 1831

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cgc aat att gca gca tgg atc gca atc gcc gcc atc atc atc gcc agc   48
Arg Asn Ile Ala Ala Trp Ile Ala Ile Ala Ala Ile Ile Ile Ala Ser
  1               5                  10                  15

ctg ggc gca ctg ctc tcg atg atc cgc gtg tgg cgt gaa gtc ttc tgg   96
Leu Gly Ala Leu Leu Ser Met Ile Arg Val Trp Arg Glu Val Phe Trp
             20                  25                  30

ggt ggc gca atg cac cag cgc ggc gtc tcg ccg cag ctg cgc atc agc   144
Gly Gly Ala Met His Gln Arg Gly Val Ser Pro Gln Leu Arg Ile Ser
         35                  40                  45

cca gca aaa atc gcc cca gcg ctc agc ctg atc att tta tcg gta ggc   192
Pro Ala Lys Ile Ala Pro Ala Leu Ser Leu Ile Ile Leu Ser Val Gly
     50                  55                  60

atg ttc atc ttc gcg ggc ccg ctt atc gac gcg acc ctc acc gcc acc   240
Met Phe Ile Phe Ala Gly Pro Leu Ile Asp Ala Thr Leu Thr Ala Thr
 65                  70                  75                  80

gac ggc ctc ttg aac acc gat gca tac caa cag gct gtg ctc ggt gaa   288
Asp Gly Leu Leu Asn Thr Asp Ala Tyr Gln Gln Ala Val Leu Gly Glu
                 85                  90                  95

aat gcc atc gga gtg cca agc cct agc tac cag gga gga aac           330
Asn Ala Ile Gly Val Pro Ser Pro Ser Tyr Gln Gly Gly Asn
            100                 105                 110

taatgcttaa cgccctgaaa ttc                                        353
```

<210> 1832
<211> 110
<212> PRT
<213> Corynebacterium glutamicum

<400> 1832

```
Arg Asn Ile Ala Ala Trp Ile Ala Ile Ala Ala Ile Ile Ile Ala Ser
  1               5                  10                  15

Leu Gly Ala Leu Leu Ser Met Ile Arg Val Trp Arg Glu Val Phe Trp
             20                  25                  30

Gly Gly Ala Met His Gln Arg Gly Val Ser Pro Gln Leu Arg Ile Ser
         35                  40                  45

Pro Ala Lys Ile Ala Pro Ala Leu Ser Leu Ile Ile Leu Ser Val Gly
     50                  55                  60

Met Phe Ile Phe Ala Gly Pro Leu Ile Asp Ala Thr Leu Thr Ala Thr
 65                  70                  75                  80

Asp Gly Leu Leu Asn Thr Asp Ala Tyr Gln Gln Ala Val Leu Gly Glu
```

```
                85                  90                  95

Asn Ala Ile Gly Val Pro Ser Pro Ser Tyr Gln Gly Gly Asn
            100                 105                 110


<210> 1833
<211> 393
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(370)
<223> RXA00597

<400> 1833
caaggagatc cgccccagcg atgctgagtg gccaagtcgc gagatcgctg acaccgccca 60

aaacaccgtc agccaagaca agagggagtt ttaaaacaac atg act gct ttt gga   115
                                            Met Thr Ala Phe Gly
                                              1               5

att gtc acc aca gtt ggc atc tgc atg ttt gcg ttc tcc ctc tta tct   163
Ile Val Thr Thr Val Gly Ile Cys Met Phe Ala Phe Ser Leu Leu Ser
                10                  15                  20

gcc ctg gtc ctt att ctg cgc acc aaa gat ttc ctc acc cgc gtg gtg   211
Ala Leu Val Leu Ile Leu Arg Thr Lys Asp Phe Leu Thr Arg Val Val
             25                  30                  35

ctt tcc gac atg gtt ttc tac tct atg atc gcg atc tac ctc atc tgg   259
Leu Ser Asp Met Val Phe Tyr Ser Met Ile Ala Ile Tyr Leu Ile Trp
         40                  45                  50

gtg ctc aac aac cca acc tca atc gcc ttt gag att gct ctt ctc gca   307
Val Leu Asn Asn Pro Thr Ser Ile Ala Phe Glu Ile Ala Leu Leu Ala
     55                  60                  65

gca gtc ctc ggc ggc gta ctt cca acc ctg tcc atg gct cgc atc att   355
Ala Val Leu Gly Gly Val Leu Pro Thr Leu Ser Met Ala Arg Ile Ile
 70                  75                  80                  85

tcg aag gga cgc agg taaatgacca ttccagagat cat                    393
Ser Lys Gly Arg Arg
                90


<210> 1834
<211> 90
<212> PRT
<213> Corynebacterium glutamicum

<400> 1834
Met Thr Ala Phe Gly Ile Val Thr Thr Val Gly Ile Cys Met Phe Ala
  1               5                  10                  15

Phe Ser Leu Leu Ser Ala Leu Val Leu Ile Leu Arg Thr Lys Asp Phe
             20                  25                  30

Leu Thr Arg Val Val Leu Ser Asp Met Val Phe Tyr Ser Met Ile Ala
```

```
         35                  40                  45

Ile Tyr Leu Ile Trp Val Leu Asn Asn Pro Thr Ser Ile Ala Phe Glu
     50                  55                  60

Ile Ala Leu Leu Ala Ala Val Leu Gly Gly Val Leu Pro Thr Leu Ser
 65                  70                  75                  80

Met Ala Arg Ile Ile Ser Lys Gly Arg Arg
                 85                  90


<210> 1835
<211> 441
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(418)
<223> RXA00598

<400> 1835
aacctcaatc gcctttgaga ttgctcttct cgcagcagtc ctcggcggcg tacttccaac 60

cctgtccatg gctcgcatca tttcgaaggg acgcaggtaa atg acc att cca gag   115
                                          Met Thr Ile Pro Glu
                                            1               5

atc atc gtc tcc atc ctc gtg atc ctc gca ggc ctg ttt tct cta ggt   163
Ile Ile Val Ser Ile Leu Val Ile Leu Ala Gly Leu Phe Ser Leu Gly
                 10                  15                  20

act gca atc gct ttg tgg cgc gca ccg gat ccg ctc acc cga gcc aac   211
Thr Ala Ile Ala Leu Trp Arg Ala Pro Asp Pro Leu Thr Arg Ala Asn
             25                  30                  35

ctg ctt ggc acc acc gtg ggt gtc tcc ata ccg ctg ctc atc att gcg   259
Leu Leu Gly Thr Thr Val Gly Val Ser Ile Pro Leu Leu Ile Ile Ala
         40                  45                  50

ctg ctg att cac acc tgg tcc gtc gac gga ttt aac ccc aac aat ttc   307
Leu Leu Ile His Thr Trp Ser Val Asp Gly Phe Asn Pro Asn Asn Phe
     55                  60                  65

atc cga gcg atc atc gcc atc atc ggc gtc tgg gtc atc ggt tcc gtt   355
Ile Arg Ala Ile Ile Ala Ile Ile Gly Val Trp Val Ile Gly Ser Val
 70                  75                  80                  85

ggt tcc tac tac atg gga cgc gcc atc tat ggt gtg acc gta gtg gat   403
Gly Ser Tyr Tyr Met Gly Arg Ala Ile Tyr Gly Val Thr Val Val Asp
                 90                  95                 100

aac aga cga tcc aaa taaactgctt ttagaaaaaa agg                     441
Asn Arg Arg Ser Lys
            105


<210> 1836
<211> 106
<212> PRT
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<213> Corynebacterium glutamicum

<400> 1836

```
Met Thr Ile Pro Glu Ile Ile Val Ser Ile Leu Val Ile Leu Ala Gly
  1               5                  10                  15

Leu Phe Ser Leu Gly Thr Ala Ile Ala Leu Trp Arg Ala Pro Asp Pro
             20                  25                  30

Leu Thr Arg Ala Asn Leu Leu Gly Thr Thr Val Gly Val Ser Ile Pro
         35                  40                  45

Leu Leu Ile Ile Ala Leu Leu Ile His Thr Trp Ser Val Asp Gly Phe
     50                  55                  60

Asn Pro Asn Asn Phe Ile Arg Ala Ile Ile Ala Ile Ile Gly Val Trp
 65                  70                  75                  80

Val Ile Gly Ser Val Gly Ser Tyr Tyr Met Gly Arg Ala Ile Tyr Gly
                 85                  90                  95

Val Thr Val Val Asp Asn Arg Arg Ser Lys
            100                 105
```

<210> 1837
<211> 414
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(391)
<223> RXA00601

<400> 1837

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tagatataga acacattcta ttgcagggaa ttatcaagtt tcatacattg tcctcgtagg 60

ggcaagtata tttcccatgc aatatttttt aggagtccca atg cgt ttc aag tca   115
                                            Met Arg Phe Lys Ser
                                              1               5

gtt gca gct atc gca ctt tcc acc gca atg atc agg ggt gga acc gca   163
Val Ala Ala Ile Ala Leu Ser Thr Ala Met Ile Arg Gly Gly Thr Ala
                 10                  15                  20

agc gtt gct aat gct cag cag gtt agc cct agt tcc acg att gag atc   211
Ser Val Ala Asn Ala Gln Gln Val Ser Pro Ser Ser Thr Ile Glu Ile
             25                  30                  35

cct caa gaa ttc gtc cac acc gtg cag aac ttc gtg cca ggt atg act   259
Pro Gln Glu Phe Val His Thr Val Gln Asn Phe Val Pro Gly Met Thr
         40                  45                  50

tac ggc gat gca ggg tcc gct atc cag agc acc gct ggt tct gtg gca   307
Tyr Gly Asp Ala Gly Ser Ala Ile Gln Ser Thr Ala Gly Ser Val Ala
     55                  60                  65

ctg aac agt acc gct gga atc atc ctt cca atc gtt ctt cca ttc ctt   355
Leu Asn Ser Thr Ala Gly Ile Ile Leu Pro Ile Val Leu Pro Phe Leu
 70                  75                  80                  85
```

```
ggt ctg gga gct gtt ggt tct gca gcg ctg tct gct taagcctttt        401
Gly Leu Gly Ala Val Gly Ser Ala Ala Leu Ser Ala
                 90                  95

ctaggttcct taa                                                   414


<210> 1838
<211> 97
<212> PRT
<213> Corynebacterium glutamicum

<400> 1838
Met Arg Phe Lys Ser Val Ala Ala Ile Ala Leu Ser Thr Ala Met Ile
  1               5                  10                  15

Arg Gly Gly Thr Ala Ser Val Ala Asn Ala Gln Gln Val Ser Pro Ser
             20                  25                  30

Ser Thr Ile Glu Ile Pro Gln Glu Phe Val His Thr Val Gln Asn Phe
         35                  40                  45

Val Pro Gly Met Thr Tyr Gly Asp Ala Gly Ser Ala Ile Gln Ser Thr
     50                  55                  60

Ala Gly Ser Val Ala Leu Asn Ser Thr Ala Gly Ile Ile Leu Pro Ile
 65                  70                  75                  80

Val Leu Pro Phe Leu Gly Leu Gly Ala Val Gly Ser Ala Ala Leu Ser
                 85                  90                  95

Ala



<210> 1839
<211> 876
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(853)
<223> RXA00602

<400> 1839
gcgcgatcaa tggaatctag cttcatatat tgcacaatag cctagttgag gtgcgcaaac 60

tggcaacaaa actacccggc aattgtgtga tgattgtagt gtg caa aaa acg caa   115
                                            Val Gln Lys Thr Gln
                                              1               5

gag att cat tca agc ctg gag gtg tcg cca tcc aag gca gcc ctg gaa   163
Glu Ile His Ser Ser Leu Glu Val Ser Pro Ser Lys Ala Ala Leu Glu
                 10                  15                  20

cca gat gat aaa ggt tat cgg cgc tac gaa atc gcg caa ggt cta aaa   211
Pro Asp Asp Lys Gly Tyr Arg Arg Tyr Glu Ile Ala Gln Gly Leu Lys
             25                  30                  35
```

```
acc tcc ctt gct gca ggt ttg ggc atg tac ccg att ggt att gcg ttt   259
Thr Ser Leu Ala Ala Gly Leu Gly Met Tyr Pro Ile Gly Ile Ala Phe
         40                  45                  50

ggt ctc ttg gtt att caa tac ggc tac gaa tgg tgg gca gcc cca ctg   307
Gly Leu Leu Val Ile Gln Tyr Gly Tyr Glu Trp Trp Ala Ala Pro Leu
     55                  60                  65

ttt tcc ggc ctg att ttc gcg ggc tcc acc gaa atg ctg gtc atc gcc   355
Phe Ser Gly Leu Ile Phe Ala Gly Ser Thr Glu Met Leu Val Ile Ala
 70                  75                  80                  85

ctc gtt gtg ggc gca gcg ccc ctg ggc gcc atc gcg ctc acc aca ttg   403
Leu Val Val Gly Ala Ala Pro Leu Gly Ala Ile Ala Leu Thr Thr Leu
                 90                  95                 100

ctg gtg aac ttc cgc cac gta ttc tat gcg ttt tca ttc ccg ctg cat   451
Leu Val Asn Phe Arg His Val Phe Tyr Ala Phe Ser Phe Pro Leu His
            105                 110                 115

gtg gtc aaa aac ccc att gcc cgt ttc tat tcg gtt ttc gcg ctt atc   499
Val Val Lys Asn Pro Ile Ala Arg Phe Tyr Ser Val Phe Ala Leu Ile
        120                 125                 130

gac gaa gcc tac gca gtc act gcg gcc agg ccc gca ggc tgg tcg gcg   547
Asp Glu Ala Tyr Ala Val Thr Ala Ala Arg Pro Ala Gly Trp Ser Ala
    135                 140                 145

tgg cga ctt atc tca atg caa ata gcg ttt cac tcc tac tgg gta ttc   595
Trp Arg Leu Ile Ser Met Gln Ile Ala Phe His Ser Tyr Trp Val Phe
150                 155                 160                 165

ggc ggt ctc acc gga gtg gcg atc gca gag ttg att cct ttt gaa att   643
Gly Gly Leu Thr Gly Val Ala Ile Ala Glu Leu Ile Pro Phe Glu Ile
                170                 175                 180

aag ggc ctc gag ttc gcc ctt tgc tct ctc ttt gtc acg ctg act ttg   691
Lys Gly Leu Glu Phe Ala Leu Cys Ser Leu Phe Val Thr Leu Thr Leu
            185                 190                 195

gat tcc tgc cga acg aaa aag cag atc cct tct ctg ctg ctc gca ggt   739
Asp Ser Cys Arg Thr Lys Lys Gln Ile Pro Ser Leu Leu Leu Ala Gly
        200                 205                 210

ttg agc ttc acc att gct ctt gtg gta att cca ggt cag gcc cta ttt   787
Leu Ser Phe Thr Ile Ala Leu Val Val Ile Pro Gly Gln Ala Leu Phe
    215                 220                 225

gcg gcg ctg ctg atc ttc ttg ggt ctg ttg acc atc cgg tac ttc ttc   835
Ala Ala Leu Leu Ile Phe Leu Gly Leu Leu Thr Ile Arg Tyr Phe Phe
230                 235                 240                 245

ttg gga aag gct gct aaa tgacaactga tttctcctgt att                 876
Leu Gly Lys Ala Ala Lys
                250
```

<210> 1840
<211> 251
<212> PRT
<213> Corynebacterium glutamicum

<400> 1840
Val Gln Lys Thr Gln Glu Ile His Ser Ser Leu Glu Val Ser Pro Ser
1 5 10 15

Lys Ala Ala Leu Glu Pro Asp Asp Lys Gly Tyr Arg Arg Tyr Glu Ile
20 25 30

Ala Gln Gly Leu Lys Thr Ser Leu Ala Ala Gly Leu Gly Met Tyr Pro
35 40 45

Ile Gly Ile Ala Phe Gly Leu Leu Val Ile Gln Tyr Gly Tyr Glu Trp
50 55 60

Trp Ala Ala Pro Leu Phe Ser Gly Leu Ile Phe Ala Gly Ser Thr Glu
65 70 75 80

Met Leu Val Ile Ala Leu Val Val Gly Ala Ala Pro Leu Gly Ala Ile
85 90 95

Ala Leu Thr Thr Leu Leu Val Asn Phe Arg His Val Phe Tyr Ala Phe
100 105 110

Ser Phe Pro Leu His Val Val Lys Asn Pro Ile Ala Arg Phe Tyr Ser
115 120 125

Val Phe Ala Leu Ile Asp Glu Ala Tyr Ala Val Thr Ala Ala Arg Pro
130 135 140

Ala Gly Trp Ser Ala Trp Arg Leu Ile Ser Met Gln Ile Ala Phe His
145 150 155 160

Ser Tyr Trp Val Phe Gly Gly Leu Thr Gly Val Ala Ile Ala Glu Leu
165 170 175

Ile Pro Phe Glu Ile Lys Gly Leu Glu Phe Ala Leu Cys Ser Leu Phe
180 185 190

Val Thr Leu Thr Leu Asp Ser Cys Arg Thr Lys Lys Gln Ile Pro Ser
195 200 205

Leu Leu Leu Ala Gly Leu Ser Phe Thr Ile Ala Leu Val Val Ile Pro
210 215 220

Gly Gln Ala Leu Phe Ala Ala Leu Leu Ile Phe Leu Gly Leu Leu Thr
225 230 235 240

Ile Arg Tyr Phe Phe Leu Gly Lys Ala Ala Lys
245 250

<210> 1841
<211> 414
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(391)
<223> RXA00604

<400> 1841
atcacgtttt gctatgaaag tggtgaaacc agctcgcccc caggtgtgaa gcatgcattt 60

tgaagcatga atctttttca tctagtgaag gactgatccc atg cgt atg aaa tca 115
Met Arg Met Lys Ser
1 5

atc gca gca att gca atc gct acc gcc gcc ctg gct ggt ggc act gga 163
Ile Ala Ala Ile Ala Ile Ala Thr Ala Ala Leu Ala Gly Gly Thr Gly
10 15 20

gtc gct agc gca cag gaa gct ggc tcg act gct ggt tcc tcc aac ctc 211
Val Ala Ser Ala Gln Glu Ala Gly Ser Thr Ala Gly Ser Ser Asn Leu
25 30 35

agc tct ggg atc cag ctt cca caa gaa gcc acc gat ctg ttg agc ttc 259
Ser Ser Gly Ile Gln Leu Pro Gln Glu Ala Thr Asp Leu Leu Ser Phe
40 45 50

ctg cct gct gct cag gct gcg cag gtt gaa gga gca att cag agc acc 307
Leu Pro Ala Ala Gln Ala Ala Gln Val Glu Gly Ala Ile Gln Ser Thr
55 60 65

gct ggt ttc ttt gcc gtt gga ctc ggc tcg acc gcc att ggt tcc act 355
Ala Gly Phe Phe Ala Val Gly Leu Gly Ser Thr Ala Ile Gly Ser Thr
70 75 80 85

gca gtg acc ttg gga att gcg gat ctg ctg tct agc taatttcctc 401
Ala Val Thr Leu Gly Ile Ala Asp Leu Leu Ser Ser
90 95

tcaatagctt caa 414

<210> 1842
<211> 97
<212> PRT
<213> Corynebacterium glutamicum

<400> 1842
Met Arg Met Lys Ser Ile Ala Ala Ile Ala Ile Ala Thr Ala Ala Leu
1 5 10 15

Ala Gly Gly Thr Gly Val Ala Ser Ala Gln Glu Ala Gly Ser Thr Ala
20 25 30

Gly Ser Ser Asn Leu Ser Ser Gly Ile Gln Leu Pro Gln Glu Ala Thr
35 40 45

Asp Leu Leu Ser Phe Leu Pro Ala Ala Gln Ala Ala Gln Val Glu Gly
50 55 60

Ala Ile Gln Ser Thr Ala Gly Phe Phe Ala Val Gly Leu Gly Ser Thr
65 70 75 80

Ala Ile Gly Ser Thr Ala Val Thr Leu Gly Ile Ala Asp Leu Leu Ser
85 90 95

Ser

<210> 1843
<211> 987
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(964)
<223> RXA00610

<400> 1843
caagcactcc caggggaacg ttcattcgaa aaactcgacg ccttatacga gcttctagag 60

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cctcggaacc aattgctcga gatcgcagtc taactagagt atg gaa ccg aaa aaa   115
                                            Met Glu Pro Lys Lys
                                              1               5

cct gtc aca tat aaa gaa ctt gcc cac gaa tat tca aga aga acg ttt   163
Pro Val Thr Tyr Lys Glu Leu Ala His Glu Tyr Ser Arg Arg Thr Phe
                 10                  15                  20

aac aaa ctc ttc acc aaa att act ggc ttc gtc tat cta aaa aac gat   211
Asn Lys Leu Phe Thr Lys Ile Thr Gly Phe Val Tyr Leu Lys Asn Asp
             25                  30                  35

cta atc aac gat ccc aac tta gtg acc caa gca ctg ctc aaa aga tgc   259
Leu Ile Asn Asp Pro Asn Leu Val Thr Gln Ala Leu Leu Lys Arg Cys
         40                  45                  50

cca gaa gga gta ctt cgc gga tat gca gca tta aag caa cgt ggc tat   307
Pro Glu Gly Val Leu Arg Gly Tyr Ala Ala Leu Lys Gln Arg Gly Tyr
     55                  60                  65

cag ctt tta gac gat cag tgg atg cca atc atc agt gtt tcc gga gat   355
Gln Leu Leu Asp Asp Gln Trp Met Pro Ile Ile Ser Val Ser Gly Asp
 70                  75                  80                  85

cta aac agg agg gac tgc tca cga ggt gaa att ctc agg cgg att gaa   403
Leu Asn Arg Arg Asp Cys Ser Arg Gly Glu Ile Leu Arg Arg Ile Glu
                 90                  95                 100

cca gaa aac acc ctg ctc agt ggc aac att agg ttc gtt aat gat gtt   451
Pro Glu Asn Thr Leu Leu Ser Gly Asn Ile Arg Phe Val Asn Asp Val
            105                 110                 115

caa gcg atc caa gac gtc ttc gac ctg cat tct ctc aac gac ttt gaa   499
Gln Ala Ile Gln Asp Val Phe Asp Leu His Ser Leu Asn Asp Phe Glu
        120                 125                 130

gac caa gta gct ctc atc gat cat ctc atc agg cag cgc ccc gaa tta   547
Asp Gln Val Ala Leu Ile Asp His Leu Ile Arg Gln Arg Pro Glu Leu
    135                 140                 145

ttc caa gaa ctc ata caa gag cca aaa ctt aag aaa cac act caa tac   595
Phe Gln Glu Leu Ile Gln Glu Pro Lys Leu Lys Lys His Thr Gln Tyr
150                 155                 160                 165

gcc aat cct ttt gct gaa tct ccg caa gaa tca cga ctt cgg gtc aga   643
Ala Asn Pro Phe Ala Glu Ser Pro Gln Glu Ser Arg Leu Arg Val Arg
                170                 175                 180
```

```
ctt cat tca ctg ggt tac cac ggc ttc atc cca cag att cat gtt gaa   691
Leu His Ser Leu Gly Tyr His Gly Phe Ile Pro Gln Ile His Val Glu
            185                 190                 195

tac gac ggt caa tcc tat ttt cta gat ctc gca gat ccg ctg tgg cag   739
Tyr Asp Gly Gln Ser Tyr Phe Leu Asp Leu Ala Asp Pro Leu Trp Gln
        200                 205                 210

gtt gcc ctc gaa tac aac ggc gga tgg cac tac acc tct gag cag cga   787
Val Ala Leu Glu Tyr Asn Gly Gly Trp His Tyr Thr Ser Glu Gln Arg
    215                 220                 225

gag aaa gat tct cat cgg aag aat gct ctg aaa agt gcg gga tgg gat   835
Glu Lys Asp Ser His Arg Lys Asn Ala Leu Lys Ser Ala Gly Trp Asp
230                 235                 240                 245

gtc cta gaa gtg aca tca aaa act ctg cag aat ccg aat tcc tgg aac   883
Val Leu Glu Val Thr Ser Lys Thr Leu Gln Asn Pro Asn Ser Trp Asn
                250                 255                 260

aac ctg ata caa cag atc aat agc tct ctc cgc cga aag cag gct cag   931
Asn Leu Ile Gln Gln Ile Asn Ser Ser Leu Arg Arg Lys Gln Ala Gln
            265                 270                 275

cga cgc cga agg tta ccc atg caa acg gtg ggc taacggcatc actgaaaaag 984
Arg Arg Arg Arg Leu Pro Met Gln Thr Val Gly
        280                 285

acc                                                               987


<210> 1844
<211> 288
<212> PRT
<213> Corynebacterium glutamicum

<400> 1844
Met Glu Pro Lys Lys Pro Val Thr Tyr Lys Glu Leu Ala His Glu Tyr
  1               5                  10                  15

Ser Arg Arg Thr Phe Asn Lys Leu Phe Thr Lys Ile Thr Gly Phe Val
             20                  25                  30

Tyr Leu Lys Asn Asp Leu Ile Asn Asp Pro Asn Leu Val Thr Gln Ala
         35                  40                  45

Leu Leu Lys Arg Cys Pro Glu Gly Val Leu Arg Gly Tyr Ala Ala Leu
     50                  55                  60

Lys Gln Arg Gly Tyr Gln Leu Leu Asp Asp Gln Trp Met Pro Ile Ile
 65                  70                  75                  80

Ser Val Ser Gly Asp Leu Asn Arg Arg Asp Cys Ser Arg Gly Glu Ile
                 85                  90                  95

Leu Arg Arg Ile Glu Pro Glu Asn Thr Leu Leu Ser Gly Asn Ile Arg
            100                 105                 110

Phe Val Asn Asp Val Gln Ala Ile Gln Asp Val Phe Asp Leu His Ser
        115                 120                 125
```

```
Leu Asn Asp Phe Glu Asp Gln Val Ala Leu Ile Asp His Leu Ile Arg
    130                 135                 140

Gln Arg Pro Glu Leu Phe Gln Glu Leu Ile Gln Glu Pro Lys Leu Lys
145                 150                 155                 160

Lys His Thr Gln Tyr Ala Asn Pro Phe Ala Glu Ser Pro Gln Glu Ser
                165                 170                 175

Arg Leu Arg Val Arg Leu His Ser Leu Gly Tyr His Gly Phe Ile Pro
            180                 185                 190

Gln Ile His Val Glu Tyr Asp Gly Gln Ser Tyr Phe Leu Asp Leu Ala
        195                 200                 205

Asp Pro Leu Trp Gln Val Ala Leu Glu Tyr Asn Gly Gly Trp His Tyr
    210                 215                 220

Thr Ser Glu Gln Arg Glu Lys Asp Ser His Arg Lys Asn Ala Leu Lys
225                 230                 235                 240

Ser Ala Gly Trp Asp Val Leu Glu Val Thr Ser Lys Thr Leu Gln Asn
                245                 250                 255

Pro Asn Ser Trp Asn Asn Leu Ile Gln Gln Ile Asn Ser Ser Leu Arg
            260                 265                 270

Arg Lys Gln Ala Gln Arg Arg Arg Arg Leu Pro Met Gln Thr Val Gly
        275                 280                 285
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<210> 1845
<211> 1599
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1576)
<223> RXA00611

<400> 1845

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ctttaaattg actatttaca aaactacttg atgagttagc aagagcacat ttcggtgcgc 60

ctccctgcta aacctcgaaa caataactag attgcacact atg tct gcc gct gct   115
                                              Met Ser Ala Ala Ala
                                                1               5

tct cga tca aga aac atc ttg act gcc ctc ctg cta ttg gtc ccg ctc   163
Ser Arg Ser Arg Asn Ile Leu Thr Ala Leu Leu Leu Leu Val Pro Leu
                10                  15                  20

atc gca ggt acc atc tac gcc tcc gcc atg ggc ttg gac gtc tcc cgc   211
Ile Ala Gly Thr Ile Tyr Ala Ser Ala Met Gly Leu Asp Val Ser Arg
            25                  30                  35

gca tgg tcc tca gca gat gaa gta acg ggg gca cct gca gcc tcc gta   259
```

```
Ala Trp Ser Ser Ala Asp Glu Val Thr Gly Ala Pro Ala Ala Ser Val
         40                  45                  50

gcc acc aac aac cag gag ctt atc gaa gcc cgt cgc gcc gcc gga gaa   307
Ala Thr Asn Asn Gln Glu Leu Ile Glu Ala Arg Arg Ala Ala Gly Glu
     55                  60                  65

gcc ggc gcc caa gcg ggg ttc ctc acc tca gga act gaa gag cta acc   355
Ala Gly Ala Gln Ala Gly Phe Leu Thr Ser Gly Thr Glu Glu Leu Thr
 70                  75                  80                  85

agc gga aca caa gag ctt atc gac ggc gca gcc cca ctc gaa gaa ggc   403
Ser Gly Thr Gln Glu Leu Ile Asp Gly Ala Ala Pro Leu Glu Glu Gly
                 90                  95                 100

gtc tca gcc gcg gct gac ggt gca gcg caa ctc cac gat ggc ctc atc   451
Val Ser Ala Ala Ala Asp Gly Ala Ala Gln Leu His Asp Gly Leu Ile
            105                 110                 115

caa ctc cag gcc ggc act gga caa atg gga acc ggc gcc acc gaa att   499
Gln Leu Gln Ala Gly Thr Gly Gln Met Gly Thr Gly Ala Thr Glu Ile
        120                 125                 130

gcc gac ggc gtc caa aac gca gtc gaa caa ctt ggc ggt ctt gtc gtt   547
Ala Asp Gly Val Gln Asn Ala Val Glu Gln Leu Gly Gly Leu Val Val
    135                 140                 145

gta cag cag caa ctc tta ggc gcc ctc aac gaa gca gac aaa caa ctc   595
Val Gln Gln Gln Leu Leu Gly Ala Leu Asn Glu Ala Asp Lys Gln Leu
150                 155                 160                 165

gcc tcg agc aaa atc ccc gaa gcc gaa gac ctg cgc aaa caa atc acc   643
Ala Ser Ser Lys Ile Pro Glu Ala Glu Asp Leu Arg Lys Gln Ile Thr
                170                 175                 180

gaa gtc cga gga cac ctc gaa aac ttc ggc atc tcc gta gaa atg acc   691
Glu Val Arg Gly His Leu Glu Asn Phe Gly Ile Ser Val Glu Met Thr
            185                 190                 195

gac caa ctc gat caa cta cgt tcc ggc acc cgc gac ctg gct aac caa   739
Asp Gln Leu Asp Gln Leu Arg Ser Gly Thr Arg Asp Leu Ala Asn Gln
        200                 205                 210

ctc gca gtc ccc ggc tac gga ttc cac gat ggt att tac agc gcc acc   787
Leu Ala Val Pro Gly Tyr Gly Phe His Asp Gly Ile Tyr Ser Ala Thr
    215                 220                 225

aat gga gca gcc gaa tta tct gca ggt ttg caa gag cta gaa gca ggc   835
Asn Gly Ala Ala Glu Leu Ser Ala Gly Leu Gln Glu Leu Glu Ala Gly
230                 235                 240                 245

gtt ggg act gcc gtc gaa ggc ttc acc gca ctc gat gaa ggt gca aac   883
Val Gly Thr Ala Val Glu Gly Phe Thr Ala Leu Asp Glu Gly Ala Asn
                250                 255                 260

cga tta gac tcc atg gcc acc ctc aac gaa gaa aaa acc tcc gca gtc   931
Arg Leu Asp Ser Met Ala Thr Leu Asn Glu Glu Lys Thr Ser Ala Val
            265                 270                 275

caa cga gcc ctc ccg gta ccc caa gta ccc gcc ggc aca atc gaa ggc   979
Gln Arg Ala Leu Pro Val Pro Gln Val Pro Ala Gly Thr Ile Glu Gly
```

```
        280                 285                 290

acc gca gac gaa gaa cgc acc agc gca cta gcg ccc atg tac gcc ttc   1027
Thr Ala Asp Glu Glu Arg Thr Ser Ala Leu Ala Pro Met Tyr Ala Phe
    295                 300                 305

tta att tca gca ttg gtc atg ctg gcc ggt gca gca ctt gga tgg gca   1075
Leu Ile Ser Ala Leu Val Met Leu Ala Gly Ala Ala Leu Gly Trp Ala
310                 315                 320                 325

aca cta aaa aac aag tgg ctg atg gcc ttt gct gtc att ggt gtc act   1123
Thr Leu Lys Asn Lys Trp Leu Met Ala Phe Ala Val Ile Gly Val Thr
                330                 335                 340

gca atc ggt ggc att atc ttg ttc acc gta gct ttg ggc ata tcc att   1171
Ala Ile Gly Gly Ile Ile Leu Phe Thr Val Ala Leu Gly Ile Ser Ile
            345                 350                 355

gga gct ttg ttt gga gcc tta gga att ttg ctt ctt gcc act gtt gtt   1219
Gly Ala Leu Phe Gly Ala Leu Gly Ile Leu Leu Leu Ala Thr Val Val
        360                 365                 370

gcc ggt att ctc tcc cgg att ttg ctt gac gtg ttg gga act acc ggg   1267
Ala Gly Ile Leu Ser Arg Ile Leu Leu Asp Val Leu Gly Thr Thr Gly
    375                 380                 385

gct att gtg gtt tct gtt ctg gga tgg gta gcc caa gct gca gta att   1315
Ala Ile Val Val Ser Val Leu Gly Trp Val Ala Gln Ala Ala Val Ile
390                 395                 400                 405

ggc cat gta tgg agt gtt acc gct gta tcc gat atc gca ctt gtt tgg   1363
Gly His Val Trp Ser Val Thr Ala Val Ser Asp Ile Ala Leu Val Trp
                410                 415                 420

cga gtc gtc gca ggc atg atg cca ctg cat tat cca acc ttt gca gtg   1411
Arg Val Val Ala Gly Met Met Pro Leu His Tyr Pro Thr Phe Ala Val
            425                 430                 435

acc tcc att ggt aat ggc gga tca gct gca gct atc tgg atg tct gtt   1459
Thr Ser Ile Gly Asn Gly Gly Ser Ala Ala Ala Ile Trp Met Ser Val
        440                 445                 450

gct gtc ttg ttg gca atg gga gcg atc gga gct gtt gcg ctt cgg aag   1507
Ala Val Leu Leu Ala Met Gly Ala Ile Gly Ala Val Ala Leu Arg Lys
    455                 460                 465

cca aag gcg gtt gcg gtt gag gtt gaa gaa gct gtt gat gct gat gca   1555
Pro Lys Ala Val Ala Val Glu Val Glu Glu Ala Val Asp Ala Asp Ala
470                 475                 480                 485

gac caa gca gcc tcg gaa tcc tgatggtttt ggtctgattc gac            1599
Asp Gln Ala Ala Ser Glu Ser
                490
```

<210> 1846
<211> 492
<212> PRT
<213> Corynebacterium glutamicum

<400> 1846

```
Met Ser Ala Ala Ala Ser Arg Ser Arg Asn Ile Leu Thr Ala Leu Leu
 1               5                  10                  15

Leu Leu Val Pro Leu Ile Ala Gly Thr Ile Tyr Ala Ser Ala Met Gly
            20                  25                  30

Leu Asp Val Ser Arg Ala Trp Ser Ser Ala Asp Glu Val Thr Gly Ala
        35                  40                  45

Pro Ala Ala Ser Val Ala Thr Asn Asn Gln Glu Leu Ile Glu Ala Arg
    50                  55                  60

Arg Ala Ala Gly Glu Ala Gly Ala Gln Ala Gly Phe Leu Thr Ser Gly
65                  70                  75                  80

Thr Glu Glu Leu Thr Ser Gly Thr Gln Glu Leu Ile Asp Gly Ala Ala
                85                  90                  95

Pro Leu Glu Glu Gly Val Ser Ala Ala Ala Asp Gly Ala Ala Gln Leu
            100                 105                 110

His Asp Gly Leu Ile Gln Leu Gln Ala Gly Thr Gly Gln Met Gly Thr
        115                 120                 125

Gly Ala Thr Glu Ile Ala Asp Gly Val Gln Asn Ala Val Glu Gln Leu
    130                 135                 140

Gly Gly Leu Val Val Val Gln Gln Gln Leu Leu Gly Ala Leu Asn Glu
145                 150                 155                 160

Ala Asp Lys Gln Leu Ala Ser Ser Lys Ile Pro Glu Ala Glu Asp Leu
                165                 170                 175

Arg Lys Gln Ile Thr Glu Val Arg Gly His Leu Glu Asn Phe Gly Ile
            180                 185                 190

Ser Val Glu Met Thr Asp Gln Leu Asp Gln Leu Arg Ser Gly Thr Arg
        195                 200                 205

Asp Leu Ala Asn Gln Leu Ala Val Pro Gly Tyr Gly Phe His Asp Gly
    210                 215                 220

Ile Tyr Ser Ala Thr Asn Gly Ala Ala Glu Leu Ser Ala Gly Leu Gln
225                 230                 235                 240

Glu Leu Glu Ala Gly Val Gly Thr Ala Val Glu Gly Phe Thr Ala Leu
                245                 250                 255

Asp Glu Gly Ala Asn Arg Leu Asp Ser Met Ala Thr Leu Asn Glu Glu
            260                 265                 270

Lys Thr Ser Ala Val Gln Arg Ala Leu Pro Val Pro Gln Val Pro Ala
        275                 280                 285

Gly Thr Ile Glu Gly Thr Ala Asp Glu Glu Arg Thr Ser Ala Leu Ala
    290                 295                 300

Pro Met Tyr Ala Phe Leu Ile Ser Ala Leu Val Met Leu Ala Gly Ala
305                 310                 315                 320

Ala Leu Gly Trp Ala Thr Leu Lys Asn Lys Trp Leu Met Ala Phe Ala
```

```
                325                 330                 335

Val Ile Gly Val Thr Ala Ile Gly Gly Ile Ile Leu Phe Thr Val Ala
            340                 345                 350

Leu Gly Ile Ser Ile Gly Ala Leu Phe Gly Ala Leu Gly Ile Leu Leu
        355                 360                 365

Leu Ala Thr Val Val Ala Gly Ile Leu Ser Arg Ile Leu Leu Asp Val
    370                 375                 380

Leu Gly Thr Thr Gly Ala Ile Val Val Ser Val Leu Gly Trp Val Ala
385                 390                 395                 400

Gln Ala Ala Val Ile Gly His Val Trp Ser Val Thr Ala Val Ser Asp
                405                 410                 415

Ile Ala Leu Val Trp Arg Val Val Ala Gly Met Met Pro Leu His Tyr
            420                 425                 430

Pro Thr Phe Ala Val Thr Ser Ile Gly Asn Gly Gly Ser Ala Ala Ala
        435                 440                 445

Ile Trp Met Ser Val Ala Val Leu Leu Ala Met Gly Ala Ile Gly Ala
    450                 455                 460

Val Ala Leu Arg Lys Pro Lys Ala Val Ala Val Glu Val Glu Glu Ala
465                 470                 475                 480

Val Asp Ala Asp Ala Asp Gln Ala Ala Ser Glu Ser
                485                 490
```

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<210> 1847
<211> 576
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(553)
<223> RXA00613

<400> 1847
tggcgatacc agctccgagt agggctgcac ttgaaaaagt gagtgtttta gcgatagttg 60

```
acaccttatt caccctacct ggggagtact ctgggcaaac atg agt gaa cta aaa   115
                                              Met Ser Glu Leu Lys
                                                1               5

gac aaa atc cgc gca gat ctg acc acc gct atg aag gcc cgc gac aag   163
Asp Lys Ile Arg Ala Asp Leu Thr Thr Ala Met Lys Ala Arg Asp Lys
                10                  15                  20

gac acc act ggt acc ttg cgc atg ctg ctt tcc gca ttg acc cag gaa   211
Asp Thr Thr Gly Thr Leu Arg Met Leu Leu Ser Ala Leu Thr Gln Glu
            25                  30                  35

gaa aca tcg gga acc aag cac gaa ctc aat gat gaa gaa gtg ttg aag   259
Glu Thr Ser Gly Thr Lys His Glu Leu Asn Asp Glu Glu Val Leu Lys
        40                  45                  50
```

```
gtg att gct cgt gag att aag aag cgt cgc gag tcc gct gag gtg tac   307
Val Ile Ala Arg Glu Ile Lys Lys Arg Arg Glu Ser Ala Glu Val Tyr
     55                  60                  65

acc gaa aat ggt cgt cag gaa ttg gct gac gtt gag ctt aaa gag gct   355
Thr Glu Asn Gly Arg Gln Glu Leu Ala Asp Val Glu Leu Lys Glu Ala
 70                  75                  80                  85

gcc att ttg gag ggc tac cag cct gag cag ctt gat gat gat cag ctg   403
Ala Ile Leu Glu Gly Tyr Gln Pro Glu Gln Leu Asp Asp Asp Gln Leu
                 90                  95                 100

aac gcg ctg atc gat gag gct atc gct gaa gtc ggc ggc gag gcc gat   451
Asn Ala Leu Ile Asp Glu Ala Ile Ala Glu Val Gly Gly Glu Ala Asp
            105                 110                 115

atg aag aag atg ggc cag atc atg aag gct gct acc gct aag gct gct   499
Met Lys Lys Met Gly Gln Ile Met Lys Ala Ala Thr Ala Lys Ala Ala
        120                 125                 130

ggc cgt gca gat gga aaa cga ctc tcc acc gca gtg aag agc cgt ttg   547
Gly Arg Ala Asp Gly Lys Arg Leu Ser Thr Ala Val Lys Ser Arg Leu
    135                 140                 145

agc aac taggtatttc tagcggaaga act                                576
Ser Asn
150
```

<210> 1848
<211> 151
<212> PRT
<213> Corynebacterium glutamicum

<400> 1848

```
Met Ser Glu Leu Lys Asp Lys Ile Arg Ala Asp Leu Thr Thr Ala Met
  1               5                  10                  15

Lys Ala Arg Asp Lys Asp Thr Thr Gly Thr Leu Arg Met Leu Leu Ser
             20                  25                  30

Ala Leu Thr Gln Glu Glu Thr Ser Gly Thr Lys His Glu Leu Asn Asp
         35                  40                  45

Glu Glu Val Leu Lys Val Ile Ala Arg Glu Ile Lys Lys Arg Arg Glu
     50                  55                  60

Ser Ala Glu Val Tyr Thr Glu Asn Gly Arg Gln Glu Leu Ala Asp Val
 65                  70                  75                  80

Glu Leu Lys Glu Ala Ala Ile Leu Glu Gly Tyr Gln Pro Glu Gln Leu
                 85                  90                  95

Asp Asp Asp Gln Leu Asn Ala Leu Ile Asp Glu Ala Ile Ala Glu Val
            100                 105                 110

Gly Gly Glu Ala Asp Met Lys Lys Met Gly Gln Ile Met Lys Ala Ala
        115                 120                 125

Thr Ala Lys Ala Ala Gly Arg Ala Asp Gly Lys Arg Leu Ser Thr Ala
```

```
    130                 135                 140

Val Lys Ser Arg Leu Ser Asn
145                 150


<210> 1849
<211> 1038
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1015)
<223> RXA00614

<400> 1849
cagtggtgtc cttgtcgcgg gccttcatag cggtggtcag atctgcgcgg attttgtctt 60

ttagttcact catgtttgcc cagagtactc cccaggtagg gtg aat aag gtg tca   115
                                            Val Asn Lys Val Ser
                                              1               5

act atc gct aaa aca ctc act ttt tca agt gca gcc cta ctc gga gct   163
Thr Ile Ala Lys Thr Leu Thr Phe Ser Ser Ala Ala Leu Leu Gly Ala
                10                  15                  20

ggt atc gcc acc gct gca tgg gga tac tca gag ctc aaa aaa ttc gag   211
Gly Ile Ala Thr Ala Ala Trp Gly Tyr Ser Glu Leu Lys Lys Phe Glu
            25                  30                  35

ctc aaa aca gta gaa ctg cca att ttg aag cct gga acg ctc cgt gga   259
Leu Lys Thr Val Glu Leu Pro Ile Leu Lys Pro Gly Thr Leu Arg Gly
        40                  45                  50

aag aag gaa ttc cgc ctt ctc cac atc tct gat ctc cac atg atc cca   307
Lys Lys Glu Phe Arg Leu Leu His Ile Ser Asp Leu His Met Ile Pro
    55                  60                  65

ggc caa gaa acc aaa aaa gca tgg gtc tcc gca ctc gat tca cta agc   355
Gly Gln Glu Thr Lys Lys Ala Trp Val Ser Ala Leu Asp Ser Leu Ser
70                  75                  80                  85

ccc gat ttg gtg atc aac acc ggt gac aac ctt agc gat gaa aaa gca   403
Pro Asp Leu Val Ile Asn Thr Gly Asp Asn Leu Ser Asp Glu Lys Ala
                90                  95                  100

gtc ccc gac gtc ctc cgc gca ctc ggc cca ctg atg aac cgc ccc ggc   451
Val Pro Asp Val Leu Arg Ala Leu Gly Pro Leu Met Asn Arg Pro Gly
            105                 110                 115

gcg ttc gtc ttc gga acc aac gat tac tgg gca ccc cgc ccc gtc aat   499
Ala Phe Val Phe Gly Thr Asn Asp Tyr Trp Ala Pro Arg Pro Val Asn
        120                 125                 130

cct ttc ggc tac ctc ttc ggt aaa aaa cgc gaa gtg agc cac atc gac   547
Pro Phe Gly Tyr Leu Phe Gly Lys Lys Arg Glu Val Ser His Ile Asp
    135                 140                 145

ctc ccc tgg cga gcc atg cga gct gct ttc atc gaa cac gga tgg caa   595
Leu Pro Trp Arg Ala Met Arg Ala Ala Phe Ile Glu His Gly Trp Gln
```

```
150                 155                 160                 165

gac gcc aac caa aag cga ctc gaa ttc caa gta ggt tcc gtc cgc ctc   643
Asp Ala Asn Gln Lys Arg Leu Glu Phe Gln Val Gly Ser Val Arg Leu
                170                 175                 180

gcc atc tca ggt gtt gat gac ccc cac cat gac ctc gac gac tac aca   691
Ala Ile Ser Gly Val Asp Asp Pro His His Asp Leu Asp Asp Tyr Thr
            185                 190                 195

gag atc gca ggg gca cca aac gtg gac gct gat ctg tcc ata gcg ttg   739
Glu Ile Ala Gly Ala Pro Asn Val Asp Ala Asp Leu Ser Ile Ala Leu
        200                 205                 210

ctt cac gca cca gaa cct cga gtc ctc gct cag ttc gaa gcc gac ggc   787
Leu His Ala Pro Glu Pro Arg Val Leu Ala Gln Phe Glu Ala Asp Gly
    215                 220                 225

tac cag ctt tcc ctc tcc ggc cac acc cac ggc ggt cag ctt tgt ctt   835
Tyr Gln Leu Ser Leu Ser Gly His Thr His Gly Gly Gln Leu Cys Leu
230                 235                 240                 245

ccg ggc agc aag cca att gtc acc aac tgt gga atc gac cgc aaa cgc   883
Pro Gly Ser Lys Pro Ile Val Thr Asn Cys Gly Ile Asp Arg Lys Arg
                250                 255                 260

gcc acc ggc ctc aac aaa ttt ggc gac atg tgg atg cac gtt tcc aac   931
Ala Thr Gly Leu Asn Lys Phe Gly Asp Met Trp Met His Val Ser Asn
            265                 270                 275

ggc ctc ggc acc tca aaa ttc gtc cca ttc cgc atc ttc tgc cga ccc   979
Gly Leu Gly Thr Ser Lys Phe Val Pro Phe Arg Ile Phe Cys Arg Pro
        280                 285                 290

agc gcc acc cta ata aag atc act gaa cag gca ctt tgacctgaaa        1025
Ser Ala Thr Leu Ile Lys Ile Thr Glu Gln Ala Leu
    295                 300                 305

aacccacagg act                                                   1038
```

<210> 1850
<211> 305
<212> PRT
<213> Corynebacterium glutamicum

<400> 1850

```
Val Asn Lys Val Ser Thr Ile Ala Lys Thr Leu Thr Phe Ser Ser Ala
  1               5                  10                  15

Ala Leu Leu Gly Ala Gly Ile Ala Thr Ala Ala Trp Gly Tyr Ser Glu
             20                  25                  30

Leu Lys Lys Phe Glu Leu Lys Thr Val Glu Leu Pro Ile Leu Lys Pro
         35                  40                  45

Gly Thr Leu Arg Gly Lys Lys Glu Phe Arg Leu Leu His Ile Ser Asp
     50                  55                  60

Leu His Met Ile Pro Gly Gln Glu Thr Lys Lys Ala Trp Val Ser Ala
 65                  70                  75                  80
```

Leu Asp Ser Leu Ser Pro Asp Leu Val Ile Asn Thr Gly Asp Asn Leu
85 90 95

Ser Asp Glu Lys Ala Val Pro Asp Val Leu Arg Ala Leu Gly Pro Leu
100 105 110

Met Asn Arg Pro Gly Ala Phe Val Phe Gly Thr Asn Asp Tyr Trp Ala
115 120 125

Pro Arg Pro Val Asn Pro Phe Gly Tyr Leu Phe Gly Lys Lys Arg Glu
130 135 140

Val Ser His Ile Asp Leu Pro Trp Arg Ala Met Arg Ala Ala Phe Ile
145 150 155 160

Glu His Gly Trp Gln Asp Ala Asn Gln Lys Arg Leu Glu Phe Gln Val
165 170 175

Gly Ser Val Arg Leu Ala Ile Ser Gly Val Asp Asp Pro His His Asp
180 185 190

Leu Asp Asp Tyr Thr Glu Ile Ala Gly Ala Pro Asn Val Asp Ala Asp
195 200 205

Leu Ser Ile Ala Leu Leu His Ala Pro Glu Pro Arg Val Leu Ala Gln
210 215 220

Phe Glu Ala Asp Gly Tyr Gln Leu Ser Leu Ser Gly His Thr His Gly
225 230 235 240

Gly Gln Leu Cys Leu Pro Gly Ser Lys Pro Ile Val Thr Asn Cys Gly
245 250 255

Ile Asp Arg Lys Arg Ala Thr Gly Leu Asn Lys Phe Gly Asp Met Trp
260 265 270

Met His Val Ser Asn Gly Leu Gly Thr Ser Lys Phe Val Pro Phe Arg
275 280 285

Ile Phe Cys Arg Pro Ser Ala Thr Leu Ile Lys Ile Thr Glu Gln Ala
290 295 300

Leu
305

<210> 1851
<211> 1183
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1183)
<223> RXA00617

<400> 1851
acgactggga cgacgactaa ctaacccctg aggcactttc tatttcatgg ctaaatcaac 60

tcctttgatt gcatcgctac gctggcgaat tgtcctgtgg atg aca gcg gtt gtt 115

```
                                                  Met Thr Ala Val Val
                                                    1               5

ttc ttg acc cta gcc agc gtt gtg atc att acc cgt tcg gtg ctg ctt   163
Phe Leu Thr Leu Ala Ser Val Val Ile Ile Thr Arg Ser Val Leu Leu
                10                  15                  20

tca gag gta acc aac acc gcg aac tcg gca gtt gag cag gaa att gag   211
Ser Glu Val Thr Asn Thr Ala Asn Ser Ala Val Glu Gln Glu Ile Glu
            25                  30                  35

gag ttt cgt cgc ttt gca gcc gaa gga att gat cca aca act gcg cag   259
Glu Phe Arg Arg Phe Ala Ala Glu Gly Ile Asp Pro Thr Thr Ala Gln
        40                  45                  50

cct ttt gag tca ggt cat cgc ctg atg gag gtt tac ctg tcg agg cag   307
Pro Phe Glu Ser Gly His Arg Leu Met Glu Val Tyr Leu Ser Arg Gln
    55                  60                  65

att ccg gat gaa aat gaa gcc att gtc ggc att ttc ccc gga gag ctc   355
Ile Pro Asp Glu Asn Glu Ala Ile Val Gly Ile Phe Pro Gly Glu Leu
70                  75                  80                  85

att cag gtt gat tac tcc cag ctc agt ggc gcc cat ccg ctt cct ttg   403
Ile Gln Val Asp Tyr Ser Gln Leu Ser Gly Ala His Pro Leu Pro Leu
                90                  95                  100

gaa cac tcc gat ccg ttg att tcg gaa atc cga cag acc acg ctg aat   451
Glu His Ser Asp Pro Leu Ile Ser Glu Ile Arg Gln Thr Thr Leu Asn
            105                 110                 115

tct gga gtt ttc agc gat ctt gaa cgc gga acc act cac tgg gga aag   499
Ser Gly Val Phe Ser Asp Leu Glu Arg Gly Thr Thr His Trp Gly Lys
        120                 125                 130

gtg aat ttc caa act gct tcc ggt gag gcc gat ggt gag ttc gtt gtc   547
Val Asn Phe Gln Thr Ala Ser Gly Glu Ala Asp Gly Glu Phe Val Val
    135                 140                 145

gca ttc ttc gct gat aat ctt aaa gac cag gtc aac ggc cag atc cag   595
Ala Phe Phe Ala Asp Asn Leu Lys Asp Gln Val Asn Gly Gln Ile Gln
150                 155                 160                 165

att ctt att ttg atc ggc aca ggg ggt ttg att gcc tca att ctg att   643
Ile Leu Ile Leu Ile Gly Thr Gly Gly Leu Ile Ala Ser Ile Leu Ile
                170                 175                 180

gct tgg ttg att gcg ggc cag atc att gcc ccg atc cgc aaa ttg agt   691
Ala Trp Leu Ile Ala Gly Gln Ile Ile Ala Pro Ile Arg Lys Leu Ser
            185                 190                 195

tcc gtg tcc gca aag atc agt aat tcg gat ctc acc tgg cgc gtc cct   739
Ser Val Ser Ala Lys Ile Ser Asn Ser Asp Leu Thr Trp Arg Val Pro
        200                 205                 210

gtg gag ggt cgt gat gag att gcg cag ctg gcc agg act ttt aat gcc   787
Val Glu Gly Arg Asp Glu Ile Ala Gln Leu Ala Arg Thr Phe Asn Ala
    215                 220                 225

atg ttg gat cgc atc gaa atc gcg tat aac gat cag cgc cag ttc gtt   835
Met Leu Asp Arg Ile Glu Ile Ala Tyr Asn Asp Gln Arg Gln Phe Val
```

```
230                 235                 240                 245

gat gat gcc ggc cac gag ctg cgc acc ccg atc aca gtg gtg cgt ggc   883
Asp Asp Ala Gly His Glu Leu Arg Thr Pro Ile Thr Val Val Arg Gly
                250                 255                 260

cag tta gag ctt ctc gcc acc acc ccg ccg gag gaa caa gcg cgg tcg   931
Gln Leu Glu Leu Leu Ala Thr Thr Pro Pro Glu Glu Gln Ala Arg Ser
            265                 270                 275

att gag ctg gcc acc act gag ttg gat cga atg tcg cga atg gtc aat   979
Ile Glu Leu Ala Thr Thr Glu Leu Asp Arg Met Ser Arg Met Val Asn
        280                 285                 290

gat ctg ctc acc ctc gca gtc gcc gat tct ggc acc ttc atc cac gcc   1027
Asp Leu Leu Thr Leu Ala Val Ala Asp Ser Gly Thr Phe Ile His Ala
    295                 300                 305

cac ccc acg gat gtc acg gat tta aca atc gat atc gaa gac aaa gcc   1075
His Pro Thr Asp Val Thr Asp Leu Thr Ile Asp Ile Glu Asp Lys Ala
310                 315                 320                 325

cgc acc atc agc gac cga att ttg ctt gtc gac gcc gcc gag ggc ctc   1123
Arg Thr Ile Ser Asp Arg Ile Leu Leu Val Asp Ala Ala Glu Gly Leu
                330                 335                 340

gtc agc ctc gac gag cag cgg gtc acc gag gca gtg ctg gag ttg ttc   1171
Val Ser Leu Asp Glu Gln Arg Val Thr Glu Ala Val Leu Glu Leu Phe
            345                 350                 355

ggc aat gcg ttg                                                  1183
Gly Asn Ala Leu
        360
```

<210> 1852
<211> 361
<212> PRT
<213> Corynebacterium glutamicum

<400> 1852

```
Met Thr Ala Val Val Phe Leu Thr Leu Ala Ser Val Val Ile Ile Thr
  1               5                  10                  15

Arg Ser Val Leu Leu Ser Glu Val Thr Asn Thr Ala Asn Ser Ala Val
             20                  25                  30

Glu Gln Glu Ile Glu Glu Phe Arg Arg Phe Ala Ala Glu Gly Ile Asp
         35                  40                  45

Pro Thr Thr Ala Gln Pro Phe Glu Ser Gly His Arg Leu Met Glu Val
     50                  55                  60

Tyr Leu Ser Arg Gln Ile Pro Asp Glu Asn Glu Ala Ile Val Gly Ile
 65                  70                  75                  80

Phe Pro Gly Glu Leu Ile Gln Val Asp Tyr Ser Gln Leu Ser Gly Ala
                 85                  90                  95

His Pro Leu Pro Leu Glu His Ser Asp Pro Leu Ile Ser Glu Ile Arg
            100                 105                 110
```

```
Gln Thr Thr Leu Asn Ser Gly Val Phe Ser Asp Leu Glu Arg Gly Thr
        115                 120                 125

Thr His Trp Gly Lys Val Asn Phe Gln Thr Ala Ser Gly Glu Ala Asp
    130                 135                 140

Gly Glu Phe Val Val Ala Phe Phe Ala Asp Asn Leu Lys Asp Gln Val
145                 150                 155                 160

Asn Gly Gln Ile Gln Ile Leu Ile Leu Ile Gly Thr Gly Gly Leu Ile
                165                 170                 175

Ala Ser Ile Leu Ile Ala Trp Leu Ile Ala Gly Gln Ile Ile Ala Pro
            180                 185                 190

Ile Arg Lys Leu Ser Ser Val Ser Ala Lys Ile Ser Asn Ser Asp Leu
        195                 200                 205

Thr Trp Arg Val Pro Val Glu Gly Arg Asp Glu Ile Ala Gln Leu Ala
    210                 215                 220

Arg Thr Phe Asn Ala Met Leu Asp Arg Ile Glu Ile Ala Tyr Asn Asp
225                 230                 235                 240

Gln Arg Gln Phe Val Asp Asp Ala Gly His Glu Leu Arg Thr Pro Ile
                245                 250                 255

Thr Val Val Arg Gly Gln Leu Glu Leu Leu Ala Thr Thr Pro Pro Glu
            260                 265                 270

Glu Gln Ala Arg Ser Ile Glu Leu Ala Thr Thr Glu Leu Asp Arg Met
        275                 280                 285

Ser Arg Met Val Asn Asp Leu Leu Thr Leu Ala Val Ala Asp Ser Gly
    290                 295                 300

Thr Phe Ile His Ala His Pro Thr Asp Val Thr Asp Leu Thr Ile Asp
305                 310                 315                 320

Ile Glu Asp Lys Ala Arg Thr Ile Ser Asp Arg Ile Leu Leu Val Asp
                325                 330                 335

Ala Ala Glu Gly Leu Val Ser Leu Asp Glu Gln Arg Val Thr Glu Ala
            340                 345                 350

Val Leu Glu Leu Phe Gly Asn Ala Leu
        355                 360
```

<210> 1853
<211> 531
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(508)
<223> RXA00628

<400> 1853

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ggttgaaagt ggcgtcgaaa agcgccttaa aatgaccggc tcacctgcat tattttatgc 60

aacctcaatt tggttgcacg ccaagtagta gtctgtgcat atg gct tct gta ttc   115
                                              Met Ala Ser Val Phe
                                                1               5

acg aaa att att aat ggc gag ctc ccc ggc cga ttt gtg tat cgt tcc   163
Thr Lys Ile Ile Asn Gly Glu Leu Pro Gly Arg Phe Val Tyr Arg Ser
                  10                  15                  20

gag aat gtc gtg gct ttt cta tcc atc gaa ccc ctc acc tac ggc cac   211
Glu Asn Val Val Ala Phe Leu Ser Ile Glu Pro Leu Thr Tyr Gly His
              25                  30                  35

acc cta gtc gta ccc gtt gca gaa gtt gac cgc tgg acc gac ctt cct   259
Thr Leu Val Val Pro Val Ala Glu Val Asp Arg Trp Thr Asp Leu Pro
          40                  45                  50

cag aac atc tgg agc gaa gta aac gag gcc tcc cag ctc atc gga aat   307
Gln Asn Ile Trp Ser Glu Val Asn Glu Ala Ser Gln Leu Ile Gly Asn
      55                  60                  65

gca atc cgc aca gca ttc gac gcc cct cga tgt ggt tac atc atc gca   355
Ala Ile Arg Thr Ala Phe Asp Ala Pro Arg Cys Gly Tyr Ile Ile Ala
  70                  75                  80                  85

gga ttc gat gtt ccc cac act cac atc cac ctc ttc ccc acc gac aaa   403
Gly Phe Asp Val Pro His Thr His Ile His Leu Phe Pro Thr Asp Lys
                  90                  95                 100

atg gcc gat tac gat ttc cgc aac gcc atg gcc gca gac gcc acc gac   451
Met Ala Asp Tyr Asp Phe Arg Asn Ala Met Ala Ala Asp Ala Thr Asp
              105                 110                 115

cct gca aaa atg gat gaa gct gca gag aag atc cgc gaa gcg ctg gac   499
Pro Ala Lys Met Asp Glu Ala Ala Glu Lys Ile Arg Glu Ala Leu Asp
          120                 125                 130

ggt ctg gtc tagttcttgt agttctaatt gct                            531
Gly Leu Val
    135


<210> 1854
<211> 136
<212> PRT
<213> Corynebacterium glutamicum

<400> 1854
Met Ala Ser Val Phe Thr Lys Ile Ile Asn Gly Glu Leu Pro Gly Arg
  1               5                  10                  15

Phe Val Tyr Arg Ser Glu Asn Val Val Ala Phe Leu Ser Ile Glu Pro
              20                  25                  30

Leu Thr Tyr Gly His Thr Leu Val Val Pro Val Ala Glu Val Asp Arg
          35                  40                  45

Trp Thr Asp Leu Pro Gln Asn Ile Trp Ser Glu Val Asn Glu Ala Ser
      50                  55                  60
```

```
Gln Leu Ile Gly Asn Ala Ile Arg Thr Ala Phe Asp Ala Pro Arg Cys
 65                  70                  75                  80

Gly Tyr Ile Ile Ala Gly Phe Asp Val Pro His Thr His Ile His Leu
                 85                  90                  95

Phe Pro Thr Asp Lys Met Ala Asp Tyr Asp Phe Arg Asn Ala Met Ala
            100                 105                 110

Ala Asp Ala Thr Asp Pro Ala Lys Met Asp Glu Ala Ala Glu Lys Ile
        115                 120                 125

Arg Glu Ala Leu Asp Gly Leu Val
    130                 135


<210> 1855
<211> 1578
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1555)
<223> RXA00631

<400> 1855
cctacctgcg ccgcaaggtg gacacccagg atccgcagct aattcagact gttcgtggcg 60

ttggatatgt tctgcgcacc ccacgtagct aaattctcct atg gaa aat cct tat   115
                                            Met Glu Asn Pro Tyr
                                              1               5

gtt gct gcg ctc gat gac gaa aac caa gaa gtc ggc gta aaa aaa gaa   163
Val Ala Ala Leu Asp Asp Glu Asn Gln Glu Val Gly Val Lys Lys Glu
                 10                  15                  20

gca gaa aaa gaa cct gaa ata ggt ccc atc aga gct gcc gga cga gcc   211
Ala Glu Lys Glu Pro Glu Ile Gly Pro Ile Arg Ala Ala Gly Arg Ala
             25                  30                  35

ata ccg ctg cgc acc cgc atc att ttg atc gtg gtg ggt atc gcc ggg   259
Ile Pro Leu Arg Thr Arg Ile Ile Leu Ile Val Val Gly Ile Ala Gly
         40                  45                  50

ctt ggt ttg ctg gtc aac gcg att gct gtc tcc agc ctc atg cgt gaa   307
Leu Gly Leu Leu Val Asn Ala Ile Ala Val Ser Ser Leu Met Arg Glu
     55                  60                  65

gtt tcc tat acc cgc atg gat caa gag cta gag acc tcg atg ggg acg   355
Val Ser Tyr Thr Arg Met Asp Gln Glu Leu Glu Thr Ser Met Gly Thr
 70                  75                  80                  85

tgg gcg cat aac gtt gag ctg ttt aat ttc gat ggc gtc cgc caa ggg   403
Trp Ala His Asn Val Glu Leu Phe Asn Phe Asp Gly Val Arg Gln Gly
                 90                  95                 100

cca ccc agc gat tat tat gtg gcc aag gtt ttt cct gat gga tcc agc   451
Pro Pro Ser Asp Tyr Tyr Val Ala Lys Val Phe Pro Asp Gly Ser Ser
            105                 110                 115
```

```
atc atc ttc aac gat gca caa tcg gca ccc gat cta gct gaa acc acc   499
Ile Ile Phe Asn Asp Ala Gln Ser Ala Pro Asp Leu Ala Glu Thr Thr
        120                 125                 130

atc ggt act ggt cca cac act gtg gat gct gct agc ggt tct gcc tcc   547
Ile Gly Thr Gly Pro His Thr Val Asp Ala Ala Ser Gly Ser Ala Ser
    135                 140                 145

aac act ccg tgg cgt gtg atg gcg gaa aag aac ggt gac att atc acc   595
Asn Thr Pro Trp Arg Val Met Ala Glu Lys Asn Gly Asp Ile Ile Thr
150                 155                 160                 165

gtg gtg ggt aaa agc atg ggg cgt gaa aca aac ctg ctg tac cga ttg   643
Val Val Gly Lys Ser Met Gly Arg Glu Thr Asn Leu Leu Tyr Arg Leu
                170                 175                 180

gtg atg gtg cag atg atc atc ggc gcg ctg att ctg gtt gct att ttg   691
Val Met Val Gln Met Ile Ile Gly Ala Leu Ile Leu Val Ala Ile Leu
            185                 190                 195

att act tca ctc ttc cta gtc aga cgc tcg ttg cgg ccg ttg aga gaa   739
Ile Thr Ser Leu Phe Leu Val Arg Arg Ser Leu Arg Pro Leu Arg Glu
        200                 205                 210

gtt gaa gag acc gcc acc agg att gcg ggc ggt gat ttg gat cga cgt   787
Val Glu Glu Thr Ala Thr Arg Ile Ala Gly Gly Asp Leu Asp Arg Arg
    215                 220                 225

gtc ccg cag tgg cca atg acc aca gaa gtc gga cag ctg tcg aat gcc   835
Val Pro Gln Trp Pro Met Thr Thr Glu Val Gly Gln Leu Ser Asn Ala
230                 235                 240                 245

ctc aat atc atg ttg gag cag ctc caa gcc tca att ctg acc gcc cag   883
Leu Asn Ile Met Leu Glu Gln Leu Gln Ala Ser Ile Leu Thr Ala Gln
                250                 255                 260

caa aaa gaa gct cag atg cgc cga ttc gtt ggc gat gcc tcc cac gag   931
Gln Lys Glu Ala Gln Met Arg Arg Phe Val Gly Asp Ala Ser His Glu
            265                 270                 275

ctc cgc aca cca ctg acc tct gtg aag ggc ttc acc gag ctg tat tca   979
Leu Arg Thr Pro Leu Thr Ser Val Lys Gly Phe Thr Glu Leu Tyr Ser
        280                 285                 290

tca ggt gca aca gat gat gcc aac tgg gtc atg tcc aag atc ggt ggc   1027
Ser Gly Ala Thr Asp Asp Ala Asn Trp Val Met Ser Lys Ile Gly Gly
    295                 300                 305

gaa gcc caa cgc atg agt gtg ctt gtg gaa gac ctc ctg tca ctg acg   1075
Glu Ala Gln Arg Met Ser Val Leu Val Glu Asp Leu Leu Ser Leu Thr
310                 315                 320                 325

cgt gcc gaa ggc cag caa atg gag aag cac cgc gtt gac gtg ctg gaa   1123
Arg Ala Glu Gly Gln Gln Met Glu Lys His Arg Val Asp Val Leu Glu
                330                 335                 340

ctc gcc ttg gca gta cgc gga tcc atg cga gca gcc tgg cca gat cgc   1171
Leu Ala Leu Ala Val Arg Gly Ser Met Arg Ala Ala Trp Pro Asp Arg
            345                 350                 355

aca gtc aat gta tcc aac aaa gct gag tcc att ccg gtt gtc aaa ggc   1219
```

```
Thr Val Asn Val Ser Asn Lys Ala Glu Ser Ile Pro Val Val Lys Gly
        360                 365                 370

gac cca act cgc ctc cac caa gtg ctt acc aac ctg gtt gcc aac gga   1267
Asp Pro Thr Arg Leu His Gln Val Leu Thr Asn Leu Val Ala Asn Gly
    375                 380                 385

cta aac cac ggc gga ccg gac gcg gaa gtc agc att gag atc aac acc   1315
Leu Asn His Gly Gly Pro Asp Ala Glu Val Ser Ile Glu Ile Asn Thr
390                 395                 400                 405

gat gga caa aac gtg agg att ctc gtg gca gac aac ggt gtc gga atg   1363
Asp Gly Gln Asn Val Arg Ile Leu Val Ala Asp Asn Gly Val Gly Met
                410                 415                 420

tct gaa gaa gat gct cag cat atc ttc gag cgt ttc tac cgc gcc gat   1411
Ser Glu Glu Asp Ala Gln His Ile Phe Glu Arg Phe Tyr Arg Ala Asp
            425                 430                 435

tcc tcc cgc tca cgc gca tcc ggc gga tcg ggc ctc ggc ctt gcg atc   1459
Ser Ser Arg Ser Arg Ala Ser Gly Gly Ser Gly Leu Gly Leu Ala Ile
        440                 445                 450

acg aaa tcc ctg gtc gaa ggc cac ggc ggc aca gtc acc gtc gac agc   1507
Thr Lys Ser Leu Val Glu Gly His Gly Gly Thr Val Thr Val Asp Ser
    455                 460                 465

gtg caa ggc gaa ggc acg gtg ttc acg atc acc ttg ccg gcg gtt tct   1555
Val Gln Gly Glu Gly Thr Val Phe Thr Ile Thr Leu Pro Ala Val Ser
470                 475                 480                 485

taaaggcatc aagggccgga aaa                                        1578


<210> 1856
<211> 485
<212> PRT
<213> Corynebacterium glutamicum

<400> 1856
Met Glu Asn Pro Tyr Val Ala Ala Leu Asp Asp Glu Asn Gln Glu Val
  1               5                  10                  15

Gly Val Lys Lys Glu Ala Glu Lys Glu Pro Glu Ile Gly Pro Ile Arg
             20                  25                  30

Ala Ala Gly Arg Ala Ile Pro Leu Arg Thr Arg Ile Ile Leu Ile Val
         35                  40                  45

Val Gly Ile Ala Gly Leu Gly Leu Leu Val Asn Ala Ile Ala Val Ser
     50                  55                  60

Ser Leu Met Arg Glu Val Ser Tyr Thr Arg Met Asp Gln Glu Leu Glu
 65                  70                  75                  80

Thr Ser Met Gly Thr Trp Ala His Asn Val Glu Leu Phe Asn Phe Asp
                 85                  90                  95

Gly Val Arg Gln Gly Pro Pro Ser Asp Tyr Tyr Val Ala Lys Val Phe
            100                 105                 110
```

Pro Asp Gly Ser Ser Ile Ile Phe Asn Asp Ala Gln Ser Ala Pro Asp
115 120 125

Leu Ala Glu Thr Thr Ile Gly Thr Gly Pro His Thr Val Asp Ala Ala
130 135 140

Ser Gly Ser Ala Ser Asn Thr Pro Trp Arg Val Met Ala Glu Lys Asn
145 150 155 160

Gly Asp Ile Ile Thr Val Val Gly Lys Ser Met Gly Arg Glu Thr Asn
165 170 175

Leu Leu Tyr Arg Leu Val Met Val Gln Met Ile Ile Gly Ala Leu Ile
180 185 190

Leu Val Ala Ile Leu Ile Thr Ser Leu Phe Leu Val Arg Arg Ser Leu
195 200 205

Arg Pro Leu Arg Glu Val Glu Glu Thr Ala Thr Arg Ile Ala Gly Gly
210 215 220

Asp Leu Asp Arg Arg Val Pro Gln Trp Pro Met Thr Thr Glu Val Gly
225 230 235 240

Gln Leu Ser Asn Ala Leu Asn Ile Met Leu Glu Gln Leu Gln Ala Ser
245 250 255

Ile Leu Thr Ala Gln Gln Lys Glu Ala Gln Met Arg Arg Phe Val Gly
260 265 270

Asp Ala Ser His Glu Leu Arg Thr Pro Leu Thr Ser Val Lys Gly Phe
275 280 285

Thr Glu Leu Tyr Ser Ser Gly Ala Thr Asp Asp Ala Asn Trp Val Met
290 295 300

Ser Lys Ile Gly Gly Glu Ala Gln Arg Met Ser Val Leu Val Glu Asp
305 310 315 320

Leu Leu Ser Leu Thr Arg Ala Glu Gly Gln Gln Met Glu Lys His Arg
325 330 335

Val Asp Val Leu Glu Leu Ala Leu Ala Val Arg Gly Ser Met Arg Ala
340 345 350

Ala Trp Pro Asp Arg Thr Val Asn Val Ser Asn Lys Ala Glu Ser Ile
355 360 365

Pro Val Val Lys Gly Asp Pro Thr Arg Leu His Gln Val Leu Thr Asn
370 375 380

Leu Val Ala Asn Gly Leu Asn His Gly Gly Pro Asp Ala Glu Val Ser
385 390 395 400

Ile Glu Ile Asn Thr Asp Gly Gln Asn Val Arg Ile Leu Val Ala Asp
405 410 415

Asn Gly Val Gly Met Ser Glu Glu Asp Ala Gln His Ile Phe Glu Arg
420 425 430

Phe Tyr Arg Ala Asp Ser Ser Arg Ser Arg Ala Ser Gly Gly Ser Gly

```
        435                 440                 445

Leu Gly Leu Ala Ile Thr Lys Ser Leu Val Glu Gly His Gly Gly Thr
    450                 455                 460

Val Thr Val Asp Ser Val Gln Gly Glu Gly Thr Val Phe Thr Ile Thr
465                 470                 475                 480

Leu Pro Ala Val Ser
                485


<210> 1857
<211> 876
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(853)
<223> RXA00637

<400> 1857
ccgatggcac tttccgtacc tggaaggtag ttgcccgcgg cagaaacaat tagggaaacc 60

tcttgacctt cacgcgacgt caaggattta actaacagtc atg aca gat cga acc   115
                                              Met Thr Asp Arg Thr
                                                1               5

att ggc gag gct gct gaa cta ctc ggt gtc acc acc cgc aca ctg cgg   163
Ile Gly Glu Ala Ala Glu Leu Leu Gly Val Thr Thr Arg Thr Leu Arg
                10                  15                  20

cat tgg gac agc atc ggg ttg ctt caa ccg agc tgg cga acc aca acg   211
His Trp Asp Ser Ile Gly Leu Leu Gln Pro Ser Trp Arg Thr Thr Thr
            25                  30                  35

gat tat cgc ctt tac aca gaa gac gat gtc gag cgc gcc ctg cag att   259
Asp Tyr Arg Leu Tyr Thr Glu Asp Asp Val Glu Arg Ala Leu Gln Ile
        40                  45                  50

ctt att tac agg gcc gcc gga atc ggg ttg aag gat att gcg gag gtg   307
Leu Ile Tyr Arg Ala Ala Gly Ile Gly Leu Lys Asp Ile Ala Glu Val
    55                  60                  65

ctt gat cag ccg gat tcg gcc aat cag cac ctg cgc cgc cag cgg gaa   355
Leu Asp Gln Pro Asp Ser Ala Asn Gln His Leu Arg Arg Gln Arg Glu
70                  75                  80                  85

ctc cta gtg gaa cag atc ggt cag ctg cat cgg atg gtc cgg gca gta   403
Leu Leu Val Glu Gln Ile Gly Gln Leu His Arg Met Val Arg Ala Val
                90                  95                  100

gat gaa atc ctt gga aag gat gcg att agc gtg aag gaa aag att gag   451
Asp Glu Ile Leu Gly Lys Asp Ala Ile Ser Val Lys Glu Lys Ile Glu
            105                 110                 115

atc ttc ggc gag gat ctg ccc aag tac caa gag gag gct ttc cag cgc   499
Ile Phe Gly Glu Asp Leu Pro Lys Tyr Gln Glu Glu Ala Phe Gln Arg
        120                 125                 130
```

```
tgg ggc gac acc ccg gag tgg aaa gaa tcc caa aag atc cag gag aag   547
Trp Gly Asp Thr Pro Glu Trp Lys Glu Ser Gln Lys Ile Gln Glu Lys
    135                 140                 145

atg acc aag gag gat ttt cag agg gcg aaa gat gaa cat gag ggg ttc   595
Met Thr Lys Glu Asp Phe Gln Arg Ala Lys Asp Glu His Glu Gly Phe
150                 155                 160                 165

gtc gaa aag ctt atc gac gcc tcc ctg cgc ggc atc gcg ccc ggc tct   643
Val Glu Lys Leu Ile Asp Ala Ser Leu Arg Gly Ile Ala Pro Gly Ser
                170                 175                 180

gca gag ggc aat gag cta gcg ctt gcg cac cgc gca agc atc ggt cag   691
Ala Glu Gly Asn Glu Leu Ala Leu Ala His Arg Ala Ser Ile Gly Gln
            185                 190                 195

tgg tac acc gtg agt gca aac aag caa gta att ttg gct cgg atg tac   739
Trp Tyr Thr Val Ser Ala Asn Lys Gln Val Ile Leu Ala Arg Met Tyr
        200                 205                 210

gtg gaa gac gag cgt ttt aac gaa act tac aaa gga cac gcc tca tat   787
Val Glu Asp Glu Arg Phe Asn Glu Thr Tyr Lys Gly His Ala Ser Tyr
    215                 220                 225

ctt tta aca ctt att gaa gca ttg gcg cag gta gaa ggc gtg gac ttg   835
Leu Leu Thr Leu Ile Glu Ala Leu Ala Gln Val Glu Gly Val Asp Leu
230                 235                 240                 245

gag aat gtg gag tgg gaa taatcccaat ttcaactctt tca                876
Glu Asn Val Glu Trp Glu
                250
```

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<210> 1858
<211> 251
<212> PRT
<213> Corynebacterium glutamicum

<400> 1858

```
Met Thr Asp Arg Thr Ile Gly Glu Ala Ala Glu Leu Leu Gly Val Thr
  1               5                  10                  15

Thr Arg Thr Leu Arg His Trp Asp Ser Ile Gly Leu Leu Gln Pro Ser
             20                  25                  30

Trp Arg Thr Thr Thr Asp Tyr Arg Leu Tyr Thr Glu Asp Asp Val Glu
         35                  40                  45

Arg Ala Leu Gln Ile Leu Ile Tyr Arg Ala Ala Gly Ile Gly Leu Lys
     50                  55                  60

Asp Ile Ala Glu Val Leu Asp Gln Pro Asp Ser Ala Asn Gln His Leu
 65                  70                  75                  80

Arg Arg Gln Arg Glu Leu Leu Val Glu Gln Ile Gly Gln Leu His Arg
                 85                  90                  95

Met Val Arg Ala Val Asp Glu Ile Leu Gly Lys Asp Ala Ile Ser Val
            100                 105                 110

Lys Glu Lys Ile Glu Ile Phe Gly Glu Asp Leu Pro Lys Tyr Gln Glu
```

```
        115                 120                 125

Glu Ala Phe Gln Arg Trp Gly Asp Thr Pro Glu Trp Lys Glu Ser Gln
    130                 135                 140

Lys Ile Gln Glu Lys Met Thr Lys Glu Asp Phe Gln Arg Ala Lys Asp
145                 150                 155                 160

Glu His Glu Gly Phe Val Glu Lys Leu Ile Asp Ala Ser Leu Arg Gly
                165                 170                 175

Ile Ala Pro Gly Ser Ala Glu Gly Asn Glu Leu Ala Leu Ala His Arg
            180                 185                 190

Ala Ser Ile Gly Gln Trp Tyr Thr Val Ser Ala Asn Lys Gln Val Ile
        195                 200                 205

Leu Ala Arg Met Tyr Val Glu Asp Glu Arg Phe Asn Glu Thr Tyr Lys
    210                 215                 220

Gly His Ala Ser Tyr Leu Leu Thr Leu Ile Glu Ala Leu Ala Gln Val
225                 230                 235                 240

Glu Gly Val Asp Leu Glu Asn Val Glu Trp Glu
                245                 250


<210> 1859
<211> 541
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(541)
<223> RXA00646

<400> 1859
aatgcaatcg gaacggttaa cgccaagtga tctggtggga tgtaggtacc gtcaggtcca 60

gcgcataaat ttcccagaaa tctctccttt acctgcaaca atg cag cgc agg gcc   115
                                               Met Gln Arg Arg Ala
                                                 1               5

cgc cgt gag gtt ggg ttg acg gaa gtt ttg gat cgt ctc cca gag cag   163
Arg Arg Glu Val Gly Leu Thr Glu Val Leu Asp Arg Leu Pro Glu Gln
                 10                  15                  20

ccc aaa aag cgg ggc cga att cct ttc acc agg gca gat cta gac aat   211
Pro Lys Lys Arg Gly Arg Ile Pro Phe Thr Arg Ala Asp Leu Asp Asn
             25                  30                  35

gac gct gaa ttg gcg gag ttt gaa acc ctc gaa gca att gca gcc ggc   259
Asp Ala Glu Leu Ala Glu Phe Glu Thr Leu Glu Ala Ile Ala Ala Gly
         40                  45                  50

gac acc ttg att acc ggc gca gtg ttc acg ggc acc ctc gaa ggg gtg   307
Asp Thr Leu Ile Thr Gly Ala Val Phe Thr Gly Thr Leu Glu Gly Val
     55                  60                  65

gca tgg gaa gtg caa gtg gat gtc ttg gtg cgc aac cct gat gga agc   355
```

```
Ala Trp Glu Val Gln Val Asp Val Leu Val Arg Asn Pro Asp Gly Ser
 70                  75                  80                  85

tac atg ccc gtg atg gtg agc aat cac cgt gtc gcc cgt ccg gat ccg   403
Tyr Met Pro Val Met Val Ser Asn His Arg Val Ala Arg Pro Asp Pro
                 90                  95                 100

cac aaa act atg cag ggc att gcc gtc acc cgc ctc ggt ttg ggt cag   451
His Lys Thr Met Gln Gly Ile Ala Val Thr Arg Leu Gly Leu Gly Gln
            105                 110                 115

ccg cta gag ctc aag gca acg ctg cgc cac cac acg atc gat ggc tat   499
Pro Leu Glu Leu Lys Ala Thr Leu Arg His His Thr Ile Asp Gly Tyr
        120                 125                 130

cgc ctc acc ctc gcg ttg atg ggt ttg gag gaa gct gga gca           541
Arg Leu Thr Leu Ala Leu Met Gly Leu Glu Glu Ala Gly Ala
    135                 140                 145
```

<210> 1860
<211> 147
<212> PRT
<213> Corynebacterium glutamicum

<400> 1860

```
Met Gln Arg Arg Ala Arg Arg Glu Val Gly Leu Thr Glu Val Leu Asp
  1               5                  10                  15

Arg Leu Pro Glu Gln Pro Lys Lys Arg Gly Arg Ile Pro Phe Thr Arg
             20                  25                  30

Ala Asp Leu Asp Asn Asp Ala Glu Leu Ala Glu Phe Glu Thr Leu Glu
         35                  40                  45

Ala Ile Ala Ala Gly Asp Thr Leu Ile Thr Gly Ala Val Phe Thr Gly
     50                  55                  60

Thr Leu Glu Gly Val Ala Trp Glu Val Gln Val Asp Val Leu Val Arg
 65                  70                  75                  80

Asn Pro Asp Gly Ser Tyr Met Pro Val Met Val Ser Asn His Arg Val
                 85                  90                  95

Ala Arg Pro Asp Pro His Lys Thr Met Gln Gly Ile Ala Val Thr Arg
            100                 105                 110

Leu Gly Leu Gly Gln Pro Leu Glu Leu Lys Ala Thr Leu Arg His His
        115                 120                 125

Thr Ile Asp Gly Tyr Arg Leu Thr Leu Ala Leu Met Gly Leu Glu Glu
    130                 135                 140

Ala Gly Ala
145
```

<210> 1861
<211> 579
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> RXA00649

<400> 1861
gtatttgatc tgtggtgtgg ctgattcggg aggactcgat gacattatgt gtatggtaca 60

cattttgtgc aagatgcaat agctggcaaa ctggagagcc atg agc acc gac ccc 115
Met Ser Thr Asp Pro
1 5

atc gcg gcc ttg gaa tac gaa tcc acc atc ttc gcc cgt cac cgg aat 163
Ile Ala Ala Leu Glu Tyr Glu Ser Thr Ile Phe Ala Arg His Arg Asn
10 15 20

caa tac acc ggc caa gca ggt acg aat gct ggc gtc ctc gat tcc agc 211
Gln Tyr Thr Gly Gln Ala Gly Thr Asn Ala Gly Val Leu Asp Ser Ser
25 30 35

ggc tac aac cta ctc acg ctg ctc cag tta cgt ggc ccc tcc acc atc 259
Gly Tyr Asn Leu Leu Thr Leu Leu Gln Leu Arg Gly Pro Ser Thr Ile
40 45 50

ggc gaa ctc agc gcc atc acc ggc cta gac gca tct acc ctt aac cgt 307
Gly Glu Leu Ser Ala Ile Thr Gly Leu Asp Ala Ser Thr Leu Asn Arg
55 60 65

cag aca aaa gcc cta cta acc aaa gga ttt gtc gaa cgc atc cca gat 355
Gln Thr Lys Ala Leu Leu Thr Lys Gly Phe Val Glu Arg Ile Pro Asp
70 75 80 85

ccc gac ggt gga atc gct cgg aaa ttc cac ccc acc gac ctc ggc aat 403
Pro Asp Gly Gly Ile Ala Arg Lys Phe His Pro Thr Asp Leu Gly Asn
90 95 100

gaa ctg ctc aac gag gaa cgc aca tcc agc caa gaa aaa tat gcc gag 451
Glu Leu Leu Asn Glu Glu Arg Thr Ser Ser Gln Glu Lys Tyr Ala Glu
105 110 115

tta ctt tca gac tgg ccc gaa gag gat cta cgc acc ttc gtc aaa ctt 499
Leu Leu Ser Asp Trp Pro Glu Glu Asp Leu Arg Thr Phe Val Lys Leu
120 125 130

ctt gaa aaa cta aat aaa gcc gtg gag aca cgc gtc gga aag cat tgg 547
Leu Glu Lys Leu Asn Lys Ala Val Glu Thr Arg Val Gly Lys His Trp
135 140 145

ccg cgc ccc tgactcagcc caagccagag ccc 579
Pro Arg Pro
150

<210> 1862
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 1862
Met Ser Thr Asp Pro Ile Ala Ala Leu Glu Tyr Glu Ser Thr Ile Phe

```
  1               5                  10                  15

Ala Arg His Arg Asn Gln Tyr Thr Gly Gln Ala Gly Thr Asn Ala Gly
            20                  25                  30

Val Leu Asp Ser Ser Gly Tyr Asn Leu Leu Thr Leu Leu Gln Leu Arg
        35                  40                  45

Gly Pro Ser Thr Ile Gly Glu Leu Ser Ala Ile Thr Gly Leu Asp Ala
    50                  55                  60

Ser Thr Leu Asn Arg Gln Thr Lys Ala Leu Leu Thr Lys Gly Phe Val
65                  70                  75                  80

Glu Arg Ile Pro Asp Pro Asp Gly Gly Ile Ala Arg Lys Phe His Pro
                85                  90                  95

Thr Asp Leu Gly Asn Glu Leu Leu Asn Glu Glu Arg Thr Ser Ser Gln
            100                 105                 110

Glu Lys Tyr Ala Glu Leu Leu Ser Asp Trp Pro Glu Glu Asp Leu Arg
        115                 120                 125

Thr Phe Val Lys Leu Leu Glu Lys Leu Asn Lys Ala Val Glu Thr Arg
    130                 135                 140

Val Gly Lys His Trp Pro Arg Pro
145                 150


<210> 1863
<211> 672
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(649)
<223> RXA00652

<400> 1863
gcgatagctc atcgcgcccg gttgattccc cttcttcaca agggtttcaa catcgagctc 60

attgcgtccg gtttccgaca cacgatctag gcttgactgc atg cgt cgt aca tta   115
                                            Met Arg Arg Thr Leu
                                              1               5

cct act atc ctc gct gct tcc atc atg ctc acc gct tgt acc ccg gcg   163
Pro Thr Ile Leu Ala Ala Ser Ile Met Leu Thr Ala Cys Thr Pro Ala
                10                  15                  20

gaa cct gaa gca acc cca gag acc acc acc gag gca gcc ccg gaa gta   211
Glu Pro Glu Ala Thr Pro Glu Thr Thr Thr Glu Ala Ala Pro Glu Val
            25                  30                  35

att act gac ggc ctt ccc atc gac gcg atg ccc gcg gtc gaa cgc acc   259
Ile Thr Asp Gly Leu Pro Ile Asp Ala Met Pro Ala Val Glu Arg Thr
        40                  45                  50

gca caa acc gca tgc ccc tac ctg ggc acc gac tgg gtc gcc gat acc   307
Ala Gln Thr Ala Cys Pro Tyr Leu Gly Thr Asp Trp Val Ala Asp Thr
```

```
     55                  60                  65

aac ggc cag cgc gtc acg ggt tac ggc aca gac gaa cgc ttt tcg acg   355
Asn Gly Gln Arg Val Thr Gly Tyr Gly Thr Asp Glu Arg Phe Ser Thr
 70                  75                  80                  85

ccc tcc tgc gtt ttt tac tcc tac ccc gaa gaa cca caa ctc acg gtg   403
Pro Ser Cys Val Phe Tyr Ser Tyr Pro Glu Glu Pro Gln Leu Thr Val
                 90                  95                 100

att gtc cgc gat atg gcc acc acg gat gac gct atc gcg gta gtg gat   451
Ile Val Arg Asp Met Ala Thr Thr Asp Asp Ala Ile Ala Val Val Asp
            105                 110                 115

tgg gca gcc ccc atc gat tcc act gag ccc gct gag gaa ccc gca ggg   499
Trp Ala Ala Pro Ile Asp Ser Thr Glu Pro Ala Glu Glu Pro Ala Gly
        120                 125                 130

tgg tcc ggt ggc cgc cga ggt gga aac gat act tca ggc gca ctc tac   547
Trp Ser Gly Gly Arg Arg Gly Gly Asn Asp Thr Ser Gly Ala Leu Tyr
    135                 140                 145

gcg gtt caa aac ggc ccc acc gcg gtc atc gtg ttc acc aat cag gat   595
Ala Val Gln Asn Gly Pro Thr Ala Val Ile Val Phe Thr Asn Gln Asp
150                 155                 160                 165

caa tcc ctc aaa gcg cag tta atc gct gag gaa gta atc cag aat ctt   643
Gln Ser Leu Lys Ala Gln Leu Ile Ala Glu Glu Val Ile Gln Asn Leu
                170                 175                 180

ggt ctc taactattag aaggccacat cgt                                672
Gly Leu
```

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```
<210> 1864
<211> 183
<212> PRT
<213> Corynebacterium glutamicum

<400> 1864
Met Arg Arg Thr Leu Pro Thr Ile Leu Ala Ala Ser Ile Met Leu Thr
  1               5                  10                  15

Ala Cys Thr Pro Ala Glu Pro Glu Ala Thr Pro Glu Thr Thr Thr Glu
             20                  25                  30

Ala Ala Pro Glu Val Ile Thr Asp Gly Leu Pro Ile Asp Ala Met Pro
         35                  40                  45

Ala Val Glu Arg Thr Ala Gln Thr Ala Cys Pro Tyr Leu Gly Thr Asp
     50                  55                  60

Trp Val Ala Asp Thr Asn Gly Gln Arg Val Thr Gly Tyr Gly Thr Asp
 65                  70                  75                  80

Glu Arg Phe Ser Thr Pro Ser Cys Val Phe Tyr Ser Tyr Pro Glu Glu
                 85                  90                  95

Pro Gln Leu Thr Val Ile Val Arg Asp Met Ala Thr Thr Asp Asp Ala
            100                 105                 110
```

```
Ile Ala Val Val Asp Trp Ala Ala Pro Ile Asp Ser Thr Glu Pro Ala
        115                 120                 125

Glu Glu Pro Ala Gly Trp Ser Gly Gly Arg Arg Gly Gly Asn Asp Thr
    130                 135                 140

Ser Gly Ala Leu Tyr Ala Val Gln Asn Gly Pro Thr Ala Val Ile Val
145                 150                 155                 160

Phe Thr Asn Gln Asp Gln Ser Leu Lys Ala Gln Leu Ile Ala Glu Glu
                165                 170                 175

Val Ile Gln Asn Leu Gly Leu
            180


<210> 1865
<211> 1389
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1366)
<223> RXA00654

<400> 1865
cagcaatagc gattattgct tgattgtgtg tttttagatc ttcggttctc ttcactcaac 60

tgctgtgaag tgccacctgt ttggaaaggc gaacacgata gtg ctc gat att ttg   115
                                              Val Leu Asp Ile Leu
                                                1               5

att tac ccg gtg tct gga gtg atg aag ctg tgg cac ctg ctt ctt cac   163
Ile Tyr Pro Val Ser Gly Val Met Lys Leu Trp His Leu Leu Leu His
                10                  15                  20

aac gtt gcg ggt ttg gac gat tca ctg gcg tgg ttc ttt tcc ctt ttc   211
Asn Val Ala Gly Leu Asp Asp Ser Leu Ala Trp Phe Phe Ser Leu Phe
            25                  30                  35

ggc ctt gtc atc acg atc cgt gca att atc gcg cct ttc acc tgg cag   259
Gly Leu Val Ile Thr Ile Arg Ala Ile Ile Ala Pro Phe Thr Trp Gln
        40                  45                  50

atg tat aag tcg ggc cgc act gcc gca cat att cgt cct cac cgc gct   307
Met Tyr Lys Ser Gly Arg Thr Ala Ala His Ile Arg Pro His Arg Ala
    55                  60                  65

gcg ctc cgg gaa gaa tac aag gga aag tac gat gaa gcg tcc att cgg   355
Ala Leu Arg Glu Glu Tyr Lys Gly Lys Tyr Asp Glu Ala Ser Ile Arg
70                  75                  80                  85

gag ttg cag aag cgc cag aat gat ttg aat aag gaa tac ggc att aac   403
Glu Leu Gln Lys Arg Gln Asn Asp Leu Asn Lys Glu Tyr Gly Ile Asn
                90                  95                  100

ccg ctg gca ggt tgt gtg cct ggg ctg atc cag ata ccg att gtc ctt   451
Pro Leu Ala Gly Cys Val Pro Gly Leu Ile Gln Ile Pro Ile Val Leu
            105                 110                 115
```

```
ggt ctt tac tgg gca ctt ctc cgc atg gct cgc cct gaa ggt ggt ttg   499
Gly Leu Tyr Trp Ala Leu Leu Arg Met Ala Arg Pro Glu Gly Gly Leu
        120                 125                 130

gaa aat ccc gtc ttc cag tcg atc ggc ttc cta act cct gag gaa gtg   547
Glu Asn Pro Val Phe Gln Ser Ile Gly Phe Leu Thr Pro Glu Glu Val
    135                 140                 145

gaa tct ttc ctc gct ggt cgc gtg agc aat gtg cct ctg ccc gct tat   595
Glu Ser Phe Leu Ala Gly Arg Val Ser Asn Val Pro Leu Pro Ala Tyr
150                 155                 160                 165

gtt tcg atg ccc act gag cag cta aaa tat ttg agc acc acg cag gcg   643
Val Ser Met Pro Thr Glu Gln Leu Lys Tyr Leu Ser Thr Thr Gln Ala
                170                 175                 180

gaa gtt ctt agt ttc gtt ttg cca ctg ttc atc aca gcc gca atc ctc   691
Glu Val Leu Ser Phe Val Leu Pro Leu Phe Ile Thr Ala Ala Ile Leu
            185                 190                 195

acc gca atc aac atg gcg atg tcc atg tac cgc agc ttc caa acc aac   739
Thr Ala Ile Asn Met Ala Met Ser Met Tyr Arg Ser Phe Gln Thr Asn
        200                 205                 210

gat tac gca tcc gga ttc tct aac ggc atg ctg aag ttc atg atc gtg   787
Asp Tyr Ala Ser Gly Phe Ser Asn Gly Met Leu Lys Phe Met Ile Val
    215                 220                 225

atg tcg atc ctc gcg ccg atc ttc cca ctg tcc ctt ggc ctc aca gga   835
Met Ser Ile Leu Ala Pro Ile Phe Pro Leu Ser Leu Gly Leu Thr Gly
230                 235                 240                 245

cca ttc ccc aca gca atc gca ctc tat tgg gtc agc aac aac ctg tgg   883
Pro Phe Pro Thr Ala Ile Ala Leu Tyr Trp Val Ser Asn Asn Leu Trp
                250                 255                 260

acg ctc ctc caa aca atc atc atg atg gtc att ttg gaa cgc aaa tac   931
Thr Leu Leu Gln Thr Ile Ile Met Met Val Ile Leu Glu Arg Lys Tyr
            265                 270                 275

cca ctt acc gac gat ttc aaa gtg cac cac cta gag cag cgc gac atc   979
Pro Leu Thr Asp Asp Phe Lys Val His His Leu Glu Gln Arg Asp Ile
        280                 285                 290

tac cgc gca aaa caa aaa gaa aag cgc atc ttc ctg tgg aca cga cgc   1027
Tyr Arg Ala Lys Gln Lys Glu Lys Arg Ile Phe Leu Trp Thr Arg Arg
    295                 300                 305

aaa aac cgc gcc ctg atg att ctc acc cca tgg aac gcc tca acg ctt   1075
Lys Asn Arg Ala Leu Met Ile Leu Thr Pro Trp Asn Ala Ser Thr Leu
310                 315                 320                 325

cac gca aca aac gtg gaa ctc acc aaa acc cgt act gcc gaa atc aac   1123
His Ala Thr Asn Val Glu Leu Thr Lys Thr Arg Thr Ala Glu Ile Asn
                330                 335                 340

gaa gca aaa cag gcc cgc aaa gaa atc gcg aac aag agg cgc gaa acg   1171
Glu Ala Lys Gln Ala Arg Lys Glu Ile Ala Asn Lys Arg Arg Glu Thr
            345                 350                 355
```

```
caa cgt gaa atg aac cgc gcc gcc atg cag cgc tta aag cag cgt cgc   1219
Gln Arg Glu Met Asn Arg Ala Ala Met Gln Arg Leu Lys Gln Arg Arg
        360                 365                 370

gct gag gtt aaa gct aaa aag aag ggg ctt atc gac gcc tcc ccc aac   1267
Ala Glu Val Lys Ala Lys Lys Lys Gly Leu Ile Asp Ala Ser Pro Asn
    375                 380                 385

gaa gat acc cct tcg gaa aat gaa gaa act aaa ttg agt agt ccg cag   1315
Glu Asp Thr Pro Ser Glu Asn Glu Glu Thr Lys Leu Ser Ser Pro Gln
390                 395                 400                 405

gtg gag ccg aca aca act gcc gag cca aat cgc gag ccg tct caa gag   1363
Val Glu Pro Thr Thr Thr Ala Glu Pro Asn Arg Glu Pro Ser Gln Glu
                410                 415                 420

gac tgatgttgtg gaccaatcga gat                                    1389
Asp
```

<210> 1866
<211> 422
<212> PRT
<213> Corynebacterium glutamicum

<400> 1866

```
Val Leu Asp Ile Leu Ile Tyr Pro Val Ser Gly Val Met Lys Leu Trp
  1               5                  10                  15

His Leu Leu Leu His Asn Val Ala Gly Leu Asp Asp Ser Leu Ala Trp
             20                  25                  30

Phe Phe Ser Leu Phe Gly Leu Val Ile Thr Ile Arg Ala Ile Ile Ala
         35                  40                  45

Pro Phe Thr Trp Gln Met Tyr Lys Ser Gly Arg Thr Ala Ala His Ile
     50                  55                  60

Arg Pro His Arg Ala Ala Leu Arg Glu Glu Tyr Lys Gly Lys Tyr Asp
 65                  70                  75                  80

Glu Ala Ser Ile Arg Glu Leu Gln Lys Arg Gln Asn Asp Leu Asn Lys
                 85                  90                  95

Glu Tyr Gly Ile Asn Pro Leu Ala Gly Cys Val Pro Gly Leu Ile Gln
            100                 105                 110

Ile Pro Ile Val Leu Gly Leu Tyr Trp Ala Leu Leu Arg Met Ala Arg
        115                 120                 125

Pro Glu Gly Gly Leu Glu Asn Pro Val Phe Gln Ser Ile Gly Phe Leu
    130                 135                 140

Thr Pro Glu Glu Val Glu Ser Phe Leu Ala Gly Arg Val Ser Asn Val
145                 150                 155                 160

Pro Leu Pro Ala Tyr Val Ser Met Pro Thr Glu Gln Leu Lys Tyr Leu
                165                 170                 175

Ser Thr Thr Gln Ala Glu Val Leu Ser Phe Val Leu Pro Leu Phe Ile
```

```
            180                 185                 190

Thr Ala Ala Ile Leu Thr Ala Ile Asn Met Ala Met Ser Met Tyr Arg
        195                 200                 205

Ser Phe Gln Thr Asn Asp Tyr Ala Ser Gly Phe Ser Asn Gly Met Leu
    210                 215                 220

Lys Phe Met Ile Val Met Ser Ile Leu Ala Pro Ile Phe Pro Leu Ser
225                 230                 235                 240

Leu Gly Leu Thr Gly Pro Phe Pro Thr Ala Ile Ala Leu Tyr Trp Val
                245                 250                 255

Ser Asn Asn Leu Trp Thr Leu Leu Gln Thr Ile Ile Met Met Val Ile
            260                 265                 270

Leu Glu Arg Lys Tyr Pro Leu Thr Asp Asp Phe Lys Val His His Leu
        275                 280                 285

Glu Gln Arg Asp Ile Tyr Arg Ala Lys Gln Lys Glu Lys Arg Ile Phe
    290                 295                 300

Leu Trp Thr Arg Arg Lys Asn Arg Ala Leu Met Ile Leu Thr Pro Trp
305                 310                 315                 320

Asn Ala Ser Thr Leu His Ala Thr Asn Val Glu Leu Thr Lys Thr Arg
                325                 330                 335

Thr Ala Glu Ile Asn Glu Ala Lys Gln Ala Arg Lys Glu Ile Ala Asn
            340                 345                 350

Lys Arg Arg Glu Thr Gln Arg Glu Met Asn Arg Ala Ala Met Gln Arg
        355                 360                 365

Leu Lys Gln Arg Arg Ala Glu Val Lys Ala Lys Lys Lys Gly Leu Ile
    370                 375                 380

Asp Ala Ser Pro Asn Glu Asp Thr Pro Ser Glu Asn Glu Glu Thr Lys
385                 390                 395                 400

Leu Ser Ser Pro Gln Val Glu Pro Thr Thr Thr Ala Glu Pro Asn Arg
                405                 410                 415

Glu Pro Ser Gln Glu Asp
            420
```

<210> 1867
<211> 384
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(361)
<223> RXA00656

<400> 1867
ccttttaata acaatacaat gaataattgg aataggtcga cacctttgga gcggagccgg 60

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ttaaaattgg cagcattcac cgaaagaaaa ggagaaccac atg ctt gcc cta ggt   115
                                             Met Leu Ala Leu Gly
                                               1               5

tgg att aca tgg atc att att ggt ggt cta gct ggt tgg att gcc tcc   163
Trp Ile Thr Trp Ile Ile Ile Gly Gly Leu Ala Gly Trp Ile Ala Ser
                 10                  15                  20

aag att aaa ggc act gat gct cag caa gga att ttg ctg aac ata gtc   211
Lys Ile Lys Gly Thr Asp Ala Gln Gln Gly Ile Leu Leu Asn Ile Val
             25                  30                  35

gtc ggt att atc ggt ggt ttg tta ggc ggc tgg ctg ctt gga atc ttc   259
Val Gly Ile Ile Gly Gly Leu Leu Gly Gly Trp Leu Leu Gly Ile Phe
         40                  45                  50

gga gtg gat gtt gcc ggt ggc ggc ttg atc ttc agc ttc atc aca tgt   307
Gly Val Asp Val Ala Gly Gly Gly Leu Ile Phe Ser Phe Ile Thr Cys
     55                  60                  65

ctg att ggt gct gtc att ttg ctg acg atc gtg cag ttc ttc act cgg   355
Leu Ile Gly Ala Val Ile Leu Leu Thr Ile Val Gln Phe Phe Thr Arg
 70                  75                  80                  85

aag aag taatctgctt taaatccgta ggg                                384
Lys Lys
```

Application Filed 2004-12-22 00:00:00

<210> 1868
<211> 87
<212> PRT
<213> Corynebacterium glutamicum

<400> 1868

```
Met Leu Ala Leu Gly Trp Ile Thr Trp Ile Ile Ile Gly Gly Leu Ala
  1               5                  10                  15

Gly Trp Ile Ala Ser Lys Ile Lys Gly Thr Asp Ala Gln Gln Gly Ile
             20                  25                  30

Leu Leu Asn Ile Val Val Gly Ile Ile Gly Gly Leu Leu Gly Gly Trp
         35                  40                  45

Leu Leu Gly Ile Phe Gly Val Asp Val Ala Gly Gly Gly Leu Ile Phe
     50                  55                  60

Ser Phe Ile Thr Cys Leu Ile Gly Ala Val Ile Leu Leu Thr Ile Val
 65                  70                  75                  80

Gln Phe Phe Thr Arg Lys Lys
                 85
```

<210> 1869
<211> 986
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (61)..(963)
<223> RXA00657

<400> 1869
gatcatgagt ttccacgaac tgtaacgcag gattcaccaa tcaatgaaag gtcgaccgac 60

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atg agc act gaa gac att gtc gtc gta gca gta gat ggc tcg gac gcc   108
Met Ser Thr Glu Asp Ile Val Val Val Ala Val Asp Gly Ser Asp Ala
  1               5                  10                  15

tca aaa caa gct gtt cgg tgg gct gca aat acc gcc aac aaa cgt ggc   156
Ser Lys Gln Ala Val Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly
             20                  25                  30

att cca ctt cgc ttg gct tcc agc tac acc atg cct cag ttc ctc tac   204
Ile Pro Leu Arg Leu Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr
         35                  40                  45

gca gag gga atg gtt cca cca caa gag ctt ttc gat gac ctc cag gcc   252
Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala
     50                  55                  60

gaa gcc ctg gaa aag att aac gaa gcc cgt gac atc gcc cat gag gta   300
Glu Ala Leu Glu Lys Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val
 65                  70                  75                  80

gcg cca gaa atc aag atc ggg cac acc atc gct gaa ggc agt ccc atc   348
Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile
                 85                  90                  95

gac atg ctg ttg gaa atg tct ccc gat gcc aca atg atc gtc atg ggt   396
Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly
            100                 105                 110

tcc cgc gga ctc ggc gga ctc tcc gga atg gtc atg ggc tcc gtc tcc   444
Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser
        115                 120                 125

ggt gca gtg gtc agc cac gca aag tgt cca gtc gtt gtt gtc cgt gaa   492
Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu
    130                 135                 140

gac agc gca gtc aac gaa gac agc aag tac ggc cca gtc gtc gtc ggt   540
Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly
145                 150                 155                 160

gtg gat ggc tcc gaa gtc tcc caa cag gca acc gaa tac gca ttt gcg   588
Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala
                165                 170                 175

gaa gct gaa gct cgt ggc gcc gaa ctc gtt gca gtt cac acc tgg atg   636
Glu Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met
            180                 185                 190

gac atg cag gta cag gca tca ctt gca ggt ctt gca gct gct caa cag   684
Asp Met Gln Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln
        195                 200                 205

cag tgg gat gaa gtg gaa cgt cag caa acc gac atg ctg atc gaa cgc   732
Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg
    210                 215                 220
```

```
ctc gca cca ctg gtg gaa aag tac cca agt gta acc gtc aag aag atc   780
Leu Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile
225                 230                 235                 240

atc acc cgt gac cgc cca gtt cgc gca ctt gca gaa gca tct gaa aac   828
Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn
                245                 250                 255

gcg cag ctc cta gtc gtt ggt tcc cat ggt cgt ggc gga ttt aag ggc   876
Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly
            260                 265                 270

atg ctc ctt ggc tcc acc tcc cgc gca ctg ctg caa tcc gca ccg tgc   924
Met Leu Leu Gly Ser Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys
        275                 280                 285

cca atg atg gtg gtt cgc cca cct gag aag att aag aag tagtttcttt   973
Pro Met Met Val Val Arg Pro Pro Glu Lys Ile Lys Lys
    290                 295                 300

taagtttcga tgc                                                  986


<210> 1870
<211> 301
<212> PRT
<213> Corynebacterium glutamicum

<400> 1870
Met Ser Thr Glu Asp Ile Val Val Val Ala Val Asp Gly Ser Asp Ala
  1               5                  10                  15

Ser Lys Gln Ala Val Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly
             20                  25                  30

Ile Pro Leu Arg Leu Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr
         35                  40                  45

Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala
     50                  55                  60

Glu Ala Leu Glu Lys Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val
 65                  70                  75                  80

Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile
                85                  90                  95

Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly
            100                 105                 110

Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser
        115                 120                 125

Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu
    130                 135                 140

Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly
145                 150                 155                 160

Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala
```

```
                165                 170                 175

Glu Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met
            180                 185                 190

Asp Met Gln Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln
        195                 200                 205

Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg
    210                 215                 220

Leu Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile
225                 230                 235                 240

Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn
                245                 250                 255

Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly
            260                 265                 270

Met Leu Leu Gly Ser Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys
        275                 280                 285

Pro Met Met Val Val Arg Pro Pro Glu Lys Ile Lys Lys
    290                 295                 300


<210> 1871
<211> 813
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(790)
<223> RXA00661

<400> 1871
cggatgcaag agaaccgtgg tttcgctgat ttttggcgaa cccggaatta aggccccgag 60

gattacatgc ttttaaatcc tttgaaaagg ggacaagatc atg aat cct ata acc   115
                                            Met Asn Pro Ile Thr
                                              1               5

gaa tta tta gac gca aca cta tgg atc ggc gga gtt ccg att ctg tgg   163
Glu Leu Leu Asp Ala Thr Leu Trp Ile Gly Gly Val Pro Ile Leu Trp
                  10                  15                  20

cgc gaa atc atc ggc aac gtt ttc gga tta ttt agc gcg tgg gca gga   211
Arg Glu Ile Ile Gly Asn Val Phe Gly Leu Phe Ser Ala Trp Ala Gly
              25                  30                  35

atg cga cgc atc gtg tgg gca tgg ccc atc ggc atc ata ggc aac gcg   259
Met Arg Arg Ile Val Trp Ala Trp Pro Ile Gly Ile Ile Gly Asn Ala
          40                  45                  50

ctg ctg ttc aca gta ttt atg ggc ggc ctt ttc cac act cca caa aac   307
Leu Leu Phe Thr Val Phe Met Gly Gly Leu Phe His Thr Pro Gln Asn
      55                  60                  65

ctc gat ctc tac ggc caa gcg ggt cgc cag atc atg ttc atc atc gtc   355
```

```
Leu Asp Leu Tyr Gly Gln Ala Gly Arg Gln Ile Met Phe Ile Ile Val
 70                  75                  80                  85

agt ggt tat ggc tgg tac caa tgg tcg gcc gca aaa cgt cgc gca ctc   403
Ser Gly Tyr Gly Trp Tyr Gln Trp Ser Ala Ala Lys Arg Arg Ala Leu
                 90                  95                 100

acc cca gaa aat gca gta gca gtg gtt cct cgc tgg gca agc acc aaa   451
Thr Pro Glu Asn Ala Val Ala Val Val Pro Arg Trp Ala Ser Thr Lys
            105                 110                 115

gaa cgc gcc ggc att gtg att gcg gcg gtt gtg gga aca ctc agc ttt   499
Glu Arg Ala Gly Ile Val Ile Ala Ala Val Val Gly Thr Leu Ser Phe
        120                 125                 130

gcc tgg att ttc caa gca ctc ggc tcc tgg ggg cca tgg gcc gac gcg   547
Ala Trp Ile Phe Gln Ala Leu Gly Ser Trp Gly Pro Trp Ala Asp Ala
    135                 140                 145

tgg att ttc gtc ggc tca atc ctg gct acc tac gga atg gct cgc gga   595
Trp Ile Phe Val Gly Ser Ile Leu Ala Thr Tyr Gly Met Ala Arg Gly
150                 155                 160                 165

tgg aca gag ttc tgg ctg atc tgg atc gcc gtc gac ata gtt ggc gtt   643
Trp Thr Glu Phe Trp Leu Ile Trp Ile Ala Val Asp Ile Val Gly Val
                170                 175                 180

cct cta ctt ttg act gct ggc tac tac cca tcc gcg gtg ctt tac ctg   691
Pro Leu Leu Leu Thr Ala Gly Tyr Tyr Pro Ser Ala Val Leu Tyr Leu
            185                 190                 195

gtg tac ggt gcg ttt gtc agc tgg gga ttt gtc gtg tgg ctg cgg gtg   739
Val Tyr Gly Ala Phe Val Ser Trp Gly Phe Val Val Trp Leu Arg Val
        200                 205                 210

caa aaa gca gac aag gct cgt gcg ctg gaa gct cag gag tct gtg aca   787
Gln Lys Ala Asp Lys Ala Arg Ala Leu Glu Ala Gln Glu Ser Val Thr
    215                 220                 225

gtc tgaaaagcgt ttactaaata gaa                                    813
Val
230


<210> 1872
<211> 230
<212> PRT
<213> Corynebacterium glutamicum

<400> 1872
Met Asn Pro Ile Thr Glu Leu Leu Asp Ala Thr Leu Trp Ile Gly Gly
  1               5                  10                  15

Val Pro Ile Leu Trp Arg Glu Ile Ile Gly Asn Val Phe Gly Leu Phe
             20                  25                  30

Ser Ala Trp Ala Gly Met Arg Arg Ile Val Trp Ala Trp Pro Ile Gly
         35                  40                  45

Ile Ile Gly Asn Ala Leu Leu Phe Thr Val Phe Met Gly Gly Leu Phe
     50                  55                  60
```

```
His Thr Pro Gln Asn Leu Asp Leu Tyr Gly Gln Ala Gly Arg Gln Ile
 65                  70                  75                  80

Met Phe Ile Ile Val Ser Gly Tyr Gly Trp Tyr Gln Trp Ser Ala Ala
                85                  90                  95

Lys Arg Arg Ala Leu Thr Pro Glu Asn Ala Val Ala Val Val Pro Arg
            100                 105                 110

Trp Ala Ser Thr Lys Glu Arg Ala Gly Ile Val Ile Ala Ala Val Val
        115                 120                 125

Gly Thr Leu Ser Phe Ala Trp Ile Phe Gln Ala Leu Gly Ser Trp Gly
    130                 135                 140

Pro Trp Ala Asp Ala Trp Ile Phe Val Gly Ser Ile Leu Ala Thr Tyr
145                 150                 155                 160

Gly Met Ala Arg Gly Trp Thr Glu Phe Trp Leu Ile Trp Ile Ala Val
                165                 170                 175

Asp Ile Val Gly Val Pro Leu Leu Leu Thr Ala Gly Tyr Tyr Pro Ser
            180                 185                 190

Ala Val Leu Tyr Leu Val Tyr Gly Ala Phe Val Ser Trp Gly Phe Val
        195                 200                 205

Val Trp Leu Arg Val Gln Lys Ala Asp Lys Ala Arg Ala Leu Glu Ala
    210                 215                 220

Gln Glu Ser Val Thr Val
225                 230
```

Sequence Listing

<210> 1873
<211> 685
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(685)
<223> RXA00667

<400> 1873

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ggcatcagtg tttgaaggga aaagcaggtc aaacaaggtg cggctgattt gagcgatcac 60

agcaccgaga tctgtgctga agaattcaat gattgggttg atg att gcg ttg aag   115
                                          Met Ile Ala Leu Lys
                                            1               5

tcc atg tct aac agg gta gta caa aag cca aaa atg aaa gcg ccg cta   163
Ser Met Ser Asn Arg Val Val Gln Lys Pro Lys Met Lys Ala Pro Leu
                10                  15                  20

ccc atc cgc gac ggc ctc aac cct tcc cgt gtg cgc ttg ccg ctc gac   211
Pro Ile Arg Asp Gly Leu Asn Pro Ser Arg Val Arg Leu Pro Leu Asp
            25                  30                  35

gcg gcg ccg atc cgc gcc atc gat ttt gtt gaa tac ctc att tcc acg   259
```

```
Ala Ala Pro Ile Arg Ala Ile Asp Phe Val Glu Tyr Leu Ile Ser Thr
         40                  45                  50

cag cgc cac cgc aat ccg gcc gac aac gcc gaa gcg ctt caa gcg cgt   307
Gln Arg His Arg Asn Pro Ala Asp Asn Ala Glu Ala Leu Gln Ala Arg
     55                  60                  65

ttc gac gcc gac ctt gtt gtc aac cac tac ggc gag ccc tac gcc ccc   355
Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly Glu Pro Tyr Ala Pro
 70                  75                  80                  85

gac acc atg gtt cag ccc gac gac gac att tgg ttc tac cgc atg ccc   403
Asp Thr Met Val Gln Pro Asp Asp Asp Ile Trp Phe Tyr Arg Met Pro
                 90                  95                 100

gcc gcc gaa cgg ccg atc cct tac aaa att cat gtc att cac gaa gac   451
Ala Ala Glu Arg Pro Ile Pro Tyr Lys Ile His Val Ile His Glu Asp
            105                 110                 115

gat gac atc ctc gtc att gac aag cca ccc tac cta gca acc atg cct   499
Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr Leu Ala Thr Met Pro
        120                 125                 130

cgt ggc cgc cac atc acc gaa acc gct ctg gtg aaa atg cgt gtg ctg   547
Arg Gly Arg His Ile Thr Glu Thr Ala Leu Val Lys Met Arg Val Leu
    135                 140                 145

act gga aac aac gat ctc acc cca gct cac cgc ctc gat cgc ctg act   595
Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg Leu Asp Arg Leu Thr
150                 155                 160                 165

tcc ggt gtg tta gtc atg gtg aaa aaa cca gaa ctc cgt ggc gct tac   643
Ser Gly Val Leu Val Met Val Lys Lys Pro Glu Leu Arg Gly Ala Tyr
                170                 175                 180

caa acc ttg ttt gcc cga cgt gag gcg tcc aaa acc tat gag           685
Gln Thr Leu Phe Ala Arg Arg Glu Ala Ser Lys Thr Tyr Glu
            185                 190                 195
```

<210> 1874
<211> 195
<212> PRT
<213> Corynebacterium glutamicum

<400> 1874

```
Met Ile Ala Leu Lys Ser Met Ser Asn Arg Val Val Gln Lys Pro Lys
  1               5                  10                  15

Met Lys Ala Pro Leu Pro Ile Arg Asp Gly Leu Asn Pro Ser Arg Val
             20                  25                  30

Arg Leu Pro Leu Asp Ala Ala Pro Ile Arg Ala Ile Asp Phe Val Glu
         35                  40                  45

Tyr Leu Ile Ser Thr Gln Arg His Arg Asn Pro Ala Asp Asn Ala Glu
     50                  55                  60

Ala Leu Gln Ala Arg Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly
 65                  70                  75                  80
```

```
Glu Pro Tyr Ala Pro Asp Thr Met Val Gln Pro Asp Asp Asp Ile Trp
                85                  90                  95

Phe Tyr Arg Met Pro Ala Ala Glu Arg Pro Ile Pro Tyr Lys Ile His
            100                 105                 110

Val Ile His Glu Asp Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr
        115                 120                 125

Leu Ala Thr Met Pro Arg Gly Arg His Ile Thr Glu Thr Ala Leu Val
    130                 135                 140

Lys Met Arg Val Leu Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg
145                 150                 155                 160

Leu Asp Arg Leu Thr Ser Gly Val Leu Val Met Val Lys Lys Pro Glu
                165                 170                 175

Leu Arg Gly Ala Tyr Gln Thr Leu Phe Ala Arg Arg Glu Ala Ser Lys
            180                 185                 190

Thr Tyr Glu
        195


<210> 1875
<211> 870
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(847)
<223> RXA00676

<400> 1875
ggtttgcgac ctccccggcg tgccgccagg ggaggaggcg ataaaacttt tttacctttc 60

gaatatcaaa atcataaaac agccttatat acttcaacgt atg gcg aag aat tct   115
                                          Met Ala Lys Asn Ser
                                           1               5

cga atc cga tac agc gcg tca atc aag cgt gcc gca gct gca atc ctc   163
Arg Ile Arg Tyr Ser Ala Ser Ile Lys Arg Ala Ala Ala Ala Ile Leu
                10                  15                  20

acc gca gct gct acc tca gtc gcg ttg atc gct gtg cca gca act gct   211
Thr Ala Ala Ala Thr Ser Val Ala Leu Ile Ala Val Pro Ala Thr Ala
            25                  30                  35

tca gca cag gac ctc gca acc ggc agc tcc cag atc cag act gat gct   259
Ser Ala Gln Asp Leu Ala Thr Gly Ser Ser Gln Ile Gln Thr Asp Ala
        40                  45                  50

cgt gaa ggt gcg tgg gca acc cgc aac acc atc caa gac caa ctt gcc   307
Arg Glu Gly Ala Trp Ala Thr Arg Asn Thr Ile Gln Asp Gln Leu Ala
    55                  60                  65

tcc att ggg cca gca gcc ctc cca gtc cgc gca gcg gta gac aat gcc   355
Ser Ile Gly Pro Ala Ala Leu Pro Val Arg Ala Ala Val Asp Asn Ala
70                  75                  80                  85
```

```
atc aac ggc atg ttc cca gga ctt gtt gat gaa aag gtt gca gca gag   403
Ile Asn Gly Met Phe Pro Gly Leu Val Asp Glu Lys Val Ala Ala Glu
                 90                  95                 100

cag gaa gct gca cgc gca gaa gct gag cgc gaa gca gca gct gca cgt   451
Gln Glu Ala Ala Arg Ala Glu Ala Glu Arg Glu Ala Ala Ala Ala Arg
            105                 110                 115

gaa gca gaa gca gcc cgc gta gcc gca gaa gaa gcc gca cgc ttt gac   499
Glu Ala Glu Ala Ala Arg Val Ala Ala Glu Glu Ala Ala Arg Phe Asp
        120                 125                 130

cgc ggc tct tgc cca gca atc gct gat gtc tgc gtg gac att gat ggt   547
Arg Gly Ser Cys Pro Ala Ile Ala Asp Val Cys Val Asp Ile Asp Gly
    135                 140                 145

gga cgt acc tgg ctg cag gaa aac ggt cag gtc acc tac ggt gca gtc   595
Gly Arg Thr Trp Leu Gln Glu Asn Gly Gln Val Thr Tyr Gly Ala Val
150                 155                 160                 165

cca gtt tcc tcc ggc gga gtt ggc cag gaa acc cct cgc gga acg ttc   643
Pro Val Ser Ser Gly Gly Val Gly Gln Glu Thr Pro Arg Gly Thr Phe
                170                 175                 180

tac atc aac cgc aag gtc aag gat gaa atc tct tac gag ttc ggt aac   691
Tyr Ile Asn Arg Lys Val Lys Asp Glu Ile Ser Tyr Glu Phe Gly Asn
            185                 190                 195

gcc cca atg ccg tac gcc atg tac ttc acc tac aac ggc cac gca ttc   739
Ala Pro Met Pro Tyr Ala Met Tyr Phe Thr Tyr Asn Gly His Ala Phe
        200                 205                 210

cac cag ggc aat gtt gcg act act tcc gct ggt tgt gtt cgc cta aac   787
His Gln Gly Asn Val Ala Thr Thr Ser Ala Gly Cys Val Arg Leu Asn
    215                 220                 225

act caa gat gcc atc tac tac ttc aac aac gtt ggc atc ggc gac atg   835
Thr Gln Asp Ala Ile Tyr Tyr Phe Asn Asn Val Gly Ile Gly Asp Met
230                 235                 240                 245

gtg tac atc tac taaaactcac cgttgctagc agg                        870
Val Tyr Ile Tyr
```

<210> 1876
<211> 249
<212> PRT
<213> Corynebacterium glutamicum

<400> 1876

```
Met Ala Lys Asn Ser Arg Ile Arg Tyr Ser Ala Ser Ile Lys Arg Ala
  1               5                  10                  15

Ala Ala Ala Ile Leu Thr Ala Ala Ala Thr Ser Val Ala Leu Ile Ala
             20                  25                  30

Val Pro Ala Thr Ala Ser Ala Gln Asp Leu Ala Thr Gly Ser Ser Gln
         35                  40                  45
```

```
Ile Gln Thr Asp Ala Arg Glu Gly Ala Trp Ala Thr Arg Asn Thr Ile
     50                  55                  60

Gln Asp Gln Leu Ala Ser Ile Gly Pro Ala Ala Leu Pro Val Arg Ala
 65                  70                  75                  80

Ala Val Asp Asn Ala Ile Asn Gly Met Phe Pro Gly Leu Val Asp Glu
                 85                  90                  95

Lys Val Ala Ala Glu Gln Glu Ala Ala Arg Ala Glu Ala Glu Arg Glu
            100                 105                 110

Ala Ala Ala Ala Arg Glu Ala Glu Ala Ala Arg Val Ala Ala Glu Glu
        115                 120                 125

Ala Ala Arg Phe Asp Arg Gly Ser Cys Pro Ala Ile Ala Asp Val Cys
    130                 135                 140

Val Asp Ile Asp Gly Gly Arg Thr Trp Leu Gln Glu Asn Gly Gln Val
145                 150                 155                 160

Thr Tyr Gly Ala Val Pro Val Ser Ser Gly Gly Val Gly Gln Glu Thr
                165                 170                 175

Pro Arg Gly Thr Phe Tyr Ile Asn Arg Lys Val Lys Asp Glu Ile Ser
            180                 185                 190

Tyr Glu Phe Gly Asn Ala Pro Met Pro Tyr Ala Met Tyr Phe Thr Tyr
        195                 200                 205

Asn Gly His Ala Phe His Gln Gly Asn Val Ala Thr Thr Ser Ala Gly
    210                 215                 220

Cys Val Arg Leu Asn Thr Gln Asp Ala Ile Tyr Tyr Phe Asn Asn Val
225                 230                 235                 240

Gly Ile Gly Asp Met Val Tyr Ile Tyr
                245
```

<210> 1877
<211> 858
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(835)
<223> RXA00678

<400> 1877

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tgcgcagtgc actttccagg aaccaaaata tccccgccga ccttgctgca gatatttcgc 60

agccgctgaa aaaactagcc gttgacctgg aggttacccg atg act cgc agt aat   115
                                            Met Thr Arg Ser Asn
                                              1               5

tta ccc gct tgg gag caa gca gac ccc agc gtc cac gcc tct gat ccc   163
Leu Pro Ala Trp Glu Gln Ala Asp Pro Ser Val His Ala Ser Asp Pro
                10                  15                  20
```

```
cgc gcc atc act ttt gcg gag gat ttt ggg att cgt ccc atc ccg gcc   211
Arg Ala Ile Thr Phe Ala Glu Asp Phe Gly Ile Arg Pro Ile Pro Ala
             25                  30                  35

gta ggt cca att gat acc acc gct atc tgt gca aca cct tca aat gga   259
Val Gly Pro Ile Asp Thr Thr Ala Ile Cys Ala Thr Pro Ser Asn Gly
         40                  45                  50

ttt gag caa tta tgg aaa gcc att gag ccg gaa acc cgc acc cgc gcc   307
Phe Glu Gln Leu Trp Lys Ala Ile Glu Pro Glu Thr Arg Thr Arg Ala
     55                  60                  65

aac gac att cat ctt ccc atc gtc gtg gcg tac gct gaa cgt ctc tgc   355
Asn Asp Ile His Leu Pro Ile Val Val Ala Tyr Ala Glu Arg Leu Cys
 70                  75                  80                  85

gac gct tac cca ctg gca gat aga gaa ttg gtt ctc gta gcc gca atc   403
Asp Ala Tyr Pro Leu Ala Asp Arg Glu Leu Val Leu Val Ala Ala Ile
                 90                  95                 100

ctc cac gac acg ggc tgg gca cat gtc gat gag agc cga atc atc tcc   451
Leu His Asp Thr Gly Trp Ala His Val Asp Glu Ser Arg Ile Ile Ser
            105                 110                 115

gaa gga ttc tcc gga aac tgg cgc aaa gca gca atc cgc ttc gaa cac   499
Glu Gly Phe Ser Gly Asn Trp Arg Lys Ala Ala Ile Arg Phe Glu His
        120                 125                 130

gaa aca gaa ggc tgc act gtg gcc cgc cga gtg ctt cca tcc ctc gga   547
Glu Thr Glu Gly Cys Thr Val Ala Arg Arg Val Leu Pro Ser Leu Gly
    135                 140                 145

tat act gtc gat ttt gtc gag cat gtc tgc gac atc atc gac gga cac   595
Tyr Thr Val Asp Phe Val Glu His Val Cys Asp Ile Ile Asp Gly His
150                 155                 160                 165

gac acc cgc caa gtg gcc tac tca cta gaa gac gct ctt gtt cgc gat   643
Asp Thr Arg Gln Val Ala Tyr Ser Leu Glu Asp Ala Leu Val Arg Asp
                170                 175                 180

tgc gac cga ctc tgg cgt ttc gac cgc gcc ggg atc acg gct tct agc   691
Cys Asp Arg Leu Trp Arg Phe Asp Arg Ala Gly Ile Thr Ala Ser Ser
            185                 190                 195

tca tgg ttc ggg atg cca gtc tca gat tat gtc gac cgc ctg cac agg   739
Ser Trp Phe Gly Met Pro Val Ser Asp Tyr Val Asp Arg Leu His Arg
        200                 205                 210

gaa atc ctc cca gaa tta atc acc gaa gct gca cac cag atg gct act   787
Glu Ile Leu Pro Glu Leu Ile Thr Glu Ala Ala His Gln Met Ala Thr
    215                 220                 225

gca gac ctc aat cgt gca aag gcc ctg tta aga acg gat gcg atc cga   835
Ala Asp Leu Asn Arg Ala Lys Ala Leu Leu Arg Thr Asp Ala Ile Arg
230                 235                 240                 245

tgaatgctgc aaccaggcgt gct                                        858
```

<210> 1878
<211> 245

<212> PRT
<213> Corynebacterium glutamicum

<400> 1878
Met Thr Arg Ser Asn Leu Pro Ala Trp Glu Gln Ala Asp Pro Ser Val
1 5 10 15

His Ala Ser Asp Pro Arg Ala Ile Thr Phe Ala Glu Asp Phe Gly Ile
20 25 30

Arg Pro Ile Pro Ala Val Gly Pro Ile Asp Thr Thr Ala Ile Cys Ala
35 40 45

Thr Pro Ser Asn Gly Phe Glu Gln Leu Trp Lys Ala Ile Glu Pro Glu
50 55 60

Thr Arg Thr Arg Ala Asn Asp Ile His Leu Pro Ile Val Val Ala Tyr
65 70 75 80

Ala Glu Arg Leu Cys Asp Ala Tyr Pro Leu Ala Asp Arg Glu Leu Val
85 90 95

Leu Val Ala Ala Ile Leu His Asp Thr Gly Trp Ala His Val Asp Glu
100 105 110

Ser Arg Ile Ile Ser Glu Gly Phe Ser Gly Asn Trp Arg Lys Ala Ala
115 120 125

Ile Arg Phe Glu His Glu Thr Glu Gly Cys Thr Val Ala Arg Arg Val
130 135 140

Leu Pro Ser Leu Gly Tyr Thr Val Asp Phe Val Glu His Val Cys Asp
145 150 155 160

Ile Ile Asp Gly His Asp Thr Arg Gln Val Ala Tyr Ser Leu Glu Asp
165 170 175

Ala Leu Val Arg Asp Cys Asp Arg Leu Trp Arg Phe Asp Arg Ala Gly
180 185 190

Ile Thr Ala Ser Ser Ser Trp Phe Gly Met Pro Val Ser Asp Tyr Val
195 200 205

Asp Arg Leu His Arg Glu Ile Leu Pro Glu Leu Ile Thr Glu Ala Ala
210 215 220

His Gln Met Ala Thr Ala Asp Leu Asn Arg Ala Lys Ala Leu Leu Arg
225 230 235 240

Thr Asp Ala Ile Arg
245

<210> 1879
<211> 1053
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1030)

<223> RXA00691

<400> 1879

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tgcagctgca gtcgcactat ggattgttct tgccatatcg ccatgggttc cttctgcgca 60

cgccttgacc acgccttgtg aagacgacca agtgacagtg atg gtt gag ggc aac   115
                                            Met Val Glu Gly Asn
                                              1               5

acc atc ggc tgt gct gac gcc ggc gga aat ggc tat caa acg ctt ctt   163
Thr Ile Gly Cys Ala Asp Ala Gly Gly Asn Gly Tyr Gln Thr Leu Leu
                 10                  15                  20

gat gcc gga ttt gat gtg gaa acc acc gtt cag ttt cca gaa ttc ttg   211
Asp Ala Gly Phe Asp Val Glu Thr Thr Val Gln Phe Pro Glu Phe Leu
             25                  30                  35

tgc cga atc aat gat ttc cca ggt cct gat gtg gac gat tgc atg acc   259
Cys Arg Ile Asn Asp Phe Pro Gly Pro Asp Val Asp Asp Cys Met Thr
         40                  45                  50

gca tca cct gct gaa gct tat tgg tct tat tgg cat gct ccc ctc ggc   307
Ala Ser Pro Ala Glu Ala Tyr Trp Ser Tyr Trp His Ala Pro Leu Gly
     55                  60                  65

gga gat gaa tgg gaa tac agc aac ctt gga gct ttc ctc tac tac ccc   355
Gly Asp Glu Trp Glu Tyr Ser Asn Leu Gly Ala Phe Leu Tyr Tyr Pro
 70                  75                  80                  85

aaa ccc ggc act gtt gaa gcg tgg tat tgg gga gat act gat cgt ccc   403
Lys Pro Gly Thr Val Glu Ala Trp Tyr Trp Gly Asp Thr Asp Arg Pro
                 90                  95                 100

ggc gcg atc ccg gtg agt aaa tct cag gcg gag ttg ggg tta gac tcc   451
Gly Ala Ile Pro Val Ser Lys Ser Gln Ala Glu Leu Gly Leu Asp Ser
             105                 110                 115

gcg gat ccg gat tac aaa att gat ttt gat cca aat gat ttc atc acc   499
Ala Asp Pro Asp Tyr Lys Ile Asp Phe Asp Pro Asn Asp Phe Ile Thr
         120                 125                 130

aca acc cca acc tcc gag tcc cct atc gcc gat tta ggg ggt gac gaa   547
Thr Thr Pro Thr Ser Glu Ser Pro Ile Ala Asp Leu Gly Gly Asp Glu
    135                 140                 145

gag ccc act gaa act act gaa gct cct atc gca ggg gct gga gct ggt   595
Glu Pro Thr Glu Thr Thr Glu Ala Pro Ile Ala Gly Ala Gly Ala Gly
150                 155                 160                 165

tcg gca aga gga caa gca gct gaa ccc act gtt gag gta aac cct gag   643
Ser Ala Arg Gly Gln Ala Ala Glu Pro Thr Val Glu Val Asn Pro Glu
                170                 175                 180

aac cct aat gag gta ttg gtg tat cag gat tct gaa gga aac tcg att   691
Asn Pro Asn Glu Val Leu Val Tyr Gln Asp Ser Glu Gly Asn Ser Ile
             185                 190                 195

act aaa ggt cag tac gag aac ttg gtt gct gca gca gcc gct aag acc   739
Thr Lys Gly Gln Tyr Glu Asn Leu Val Ala Ala Ala Ala Ala Lys Thr
         200                 205                 210
```

```
act gct gct gtc caa gcc cca gct ggg gct ggt gaa gca aat agc caa   787
Thr Ala Ala Val Gln Ala Pro Ala Gly Ala Gly Glu Ala Asn Ser Gln
    215                 220                 225

ccg cag gca aca gcg gtg gca gaa gct cct gaa gtt gat ccg atg acc   835
Pro Gln Ala Thr Ala Val Ala Glu Ala Pro Glu Val Asp Pro Met Thr
230                 235                 240                 245

acg cag gtt ctt atg gcg cct gcg ggc caa gat gga gac gtc atg gct   883
Thr Gln Val Leu Met Ala Pro Ala Gly Gln Asp Gly Asp Val Met Ala
                250                 255                 260

gag ggt tcg acg cag cag acg tac gcc aca ggc acg gtg gat tct tct   931
Glu Gly Ser Thr Gln Gln Thr Tyr Ala Thr Gly Thr Val Asp Ser Ser
            265                 270                 275

gct cag gga tgg atc att gga ctc aca ctg gct gtc att tcc ttg gtt   979
Ala Gln Gly Trp Ile Ile Gly Leu Thr Leu Ala Val Ile Ser Leu Val
        280                 285                 290

tca gcg tct gct gtg gcg gcg tgg gcg att cgt cgt tca gag gtc cag   1027
Ser Ala Ser Ala Val Ala Ala Trp Ala Ile Arg Arg Ser Glu Val Gln
    295                 300                 305

ggt taaagcttcg tgaaatggat tga                                    1053
Gly
310
```

Sequence Listing - 2141 - BGI-129CP

<210> 1880
<211> 310
<212> PRT
<213> Corynebacterium glutamicum

<400> 1880

```
Met Val Glu Gly Asn Thr Ile Gly Cys Ala Asp Ala Gly Gly Asn Gly
  1               5                  10                  15

Tyr Gln Thr Leu Leu Asp Ala Gly Phe Asp Val Glu Thr Thr Val Gln
             20                  25                  30

Phe Pro Glu Phe Leu Cys Arg Ile Asn Asp Phe Pro Gly Pro Asp Val
         35                  40                  45

Asp Asp Cys Met Thr Ala Ser Pro Ala Glu Ala Tyr Trp Ser Tyr Trp
     50                  55                  60

His Ala Pro Leu Gly Gly Asp Glu Trp Glu Tyr Ser Asn Leu Gly Ala
 65                  70                  75                  80

Phe Leu Tyr Tyr Pro Lys Pro Gly Thr Val Glu Ala Trp Tyr Trp Gly
                 85                  90                  95

Asp Thr Asp Arg Pro Gly Ala Ile Pro Val Ser Lys Ser Gln Ala Glu
            100                 105                 110

Leu Gly Leu Asp Ser Ala Asp Pro Asp Tyr Lys Ile Asp Phe Asp Pro
        115                 120                 125

Asn Asp Phe Ile Thr Thr Thr Pro Thr Ser Glu Ser Pro Ile Ala Asp
    130                 135                 140
```

```
Leu Gly Gly Asp Glu Glu Pro Thr Glu Thr Thr Glu Ala Pro Ile Ala
145                 150                 155                 160

Gly Ala Gly Ala Gly Ser Ala Arg Gly Gln Ala Ala Glu Pro Thr Val
                165                 170                 175

Glu Val Asn Pro Glu Asn Pro Asn Glu Val Leu Val Tyr Gln Asp Ser
            180                 185                 190

Glu Gly Asn Ser Ile Thr Lys Gly Gln Tyr Glu Asn Leu Val Ala Ala
        195                 200                 205

Ala Ala Ala Lys Thr Thr Ala Ala Val Gln Ala Pro Ala Gly Ala Gly
    210                 215                 220

Glu Ala Asn Ser Gln Pro Gln Ala Thr Ala Val Ala Glu Ala Pro Glu
225                 230                 235                 240

Val Asp Pro Met Thr Thr Gln Val Leu Met Ala Pro Ala Gly Gln Asp
                245                 250                 255

Gly Asp Val Met Ala Glu Gly Ser Thr Gln Gln Thr Tyr Ala Thr Gly
            260                 265                 270

Thr Val Asp Ser Ser Ala Gln Gly Trp Ile Ile Gly Leu Thr Leu Ala
        275                 280                 285

Val Ile Ser Leu Val Ser Ala Ser Ala Val Ala Ala Trp Ala Ile Arg
    290                 295                 300

Arg Ser Glu Val Gln Gly
305                 310


<210> 1881
<211> 1257
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1234)
<223> RXA00692

<400> 1881
ccttaaagcg gggtcagaac atttctccaa ttcattttaa ggacatgttt tcatggctca 60

tctacgtggg aagagaacca ttcgctggtc tgctgcaacc gtg gct tta gca acc   115
                                              Val Ala Leu Ala Thr
                                                1               5

ggt gtt tcc ctg ttg gct cca cag gtc gtt gct gca cag gat gca tca   163
Gly Val Ser Leu Leu Ala Pro Gln Val Val Ala Ala Gln Asp Ala Ser
                10                  15                  20

tcg gat att caa tta gct acc caa ttc atc gaa aaa gaa ttt gca acg   211
Ser Asp Ile Gln Leu Ala Thr Gln Phe Ile Glu Lys Glu Phe Ala Thr
            25                  30                  35

aat ggc ctc atc cct ggg cct gta ggt act cca gat att ggg ctc aat   259
```

```
Asn Gly Leu Ile Pro Gly Pro Val Gly Thr Pro Asp Ile Gly Leu Asn
         40                  45                  50

cag gat ctg ttg ctg tcc cta aat gcg ctt gcc cct gat tct cca gag   307
Gln Asp Leu Leu Leu Ser Leu Asn Ala Leu Ala Pro Asp Ser Pro Glu
     55                  60                  65

atc gac gct gca tat gct gca att gct ccg gag ctc gag ggc tat gtc   355
Ile Asp Ala Ala Tyr Ala Ala Ile Ala Pro Glu Leu Glu Gly Tyr Val
 70                  75                  80                  85

tca gtt tct gac tac atc ttc agc gat cgt cta gcc aag acc gta gct   403
Ser Val Ser Asp Tyr Ile Phe Ser Asp Arg Leu Ala Lys Thr Val Ala
                90                  95                 100

ttc caa gat gcc ctc ggc gtc aga gat gct gat ttt atc gcg caa ctt   451
Phe Gln Asp Ala Leu Gly Val Arg Asp Ala Asp Phe Ile Ala Gln Leu
            105                 110                 115

gtc agc gct gtt caa gaa aac ggt cag atc aaa aac tta gat aat ggt   499
Val Ser Ala Val Gln Glu Asn Gly Gln Ile Lys Asn Leu Asp Asn Gly
        120                 125                 130

gaa gcc aca act gca att aat aac ttc agc cag gcc tgg ggc gtt cta   547
Glu Ala Thr Thr Ala Ile Asn Asn Phe Ser Gln Ala Trp Gly Val Leu
    135                 140                 145

gct ctg cac cgc gtc ggt gaa acc gaa gca gcc gag cgc gca aca gaa   595
Ala Leu His Arg Val Gly Glu Thr Glu Ala Ala Glu Arg Ala Thr Glu
150                 155                 160                 165

ttc ctt aaa act caa gtg tgc tcc gac ggt ggt gtc caa tta gcc tca   643
Phe Leu Lys Thr Gln Val Cys Ser Asp Gly Gly Val Gln Leu Ala Ser
                170                 175                 180

gca atc gaa cct aca tgc aaa acc acg gat tcc gat gtc act gca atg   691
Ala Ile Glu Pro Thr Cys Lys Thr Thr Asp Ser Asp Val Thr Ala Met
            185                 190                 195

gct gca cag gct ttg act ctg gca aat ggt gcg cag gat cca acc aca   739
Ala Ala Gln Ala Leu Thr Leu Ala Asn Gly Ala Gln Asp Pro Thr Thr
        200                 205                 210

caa gcc act ctc gat tac ctc gtc acc acg atg gat gag acc ggt ggt   787
Gln Ala Thr Leu Asp Tyr Leu Val Thr Thr Met Asp Glu Thr Gly Gly
    215                 220                 225

gtc aaa aat act tgg acc ggt gtg aat tcc aac tcc acg gga att gtc   835
Val Lys Asn Thr Trp Thr Gly Val Asn Ser Asn Ser Thr Gly Ile Val
230                 235                 240                 245

gga tcc gct ttt gct ctt gcg ggc gat gag gaa aac tac ctc aag gct   883
Gly Ser Ala Phe Ala Leu Ala Gly Asp Glu Glu Asn Tyr Leu Lys Ala
                250                 255                 260

cgt gaa tac ctg gca tct gtt caa ttt ggc gaa gat gca gac cca tcg   931
Arg Glu Tyr Leu Ala Ser Val Gln Phe Gly Glu Asp Ala Asp Pro Ser
            265                 270                 275

att cag ggt ggc ttt gct ttc acc gtg aag gct aag gaa acc aac act   979
Ile Gln Gly Gly Phe Ala Phe Thr Val Lys Ala Lys Glu Thr Asn Thr
```

```
        280                 285                 290

gcg att agc gat cag att cga cgc gca act ggc caa gca gca tta ggt   1027
Ala Ile Ser Asp Gln Ile Arg Arg Ala Thr Gly Gln Ala Ala Leu Gly
    295                 300                 305

ttt gca ggc ggt aac tac gcc aac gat aaa ctg atc acc att gcg aac   1075
Phe Ala Gly Gly Asn Tyr Ala Asn Asp Lys Leu Ile Thr Ile Ala Asn
310                 315                 320                 325

cca gta gat cca act cca gat cca gaa att cca act ccc cca gct gat   1123
Pro Val Asp Pro Thr Pro Asp Pro Glu Ile Pro Thr Pro Pro Ala Asp
                330                 335                 340

tca gag gga tcc acc ggt gga att ggc ggc gct gga att atc atc gcc   1171
Ser Glu Gly Ser Thr Gly Gly Ile Gly Gly Ala Gly Ile Ile Ile Ala
            345                 350                 355

atc ttg gcc atc ctt gcc gcc atc gct ggt gtc atg gga cca atg atg   1219
Ile Leu Ala Ile Leu Ala Ala Ile Ala Gly Val Met Gly Pro Met Met
        360                 365                 370

gct aac ctg cag ttt taacatctga gagaagtaca gtg                    1257
Ala Asn Leu Gln Phe
    375
```

<210> 1882
<211> 378
<212> PRT
<213> Corynebacterium glutamicum

<400> 1882

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Val Ala Leu Ala Thr Gly Val Ser Leu Leu Ala Pro Gln Val Val Ala
  1               5                  10                  15

Ala Gln Asp Ala Ser Ser Asp Ile Gln Leu Ala Thr Gln Phe Ile Glu
             20                  25                  30

Lys Glu Phe Ala Thr Asn Gly Leu Ile Pro Gly Pro Val Gly Thr Pro
         35                  40                  45

Asp Ile Gly Leu Asn Gln Asp Leu Leu Leu Ser Leu Asn Ala Leu Ala
     50                  55                  60

Pro Asp Ser Pro Glu Ile Asp Ala Ala Tyr Ala Ala Ile Ala Pro Glu
 65                  70                  75                  80

Leu Glu Gly Tyr Val Ser Val Ser Asp Tyr Ile Phe Ser Asp Arg Leu
                 85                  90                  95

Ala Lys Thr Val Ala Phe Gln Asp Ala Leu Gly Val Arg Asp Ala Asp
            100                 105                 110

Phe Ile Ala Gln Leu Val Ser Ala Val Gln Glu Asn Gly Gln Ile Lys
        115                 120                 125

Asn Leu Asp Asn Gly Glu Ala Thr Thr Ala Ile Asn Asn Phe Ser Gln
    130                 135                 140

Ala Trp Gly Val Leu Ala Leu His Arg Val Gly Glu Thr Glu Ala Ala
```

```
145                 150                 155                 160

Glu Arg Ala Thr Glu Phe Leu Lys Thr Gln Val Cys Ser Asp Gly Gly
                165                 170                 175

Val Gln Leu Ala Ser Ala Ile Glu Pro Thr Cys Lys Thr Thr Asp Ser
            180                 185                 190

Asp Val Thr Ala Met Ala Ala Gln Ala Leu Thr Leu Ala Asn Gly Ala
        195                 200                 205

Gln Asp Pro Thr Thr Gln Ala Thr Leu Asp Tyr Leu Val Thr Thr Met
    210                 215                 220

Asp Glu Thr Gly Gly Val Lys Asn Thr Trp Thr Gly Val Asn Ser Asn
225                 230                 235                 240

Ser Thr Gly Ile Val Gly Ser Ala Phe Ala Leu Ala Gly Asp Glu Glu
                245                 250                 255

Asn Tyr Leu Lys Ala Arg Glu Tyr Leu Ala Ser Val Gln Phe Gly Glu
            260                 265                 270

Asp Ala Asp Pro Ser Ile Gln Gly Gly Phe Ala Phe Thr Val Lys Ala
        275                 280                 285

Lys Glu Thr Asn Thr Ala Ile Ser Asp Gln Ile Arg Arg Ala Thr Gly
    290                 295                 300

Gln Ala Ala Leu Gly Phe Ala Gly Gly Asn Tyr Ala Asn Asp Lys Leu
305                 310                 315                 320

Ile Thr Ile Ala Asn Pro Val Asp Pro Thr Pro Asp Pro Glu Ile Pro
                325                 330                 335

Thr Pro Pro Ala Asp Ser Glu Gly Ser Thr Gly Gly Ile Gly Gly Ala
            340                 345                 350

Gly Ile Ile Ile Ala Ile Leu Ala Ile Leu Ala Ala Ile Ala Gly Val
        355                 360                 365

Met Gly Pro Met Met Ala Asn Leu Gln Phe
    370                 375


<210> 1883
<211> 606
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(583)
<223> RXA00693

<400> 1883
tccatcagcc ctccccgcg tgccccacgc ggggcacggt tagcgctgct aacctggccc 60

gatgtacaaa ttaatctcac cgcatttgtc aggccacgcc atg tgg aaa gag gct   115
                                              Met Trp Lys Glu Ala
                                                1               5
```

```
ttg gaa gaa ttc gga tca ggc ccc atc cac ggc tcg ggt tat ttc gag   163
Leu Glu Glu Phe Gly Ser Gly Pro Ile His Gly Ser Gly Tyr Phe Glu
                10                  15                  20

aac tat ctt ccc atc gac tat tcc gaa gca gga ttt cac cac tac ctc   211
Asn Tyr Leu Pro Ile Asp Tyr Ser Glu Ala Gly Phe His His Tyr Leu
            25                  30                  35

aag gag cgc act gac gcg gcc gat cct tcg gtt cca cca ccg gaa ggt   259
Lys Glu Arg Thr Asp Ala Ala Asp Pro Ser Val Pro Pro Pro Glu Gly
        40                  45                  50

ttt gtg cac tgc agc tat ttc tgg atc gtt gat gat gac gat gtt ctt   307
Phe Val His Cys Ser Tyr Phe Trp Ile Val Asp Asp Asp Asp Val Leu
    55                  60                  65

gtc gga ttc tta gct tta agg cac gag ctg aac caa cat ctc ctg gaa   355
Val Gly Phe Leu Ala Leu Arg His Glu Leu Asn Gln His Leu Leu Glu
70                  75                  80                  85

gtc gcg ggc cac att ggt tac ggc gtg cgc ccg tct gcg cgt cga aaa   403
Val Ala Gly His Ile Gly Tyr Gly Val Arg Pro Ser Ala Arg Arg Lys
                90                  95                  100

ggt gct gca acc gca gcg ctg aaa ctc ggt gtt cat gaa gct cag gcc   451
Gly Ala Ala Thr Ala Ala Leu Lys Leu Gly Val His Glu Ala Gln Ala
            105                 110                 115

ttg ggc atc gac aag gtt ttg ctg tgc gtc gca gga gat aac gaa gcg   499
Leu Gly Ile Asp Lys Val Leu Leu Cys Val Ala Gly Asp Asn Glu Ala
        120                 125                 130

tcc agg aac gtc atc gaa aag tgc ggt gga gtt tat gaa tcc acg atc   547
Ser Arg Asn Val Ile Glu Lys Cys Gly Gly Val Tyr Glu Ser Thr Ile
    135                 140                 145

cgt gga atg cga cgc tat tgg ata gcc aca gat tct taaaaaatct        593
Arg Gly Met Arg Arg Tyr Trp Ile Ala Thr Asp Ser
150                 155                 160

tcgcaagaac tta                                                   606
```

<210> 1884
<211> 161
<212> PRT
<213> Corynebacterium glutamicum

<400> 1884

```
Met Trp Lys Glu Ala Leu Glu Glu Phe Gly Ser Gly Pro Ile His Gly
  1               5                  10                  15

Ser Gly Tyr Phe Glu Asn Tyr Leu Pro Ile Asp Tyr Ser Glu Ala Gly
            20                  25                  30

Phe His His Tyr Leu Lys Glu Arg Thr Asp Ala Ala Asp Pro Ser Val
        35                  40                  45

Pro Pro Pro Glu Gly Phe Val His Cys Ser Tyr Phe Trp Ile Val Asp
    50                  55                  60
```

```
Asp Asp Asp Val Leu Val Gly Phe Leu Ala Leu Arg His Glu Leu Asn
 65                  70                  75                  80

Gln His Leu Leu Glu Val Ala Gly His Ile Gly Tyr Gly Val Arg Pro
                85                  90                  95

Ser Ala Arg Arg Lys Gly Ala Ala Thr Ala Ala Leu Lys Leu Gly Val
            100                 105                 110

His Glu Ala Gln Ala Leu Gly Ile Asp Lys Val Leu Leu Cys Val Ala
        115                 120                 125

Gly Asp Asn Glu Ala Ser Arg Asn Val Ile Glu Lys Cys Gly Gly Val
    130                 135                 140

Tyr Glu Ser Thr Ile Arg Gly Met Arg Arg Tyr Trp Ile Ala Thr Asp
145                 150                 155                 160

Ser
```

US20090275107A1

<210> 1885
<211> 498
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(475)
<223> RXA00701

<400> 1885
aagagacgat ggcgtatagg acgatgatga gcatttcctt tttgccgcgt acttggggga 60

```
gtaggccggc gccgaagctg acccaggcgg ctgcgagcat ttg gta ggg gag cca   115
                                               Leu Val Gly Glu Pro
                                                 1               5

cgg tcc gat tcc tgc ggt gag cag cgc gga tgc gaa cag tcc ggt gtt   163
Arg Ser Asp Ser Cys Gly Glu Gln Arg Gly Cys Glu Gln Ser Gly Val
                10                  15                  20

gcc gag gat gaa tcc gaa gcc ggg tcc gaa ggc tcg tcc gcc gag gat   211
Ala Glu Asp Glu Ser Glu Ala Gly Ser Glu Gly Ser Ser Ala Glu Asp
            25                  30                  35

gag gac aaa gaa gac tgc ttc aaa gcc tgc tgc gcc ggc acc gaa tgg   259
Glu Asp Lys Glu Asp Cys Phe Lys Ala Cys Cys Ala Gly Thr Glu Trp
        40                  45                  50

tcg gac tac ggc aac cat ggc ggt gag gac gcc gag cat ggc tac ggc   307
Ser Asp Tyr Gly Asn His Gly Gly Glu Asp Ala Glu His Gly Tyr Gly
    55                  60                  65

ttt aac gtc gaa tcc gtt ttc act gat ttc ggc gat gac agc ggc cag   355
Phe Asn Val Glu Ser Val Phe Thr Asp Phe Gly Asp Asp Ser Gly Gln
70                  75                  80                  85

cac gag ggg aat gac gat cgc gat gta gag ggg cgc ttg ggc ttt gtc   403
```

```
His Glu Gly Asn Asp Asp Arg Asp Val Glu Gly Arg Leu Gly Phe Val
                 90                  95                 100

gga cag gaa gga ttc cgg gtt gac gat cag cgg cca gaa gaa aat cac   451
Gly Gln Glu Gly Phe Arg Val Asp Asp Gln Arg Pro Glu Glu Asn His
            105                 110                 115

gat gct caa aac cgc aag gaa gct taaggtgagg aaggttttgg gct         498
Asp Ala Gln Asn Arg Lys Glu Ala
        120                 125


<210> 1886
<211> 125
<212> PRT
<213> Corynebacterium glutamicum

<400> 1886
Leu Val Gly Glu Pro Arg Ser Asp Ser Cys Gly Glu Gln Arg Gly Cys
  1               5                  10                  15

Glu Gln Ser Gly Val Ala Glu Asp Glu Ser Glu Ala Gly Ser Glu Gly
             20                  25                  30

Ser Ser Ala Glu Asp Glu Asp Lys Glu Asp Cys Phe Lys Ala Cys Cys
         35                  40                  45

Ala Gly Thr Glu Trp Ser Asp Tyr Gly Asn His Gly Gly Glu Asp Ala
     50                  55                  60

Glu His Gly Tyr Gly Phe Asn Val Glu Ser Val Phe Thr Asp Phe Gly
 65                  70                  75                  80

Asp Asp Ser Gly Gln His Glu Gly Asn Asp Asp Arg Asp Val Glu Gly
                 85                  90                  95

Arg Leu Gly Phe Val Gly Gln Glu Gly Phe Arg Val Asp Asp Gln Arg
            100                 105                 110

Pro Glu Glu Asn His Asp Ala Gln Asn Arg Lys Glu Ala
        115                 120                 125


<210> 1887
<211> 1095
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1072)
<223> RXA00707

<400> 1887
tagttaaaag cacttacctt aactggtagg tgctttttc atgtctacgc agtgggtaac 60

tttcagagga aaattaccca accaaaacaa aggaactttc atg aac gtg caa cgc   115
                                           Met Asn Val Gln Arg
                                             1               5

aaa ctg ctg gcg atc gta ggg gct ttc atg gca ggg tct tta gcc ttg   163
```

```
Lys Leu Leu Ala Ile Val Gly Ala Phe Met Ala Gly Ser Leu Ala Leu
                10                  15                  20

gga aca cca act gca cag gcc caa agc att ggc agc agt gcc tca cag   211
Gly Thr Pro Thr Ala Gln Ala Gln Ser Ile Gly Ser Ser Ala Ser Gln
            25                  30                  35

aga act gaa gtc tta cgt ggg ctg acc tca tct gcc gga ata cca gat   259
Arg Thr Glu Val Leu Arg Gly Leu Thr Ser Ser Ala Gly Ile Pro Asp
        40                  45                  50

gcc aca gcg ccg gaa ggc ggg gca aaa gtc gtg gtc ttt gga gat tca   307
Ala Thr Ala Pro Glu Gly Gly Ala Lys Val Val Val Phe Gly Asp Ser
    55                  60                  65

cat gca tca gga acc aat gca cca ttt gat gtg gat gaa cgc ggc tgc   355
His Ala Ser Gly Thr Asn Ala Pro Phe Asp Val Asp Glu Arg Gly Cys
70                  75                  80                  85

ctc aag ggg aac caa tcg tgg cct gat caa ttg caa gca caa caa gga   403
Leu Lys Gly Asn Gln Ser Trp Pro Asp Gln Leu Gln Ala Gln Gln Gly
                90                  95                  100

ttg cag cag ggg gag ctc att gac ctt tcc tgc aac ggc gcc tcc atc   451
Leu Gln Gln Gly Glu Leu Ile Asp Leu Ser Cys Asn Gly Ala Ser Ile
            105                 110                 115

aac tcg acg ggt ttc cac ttt tcc gat gaa gtt cgg cat gca gaa gca   499
Asn Ser Thr Gly Phe His Phe Ser Asp Glu Val Arg His Ala Glu Ala
        120                 125                 130

cta ggg gcc att gga cca aat acc gag aac atc ttc atc caa ttt ggc   547
Leu Gly Ala Ile Gly Pro Asn Thr Glu Asn Ile Phe Ile Gln Phe Gly
    135                 140                 145

aag aat gat cag tgg gga cac tca cca atc aat ttg cgc tat tcc gtg   595
Lys Asn Asp Gln Trp Gly His Ser Pro Ile Asn Leu Arg Tyr Ser Val
150                 155                 160                 165

atc aac tgc ctt ttt gat gcg gcc aac gga tgc ggt gag aaa gct gta   643
Ile Asn Cys Leu Phe Asp Ala Ala Asn Gly Cys Gly Glu Lys Ala Val
                170                 175                 180

gcg gct gga acc atg cag gat ccc tcc tcg gtc acc ggc gaa aac tat   691
Ala Ala Gly Thr Met Gln Asp Pro Ser Ser Val Thr Gly Glu Asn Tyr
            185                 190                 195

gct cag cgg atg aaa cct gtc atc gac tac ctc aag tac tac gct cca   739
Ala Gln Arg Met Lys Pro Val Ile Asp Tyr Leu Lys Tyr Tyr Ala Pro
        200                 205                 210

aat gcg cag atc acg ttg ctg gga tac cag gaa tac acc cca cga agc   787
Asn Ala Gln Ile Thr Leu Leu Gly Tyr Gln Glu Tyr Thr Pro Arg Ser
    215                 220                 225

gga agc gag att tgt gtc cgc gtg gga ggt acg gaa cta agg aaa cca   835
Gly Ser Glu Ile Cys Val Arg Val Gly Gly Thr Glu Leu Arg Lys Pro
230                 235                 240                 245

gac gcc acc aac ctg gtg tcc tat atg aac aat ctt gag tcg gcc att   883
Asp Ala Thr Asn Leu Val Ser Tyr Met Asn Asn Leu Glu Ser Ala Ile
```

```
                250                 255                 260

ttt gaa gcc tct gag att ctt gac gtc cag cat gcc aat ctc cgt gag   931
Phe Glu Ala Ser Glu Ile Leu Asp Val Gln His Ala Asn Leu Arg Glu
            265                 270                 275

gcc act gca gga cac agc agc tgc tca gct gaa ccg tgg gtc aac gga   979
Ala Thr Ala Gly His Ser Ser Cys Ser Ala Glu Pro Trp Val Asn Gly
        280                 285                 290

gtg ctg gat atg cgg gta aac gct gta gga ggc acc tgg cac cca tct   1027
Val Leu Asp Met Arg Val Asn Ala Val Gly Gly Thr Trp His Pro Ser
    295                 300                 305

cca aag gga gat gaa gtg acc gcg ggc ctc ctc gga acc ttg atg       1072
Pro Lys Gly Asp Glu Val Thr Ala Gly Leu Leu Gly Thr Leu Met
310                 315                 320

taactatcta gaattcttca tag                                        1095
```

<210> 1888
<211> 324
<212> PRT
<213> Corynebacterium glutamicum

<400> 1888

```
Met Asn Val Gln Arg Lys Leu Leu Ala Ile Val Gly Ala Phe Met Ala
  1               5                  10                  15

Gly Ser Leu Ala Leu Gly Thr Pro Thr Ala Gln Ala Gln Ser Ile Gly
             20                  25                  30

Ser Ser Ala Ser Gln Arg Thr Glu Val Leu Arg Gly Leu Thr Ser Ser
         35                  40                  45

Ala Gly Ile Pro Asp Ala Thr Ala Pro Glu Gly Gly Ala Lys Val Val
     50                  55                  60

Val Phe Gly Asp Ser His Ala Ser Gly Thr Asn Ala Pro Phe Asp Val
 65                  70                  75                  80

Asp Glu Arg Gly Cys Leu Lys Gly Asn Gln Ser Trp Pro Asp Gln Leu
                 85                  90                  95

Gln Ala Gln Gln Gly Leu Gln Gln Gly Glu Leu Ile Asp Leu Ser Cys
            100                 105                 110

Asn Gly Ala Ser Ile Asn Ser Thr Gly Phe His Phe Ser Asp Glu Val
        115                 120                 125

Arg His Ala Glu Ala Leu Gly Ala Ile Gly Pro Asn Thr Glu Asn Ile
    130                 135                 140

Phe Ile Gln Phe Gly Lys Asn Asp Gln Trp Gly His Ser Pro Ile Asn
145                 150                 155                 160

Leu Arg Tyr Ser Val Ile Asn Cys Leu Phe Asp Ala Ala Asn Gly Cys
                165                 170                 175

Gly Glu Lys Ala Val Ala Ala Gly Thr Met Gln Asp Pro Ser Ser Val
```

```
            180                 185                 190

Thr Gly Glu Asn Tyr Ala Gln Arg Met Lys Pro Val Ile Asp Tyr Leu
        195                 200                 205

Lys Tyr Tyr Ala Pro Asn Ala Gln Ile Thr Leu Leu Gly Tyr Gln Glu
    210                 215                 220

Tyr Thr Pro Arg Ser Gly Ser Glu Ile Cys Val Arg Val Gly Gly Thr
225                 230                 235                 240

Glu Leu Arg Lys Pro Asp Ala Thr Asn Leu Val Ser Tyr Met Asn Asn
                245                 250                 255

Leu Glu Ser Ala Ile Phe Glu Ala Ser Glu Ile Leu Asp Val Gln His
            260                 265                 270

Ala Asn Leu Arg Glu Ala Thr Ala Gly His Ser Ser Cys Ser Ala Glu
        275                 280                 285

Pro Trp Val Asn Gly Val Leu Asp Met Arg Val Asn Ala Val Gly Gly
    290                 295                 300

Thr Trp His Pro Ser Pro Lys Gly Asp Glu Val Thr Ala Gly Leu Leu
305                 310                 315                 320

Gly Thr Leu Met
```

20040229 09:39:37 a

<210> 1889
<211> 1056
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (71)..(1033)
<223> RXA00713

<400> 1889

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aaccacgcct ccttgtgcgg gcctgtcagt aactgttatc gcaggttcat gcgttaaggt 60

gtggaagacc atg aca aaa gta gcg gag ctg gac caa gag tgg tcc gaa    109
           Met Thr Lys Val Ala Glu Leu Asp Gln Glu Trp Ser Glu
             1               5                  10

gta gat gac gcg gaa tta gac gcg caa agc gct ggc act tct gat agt   157
Val Asp Asp Ala Glu Leu Asp Ala Gln Ser Ala Gly Thr Ser Asp Ser
     15                  20                  25

tcc agc aca gac gac ttc gct gac gca gaa aac act tct gaa aat ctg   205
Ser Ser Thr Asp Asp Phe Ala Asp Ala Glu Asn Thr Ser Glu Asn Leu
 30                  35                  40                  45

gga ccc atc ggc cca gaa cca ctc cct gaa cca gat ggg gat gtt ccg   253
Gly Pro Ile Gly Pro Glu Pro Leu Pro Glu Pro Asp Gly Asp Val Pro
                 50                  55                  60

gca tcg ggt ttc caa gtg cag ctc gat aat ttt gaa ggt cct ttt gac   301
Ala Ser Gly Phe Gln Val Gln Leu Asp Asn Phe Glu Gly Pro Phe Asp
```

```
                65                  70                  75

ctt ctc ctg cag ctg att acc aag aag aaa ctt gat gtc act gaa gtt   349
Leu Leu Leu Gln Leu Ile Thr Lys Lys Lys Leu Asp Val Thr Glu Val
         80                  85                  90

gcc ttg gcc cag gtg acc gac gag ttt att gct tac acc cga aaa ctg   397
Ala Leu Ala Gln Val Thr Asp Glu Phe Ile Ala Tyr Thr Arg Lys Leu
     95                 100                 105

ggc gaa acc agc gat ttg gat gag acc aca gag ttc tta gtg gtg gcc   445
Gly Glu Thr Ser Asp Leu Asp Glu Thr Thr Glu Phe Leu Val Val Ala
110                 115                 120                 125

gca acg ctg ttg gat ctt aaa aca gct cgc ctg ctc ccg cgt ggt gaa   493
Ala Thr Leu Leu Asp Leu Lys Thr Ala Arg Leu Leu Pro Arg Gly Glu
                130                 135                 140

gtc gac gat gaa gat gat ctc gaa ttg ctc gaa ata aag gat ctc ctt   541
Val Asp Asp Glu Asp Asp Leu Glu Leu Leu Glu Ile Lys Asp Leu Leu
            145                 150                 155

ttc gcc agg ttg ttg cag tat cgc gct tac aag caa gtt gcg gaa atg   589
Phe Ala Arg Leu Leu Gln Tyr Arg Ala Tyr Lys Gln Val Ala Glu Met
        160                 165                 170

ttt gcg caa tgg cag cga gat gct cga cgc agg tac ccg cgc gct gtc   637
Phe Ala Gln Trp Gln Arg Asp Ala Arg Arg Arg Tyr Pro Arg Ala Val
    175                 180                 185

tca tta gaa act cag ttt gcc aac ctc ttg ccg ccc gtt tcc ttg ggt   685
Ser Leu Glu Thr Gln Phe Ala Asn Leu Leu Pro Pro Val Ser Leu Gly
190                 195                 200                 205

cat tcc tta aaa agt ttc agc gag ttg gct gct gtg gtg ttt cgt ccg   733
His Ser Leu Lys Ser Phe Ser Glu Leu Ala Ala Val Val Phe Arg Pro
                210                 215                 220

aaa ccc cca gag acg gtg aaa aca gat cac gtg cac caa gtt gcg gtg   781
Lys Pro Pro Glu Thr Val Lys Thr Asp His Val His Gln Val Ala Val
            225                 230                 235

tca gtt cca gag caa gcg ggc agg att ctt aac acg ttg aaa ctt gcc   829
Ser Val Pro Glu Gln Ala Gly Arg Ile Leu Asn Thr Leu Lys Leu Ala
        240                 245                 250

gga att gat cat tat ttg agc ttt cag ctg ctc aca cgt gat tgt acc   877
Gly Ile Asp His Tyr Leu Ser Phe Gln Leu Leu Thr Arg Asp Cys Thr
    255                 260                 265

gcg tca atg gaa gtg att ggc cgc ttc ctt gcc ttg ctg gaa ttg tat   925
Ala Ser Met Glu Val Ile Gly Arg Phe Leu Ala Leu Leu Glu Leu Tyr
270                 275                 280                 285

aag gca cgc gct att gaa acc ttg caa gaa gag cca ctc ggc gag ctt   973
Lys Ala Arg Ala Ile Glu Thr Leu Gln Glu Glu Pro Leu Gly Glu Leu
                290                 295                 300

aaa gtt tcg tgg act ggc att gat gtc gat cca gca gtc gtc gcg gcg   1021
Lys Val Ser Trp Thr Gly Ile Asp Val Asp Pro Ala Val Val Ala Ala
            305                 310                 315
```

agt gac tgg gag taatcagttt ttcttaagga aac 1056
Ser Asp Trp Glu
320

<210> 1890
<211> 321
<212> PRT
<213> Corynebacterium glutamicum

<400> 1890
Met Thr Lys Val Ala Glu Leu Asp Gln Glu Trp Ser Glu Val Asp Asp
1 5 10 15

Ala Glu Leu Asp Ala Gln Ser Ala Gly Thr Ser Asp Ser Ser Ser Thr
20 25 30

Asp Asp Phe Ala Asp Ala Glu Asn Thr Ser Glu Asn Leu Gly Pro Ile
35 40 45

Gly Pro Glu Pro Leu Pro Glu Pro Asp Gly Asp Val Pro Ala Ser Gly
50 55 60

Phe Gln Val Gln Leu Asp Asn Phe Glu Gly Pro Phe Asp Leu Leu Leu
65 70 75 80

Gln Leu Ile Thr Lys Lys Lys Leu Asp Val Thr Glu Val Ala Leu Ala
85 90 95

Gln Val Thr Asp Glu Phe Ile Ala Tyr Thr Arg Lys Leu Gly Glu Thr
100 105 110

Ser Asp Leu Asp Glu Thr Thr Glu Phe Leu Val Val Ala Ala Thr Leu
115 120 125

Leu Asp Leu Lys Thr Ala Arg Leu Leu Pro Arg Gly Glu Val Asp Asp
130 135 140

Glu Asp Asp Leu Glu Leu Leu Glu Ile Lys Asp Leu Leu Phe Ala Arg
145 150 155 160

Leu Leu Gln Tyr Arg Ala Tyr Lys Gln Val Ala Glu Met Phe Ala Gln
165 170 175

Trp Gln Arg Asp Ala Arg Arg Arg Tyr Pro Arg Ala Val Ser Leu Glu
180 185 190

Thr Gln Phe Ala Asn Leu Leu Pro Pro Val Ser Leu Gly His Ser Leu
195 200 205

Lys Ser Phe Ser Glu Leu Ala Ala Val Val Phe Arg Pro Lys Pro Pro
210 215 220

Glu Thr Val Lys Thr Asp His Val His Gln Val Ala Val Ser Val Pro
225 230 235 240

Glu Gln Ala Gly Arg Ile Leu Asn Thr Leu Lys Leu Ala Gly Ile Asp
245 250 255

His Tyr Leu Ser Phe Gln Leu Leu Thr Arg Asp Cys Thr Ala Ser Met

```
            260                 265                 270

Glu Val Ile Gly Arg Phe Leu Ala Leu Leu Glu Leu Tyr Lys Ala Arg
        275                 280                 285

Ala Ile Glu Thr Leu Gln Glu Glu Pro Leu Gly Glu Leu Lys Val Ser
    290                 295                 300

Trp Thr Gly Ile Asp Val Asp Pro Ala Val Val Ala Ala Ser Asp Trp
305                 310                 315                 320

Glu
```

<210> 1891
<211> 684
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(661)
<223> RXA00714

<400> 1891

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cgtcaatcaa gctgtcaaaa aaaatacaag ttaggtcaca aaatgatttc agtcgtgaga 60

accatcacat ataagacatc tcatgatcta acatttcttc atg gct acg att aca   115
                                              Met Ala Thr Ile Thr
                                                1               5

cgc acc gac aga ctg atc ctc gta ccg ctc act gtt gag ctc gaa gac   163
Arg Thr Asp Arg Leu Ile Leu Val Pro Leu Thr Val Glu Leu Glu Asp
                10                  15                  20

gag gcc cac cag att tac tct gat tct cga atc tgg gaa cac cgc ccc   211
Glu Ala His Gln Ile Tyr Ser Asp Ser Arg Ile Trp Glu His Arg Pro
            25                  30                  35

cag gcg cgt cac acc aac gtg cgt gtc acg cgc gac atc atc aag cgc   259
Gln Ala Arg His Thr Asn Val Arg Val Thr Arg Asp Ile Ile Lys Arg
        40                  45                  50

acc aat gaa agc tgg ggc aag aaa gac ctt ggc ccc tgg ggt gtt tac   307
Thr Asn Glu Ser Trp Gly Lys Lys Asp Leu Gly Pro Trp Gly Val Tyr
    55                  60                  65

ctc cgt gac cgc cca tcg gaa ttc gtt ggc gtt ggt ggc gtt gaa ctc   355
Leu Arg Asp Arg Pro Ser Glu Phe Val Gly Val Gly Gly Val Glu Leu
70                  75                  80                  85

atc gac gga aaa gta tgg gac ctc aag tac cgc ctc cgc ccc gac cta   403
Ile Asp Gly Lys Val Trp Asp Leu Lys Tyr Arg Leu Arg Pro Asp Leu
                90                  95                  100

tgg ggc aat gga tac gcc acg gaa atc tcc aac gcc gca aca ctg gcc   451
Trp Gly Asn Gly Tyr Ala Thr Glu Ile Ser Asn Ala Ala Thr Leu Ala
            105                 110                 115

acc aag cgt atc gac gac agc ctc cca ctc acg gcc agg gtg act acc   499
```

```
Thr Lys Arg Ile Asp Asp Ser Leu Pro Leu Thr Ala Arg Val Thr Thr
        120                 125                 130

aac cac cct gcc tca ttc cgt att ttg gaa aaa ctg gga ctc acc ccc   547
Asn His Pro Ala Ser Phe Arg Ile Leu Glu Lys Leu Gly Leu Thr Pro
    135                 140                 145

gta tgg gaa ggc cga cga gtc gga acg gaa gat gac ccc aac gag cct   595
Val Trp Glu Gly Arg Arg Val Gly Thr Glu Asp Asp Pro Asn Glu Pro
150                 155                 160                 165

gat gtg aga att tat tct gac cgt ccg cta tcg gat gaa att ctt gaa   643
Asp Val Arg Ile Tyr Ser Asp Arg Pro Leu Ser Asp Glu Ile Leu Glu
                170                 175                 180

atg ctc aag caa cga cca tagaccagaa aatctcaccc ctt                684
Met Leu Lys Gln Arg Pro
            185
```

<210> 1892
<211> 187
<212> PRT
<213> Corynebacterium glutamicum

<400> 1892

```
Met Ala Thr Ile Thr Arg Thr Asp Arg Leu Ile Leu Val Pro Leu Thr
  1               5                  10                  15

Val Glu Leu Glu Asp Glu Ala His Gln Ile Tyr Ser Asp Ser Arg Ile
             20                  25                  30

Trp Glu His Arg Pro Gln Ala Arg His Thr Asn Val Arg Val Thr Arg
         35                  40                  45

Asp Ile Ile Lys Arg Thr Asn Glu Ser Trp Gly Lys Lys Asp Leu Gly
     50                  55                  60

Pro Trp Gly Val Tyr Leu Arg Asp Arg Pro Ser Glu Phe Val Gly Val
 65                  70                  75                  80

Gly Gly Val Glu Leu Ile Asp Gly Lys Val Trp Asp Leu Lys Tyr Arg
                 85                  90                  95

Leu Arg Pro Asp Leu Trp Gly Asn Gly Tyr Ala Thr Glu Ile Ser Asn
            100                 105                 110

Ala Ala Thr Leu Ala Thr Lys Arg Ile Asp Asp Ser Leu Pro Leu Thr
        115                 120                 125

Ala Arg Val Thr Thr Asn His Pro Ala Ser Phe Arg Ile Leu Glu Lys
    130                 135                 140

Leu Gly Leu Thr Pro Val Trp Glu Gly Arg Arg Val Gly Thr Glu Asp
145                 150                 155                 160

Asp Pro Asn Glu Pro Asp Val Arg Ile Tyr Ser Asp Arg Pro Leu Ser
                165                 170                 175

Asp Glu Ile Leu Glu Met Leu Lys Gln Arg Pro
            180                 185
```

<210> 1893
<211> 636
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(613)
<223> RXA00716

<400> 1893
aaagccgatt gcttaacgcc cgctatgata accactcatg aatgatttcg atccagcatt 60

gatttccgcg atgagcctta tccctcagac gaggtctcgg atg gaa tca atc ttg 115
Met Glu Ser Ile Leu
1 5

ttg gtg gtc gat acc cca gtt tca gca cgc acg ctg gct ggg gtg ttg 163
Leu Val Val Asp Thr Pro Val Ser Ala Arg Thr Leu Ala Gly Val Leu
10 15 20

ggc att gac gtg cct gca aca gag gca att ttg aag gaa atg gcc ttt 211
Gly Ile Asp Val Pro Ala Thr Glu Ala Ile Leu Lys Glu Met Ala Phe
25 30 35

gag ctt tct gaa cgg ggc agc ggc att gat ctg cgg gaa acg gca gaa 259
Glu Leu Ser Glu Arg Gly Ser Gly Ile Asp Leu Arg Glu Thr Ala Glu
40 45 50

gga tgg cgc tat tac acc cgc ccg gaa aat gcg gac atc gtc gag caa 307
Gly Trp Arg Tyr Tyr Thr Arg Pro Glu Asn Ala Asp Ile Val Glu Gln
55 60 65

ttc ctc ctc gat gga aac caa acc aga ctg tcc cgt gca gca ttg gaa 355
Phe Leu Leu Asp Gly Asn Gln Thr Arg Leu Ser Arg Ala Ala Leu Glu
70 75 80 85

aca ctc gcg gtg gtg gca tat cgg cag ccg gtc aca cgc tcc cag att 403
Thr Leu Ala Val Val Ala Tyr Arg Gln Pro Val Thr Arg Ser Gln Ile
90 95 100

tca gca gtg cgc gga gta aat gtc gac ggc gtc atg aga acc ttg cag 451
Ser Ala Val Arg Gly Val Asn Val Asp Gly Val Met Arg Thr Leu Gln
105 110 115

ctt cga ggc cta gtc aaa gaa gtc gat gtg gac gaa tca acg ggc gca 499
Leu Arg Gly Leu Val Lys Glu Val Asp Val Asp Glu Ser Thr Gly Ala
120 125 130

cac cgc tat ggc aca acg gaa ttg ctg ctt gag ctg ttg ggt att gat 547
His Arg Tyr Gly Thr Thr Glu Leu Leu Leu Glu Leu Leu Gly Ile Asp
135 140 145

tct ttg gat aaa tta cca gat cta gca ccg ctt ttg ccg gat gtt gac 595
Ser Leu Asp Lys Leu Pro Asp Leu Ala Pro Leu Leu Pro Asp Val Asp
150 155 160 165

tcc att gat gaa gac ttc taaagcatca gttaaagccc cga 636
Ser Ile Asp Glu Asp Phe

170

<210> 1894
<211> 171
<212> PRT
<213> Corynebacterium glutamicum

<400> 1894
Met Glu Ser Ile Leu Leu Val Val Asp Thr Pro Val Ser Ala Arg Thr
1 5 10 15

Leu Ala Gly Val Leu Gly Ile Asp Val Pro Ala Thr Glu Ala Ile Leu
20 25 30

Lys Glu Met Ala Phe Glu Leu Ser Glu Arg Gly Ser Gly Ile Asp Leu
35 40 45

Arg Glu Thr Ala Glu Gly Trp Arg Tyr Tyr Thr Arg Pro Glu Asn Ala
50 55 60

Asp Ile Val Glu Gln Phe Leu Leu Asp Gly Asn Gln Thr Arg Leu Ser
65 70 75 80

Arg Ala Ala Leu Glu Thr Leu Ala Val Val Ala Tyr Arg Gln Pro Val
85 90 95

Thr Arg Ser Gln Ile Ser Ala Val Arg Gly Val Asn Val Asp Gly Val
100 105 110

Met Arg Thr Leu Gln Leu Arg Gly Leu Val Lys Glu Val Asp Val Asp
115 120 125

Glu Ser Thr Gly Ala His Arg Tyr Gly Thr Thr Glu Leu Leu Leu Glu
130 135 140

Leu Leu Gly Ile Asp Ser Leu Asp Lys Leu Pro Asp Leu Ala Pro Leu
145 150 155 160

Leu Pro Asp Val Asp Ser Ile Asp Glu Asp Phe
165 170

<210> 1895
<211> 1752
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1729)
<223> RXA00719

<400> 1895
cagatgatgc acacatcgtg gacacctctg atatgaccat ggatcaagta cttgatcacc 60

tcatccacct agtggaagcc tccgctgaaa ggagcaacca gtg act gat aaa cac 115
Val Thr Asp Lys His
1 5

acc atg cct ggt gaa gag gac gac acc gta ttc gtc tac cac acc cac 163

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Thr Met Pro Gly Glu Glu Asp Asp Thr Val Phe Val Tyr His Thr His
                10                  15                  20

aaa ggc gaa atg gac gtc gaa ggt gcg ttt gct gac gaa gaa gaa cta   211
Lys Gly Glu Met Asp Val Glu Gly Ala Phe Ala Asp Glu Glu Glu Leu
            25                  30                  35

gca cca cac ggc ggt tgg gct tcc gca gat ttc gac cca gca gaa ttc   259
Ala Pro His Gly Gly Trp Ala Ser Ala Asp Phe Asp Pro Ala Glu Phe
        40                  45                  50

ggc tac gaa gac tct gac gat gac ttc gat gca gag gac ttt gac gaa   307
Gly Tyr Glu Asp Ser Asp Asp Asp Phe Asp Ala Glu Asp Phe Asp Glu
    55                  60                  65

aca gag ttc tcc aac cct gat ttc ggc gaa gac tac tct gat gaa gac   355
Thr Glu Phe Ser Asn Pro Asp Phe Gly Glu Asp Tyr Ser Asp Glu Asp
70                  75                  80                  85

tgg gaa gaa atc gag acc gca ttc gga ttc gac cca agc cac ctt gaa   403
Trp Glu Glu Ile Glu Thr Ala Phe Gly Phe Asp Pro Ser His Leu Glu
                90                  95                  100

gaa gct ctc tgc acg gtc gct atc gtc gga cgc cca aat gtt ggt aaa   451
Glu Ala Leu Cys Thr Val Ala Ile Val Gly Arg Pro Asn Val Gly Lys
            105                 110                 115

tca acc ttg gtg aac cgc ttt att gga cgt cga gaa gca gtc gtg gaa   499
Ser Thr Leu Val Asn Arg Phe Ile Gly Arg Arg Glu Ala Val Val Glu
        120                 125                 130

gat ttc ccc ggc gta acc cgt gac cgc atc tcc tac atc tct gac tgg   547
Asp Phe Pro Gly Val Thr Arg Asp Arg Ile Ser Tyr Ile Ser Asp Trp
    135                 140                 145

ggt gga cac cgt ttc tgg gtt cag gac aca ggc gga tgg gat cct aac   595
Gly Gly His Arg Phe Trp Val Gln Asp Thr Gly Gly Trp Asp Pro Asn
150                 155                 160                 165

gtc aag ggc atc cac gca tcg atc gca cag caa gca gaa gtt gct atg   643
Val Lys Gly Ile His Ala Ser Ile Ala Gln Gln Ala Glu Val Ala Met
                170                 175                 180

agc act gcc gat gtc atc gta ttc gtc gtg gac acc aag gtg ggc atc   691
Ser Thr Ala Asp Val Ile Val Phe Val Val Asp Thr Lys Val Gly Ile
            185                 190                 195

acc gaa act gac tca gtg atg gca gca aaa ctg ttg cgc tcg gaa gtg   739
Thr Glu Thr Asp Ser Val Met Ala Ala Lys Leu Leu Arg Ser Glu Val
        200                 205                 210

cca gtg atc ttg gtt gcg aac aaa ttc gac tcc gac agc cag tgg gct   787
Pro Val Ile Leu Val Ala Asn Lys Phe Asp Ser Asp Ser Gln Trp Ala
    215                 220                 225

gac atg gct gag ttc tac agc ctc ggc ctt ggc gat cca tac cca gtt   835
Asp Met Ala Glu Phe Tyr Ser Leu Gly Leu Gly Asp Pro Tyr Pro Val
230                 235                 240                 245

tca gcc cag cat gga cgt ggt ggc gct gac gtt ttg gac aaa gtc ctt   883
Ser Ala Gln His Gly Arg Gly Gly Ala Asp Val Leu Asp Lys Val Leu
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                250                 255                 260

gaa ctc ttc cca gaa gag cct cgc tcc aag tcc atc gtg gaa ggc cct   931
Glu Leu Phe Pro Glu Glu Pro Arg Ser Lys Ser Ile Val Glu Gly Pro
            265                 270                 275

cgt cgt gtc gcc ctt gtg ggt aag cca aac gtg ggt aag tct tca ctg   979
Arg Arg Val Ala Leu Val Gly Lys Pro Asn Val Gly Lys Ser Ser Leu
        280                 285                 290

ctc aac aag ttt gct ggc gag acc cgc tct gtc gtg gac aat gtt gca   1027
Leu Asn Lys Phe Ala Gly Glu Thr Arg Ser Val Val Asp Asn Val Ala
    295                 300                 305

gga acc acc gtt gac ccc gtt gac tcc ctg att cag ctg gat caa aaa   1075
Gly Thr Thr Val Asp Pro Val Asp Ser Leu Ile Gln Leu Asp Gln Lys
310                 315                 320                 325

ctg tgg aaa ttc gtg gat act gct ggt ctt cgc aaa aag gtc aag act   1123
Leu Trp Lys Phe Val Asp Thr Ala Gly Leu Arg Lys Lys Val Lys Thr
                330                 335                 340

gca tct ggc cac gag tac tac gca tca ctg cgt acc cac ggt gcc atc   1171
Ala Ser Gly His Glu Tyr Tyr Ala Ser Leu Arg Thr His Gly Ala Ile
            345                 350                 355

gat gca gct gag ctg tgt gtt ttg ctt atc gat tcc tcc gaa ccc atc   1219
Asp Ala Ala Glu Leu Cys Val Leu Leu Ile Asp Ser Ser Glu Pro Ile
        360                 365                 370

acc gag cag gat cag cgc gtg ctc gca atg atc acc gat gcc ggt aag   1267
Thr Glu Gln Asp Gln Arg Val Leu Ala Met Ile Thr Asp Ala Gly Lys
    375                 380                 385

gca ctg gtt att gcg ttc aac aag tgg gat ctc atg gat gaa gat cgc   1315
Ala Leu Val Ile Ala Phe Asn Lys Trp Asp Leu Met Asp Glu Asp Arg
390                 395                 400                 405

cgc atc gat ttg gat cgc gaa ctt gat ctc cag ttg gca cac gtg cct   1363
Arg Ile Asp Leu Asp Arg Glu Leu Asp Leu Gln Leu Ala His Val Pro
                410                 415                 420

tgg gca aag cgc atc aac atc tcc gcc aaa acc ggt cgt gca ctg cag   1411
Trp Ala Lys Arg Ile Asn Ile Ser Ala Lys Thr Gly Arg Ala Leu Gln
            425                 430                 435

cgc ctc gag cca gca atg ttg gaa gcg ctc gac aac tgg gat cgc cgt   1459
Arg Leu Glu Pro Ala Met Leu Glu Ala Leu Asp Asn Trp Asp Arg Arg
        440                 445                 450

atc tcc act ggt cag ctg aac acc tgg ctg cgt gaa gca att gct gcg   1507
Ile Ser Thr Gly Gln Leu Asn Thr Trp Leu Arg Glu Ala Ile Ala Ala
    455                 460                 465

aac cca cca cca atg cgt ggc gga cgt ttg cct cga gtg ctg ttt gcc   1555
Asn Pro Pro Pro Met Arg Gly Gly Arg Leu Pro Arg Val Leu Phe Ala
470                 475                 480                 485

acc cag gca tct act cag cca cca gtg atc gta ctg ttc acc acc ggc   1603
Thr Gln Ala Ser Thr Gln Pro Pro Val Ile Val Leu Phe Thr Thr Gly
                490                 495                 500
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ttc ctc gaa gca ggt tac cga cga tac ctg gag cgc aag ttc cgt gaa   1651
Phe Leu Glu Ala Gly Tyr Arg Arg Tyr Leu Glu Arg Lys Phe Arg Glu
            505                 510                 515

cgt ttc ggc ttt gaa ggc act cca gtg cga atc gct gtg cgt gtt cgc   1699
Arg Phe Gly Phe Glu Gly Thr Pro Val Arg Ile Ala Val Arg Val Arg
        520                 525                 530

gag cgc cgc ggc aag ggc gga aac aag cag taaagcttga ttttccctaa     1749
Glu Arg Arg Gly Lys Gly Gly Asn Lys Gln
    535                 540

aag                                                               1752


<210> 1896
<211> 543
<212> PRT
<213> Corynebacterium glutamicum

<400> 1896
Val Thr Asp Lys His Thr Met Pro Gly Glu Glu Asp Asp Thr Val Phe
  1               5                  10                  15

Val Tyr His Thr His Lys Gly Glu Met Asp Val Glu Gly Ala Phe Ala
             20                  25                  30

Asp Glu Glu Glu Leu Ala Pro His Gly Gly Trp Ala Ser Ala Asp Phe
         35                  40                  45

Asp Pro Ala Glu Phe Gly Tyr Glu Asp Ser Asp Asp Asp Phe Asp Ala
     50                  55                  60

Glu Asp Phe Asp Glu Thr Glu Phe Ser Asn Pro Asp Phe Gly Glu Asp
 65                  70                  75                  80

Tyr Ser Asp Glu Asp Trp Glu Glu Ile Glu Thr Ala Phe Gly Phe Asp
                 85                  90                  95

Pro Ser His Leu Glu Glu Ala Leu Cys Thr Val Ala Ile Val Gly Arg
            100                 105                 110

Pro Asn Val Gly Lys Ser Thr Leu Val Asn Arg Phe Ile Gly Arg Arg
        115                 120                 125

Glu Ala Val Val Glu Asp Phe Pro Gly Val Thr Arg Asp Arg Ile Ser
    130                 135                 140

Tyr Ile Ser Asp Trp Gly Gly His Arg Phe Trp Val Gln Asp Thr Gly
145                 150                 155                 160

Gly Trp Asp Pro Asn Val Lys Gly Ile His Ala Ser Ile Ala Gln Gln
                165                 170                 175

Ala Glu Val Ala Met Ser Thr Ala Asp Val Ile Val Phe Val Val Asp
            180                 185                 190

Thr Lys Val Gly Ile Thr Glu Thr Asp Ser Val Met Ala Ala Lys Leu
        195                 200                 205
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Leu Arg Ser Glu Val Pro Val Ile Leu Val Ala Asn Lys Phe Asp Ser
    210                 215                 220

Asp Ser Gln Trp Ala Asp Met Ala Glu Phe Tyr Ser Leu Gly Leu Gly
225                 230                 235                 240

Asp Pro Tyr Pro Val Ser Ala Gln His Gly Arg Gly Gly Ala Asp Val
                245                 250                 255

Leu Asp Lys Val Leu Glu Leu Phe Pro Glu Glu Pro Arg Ser Lys Ser
            260                 265                 270

Ile Val Glu Gly Pro Arg Arg Val Ala Leu Val Gly Lys Pro Asn Val
        275                 280                 285

Gly Lys Ser Ser Leu Leu Asn Lys Phe Ala Gly Glu Thr Arg Ser Val
    290                 295                 300

Val Asp Asn Val Ala Gly Thr Thr Val Asp Pro Val Asp Ser Leu Ile
305                 310                 315                 320

Gln Leu Asp Gln Lys Leu Trp Lys Phe Val Asp Thr Ala Gly Leu Arg
                325                 330                 335

Lys Lys Val Lys Thr Ala Ser Gly His Glu Tyr Tyr Ala Ser Leu Arg
            340                 345                 350

Thr His Gly Ala Ile Asp Ala Ala Glu Leu Cys Val Leu Leu Ile Asp
        355                 360                 365

Ser Ser Glu Pro Ile Thr Glu Gln Asp Gln Arg Val Leu Ala Met Ile
    370                 375                 380

Thr Asp Ala Gly Lys Ala Leu Val Ile Ala Phe Asn Lys Trp Asp Leu
385                 390                 395                 400

Met Asp Glu Asp Arg Arg Ile Asp Leu Asp Arg Glu Leu Asp Leu Gln
                405                 410                 415

Leu Ala His Val Pro Trp Ala Lys Arg Ile Asn Ile Ser Ala Lys Thr
            420                 425                 430

Gly Arg Ala Leu Gln Arg Leu Glu Pro Ala Met Leu Glu Ala Leu Asp
        435                 440                 445

Asn Trp Asp Arg Arg Ile Ser Thr Gly Gln Leu Asn Thr Trp Leu Arg
    450                 455                 460

Glu Ala Ile Ala Ala Asn Pro Pro Pro Met Arg Gly Gly Arg Leu Pro
465                 470                 475                 480

Arg Val Leu Phe Ala Thr Gln Ala Ser Thr Gln Pro Pro Val Ile Val
                485                 490                 495

Leu Phe Thr Thr Gly Phe Leu Glu Ala Gly Tyr Arg Arg Tyr Leu Glu
            500                 505                 510

Arg Lys Phe Arg Glu Arg Phe Gly Phe Glu Gly Thr Pro Val Arg Ile
        515                 520                 525

Ala Val Arg Val Arg Glu Arg Arg Gly Lys Gly Gly Asn Lys Gln
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    530                 535                 540


<210> 1897
<211> 671
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(648)
<223> RXA00724

<400> 1897
atc ggt gag gaa gtc ctc gcc gga cgc caa gcc tat gtg gtg tgt ccg   48
Ile Gly Glu Glu Val Leu Ala Gly Arg Gln Ala Tyr Val Val Cys Pro
  1               5                  10                  15

cgc att gaa ggc gaa ggc ggc gtg ctg gaa atc cac gcc tat ctt tcc   96
Arg Ile Glu Gly Glu Gly Gly Val Leu Glu Ile His Ala Tyr Leu Ser
             20                  25                  30

gaa cag gta tat cca gga ttg aat gtt gga atg ctg cac ggt cgc atg   144
Glu Gln Val Tyr Pro Gly Leu Asn Val Gly Met Leu His Gly Arg Met
         35                  40                  45

gac acg gat ctc aaa gat tcg gtc atg cag gaa ttc gcc caa ggt gag   192
Asp Thr Asp Leu Lys Asp Ser Val Met Gln Glu Phe Ala Gln Gly Glu
     50                  55                  60

atc gat att ttg gtc gcc acc acg gtc att gag gtc ggt att gac gtt   240
Ile Asp Ile Leu Val Ala Thr Thr Val Ile Glu Val Gly Ile Asp Val
 65                  70                  75                  80

gcc aac gcc acc gtc atg ctc atc cgc gag gcg gaa cgc ttc ggc gtt   288
Ala Asn Ala Thr Val Met Leu Ile Arg Glu Ala Glu Arg Phe Gly Val
                 85                  90                  95

tcc cag atc cac cag ctg cgc ggc cgt gtt ggc cgt ggg cag cac gat   336
Ser Gln Ile His Gln Leu Arg Gly Arg Val Gly Arg Gly Gln His Asp
            100                 105                 110

tcc ctc tgc ctg ctg cac acc acc ttc gac gag gac tcc cca caa ggc   384
Ser Leu Cys Leu Leu His Thr Thr Phe Asp Glu Asp Ser Pro Gln Gly
        115                 120                 125

caa cgc ctc gcc gca att tcc acc aca acc gac ggt ttt caa ctc tct   432
Gln Arg Leu Ala Ala Ile Ser Thr Thr Thr Asp Gly Phe Gln Leu Ser
    130                 135                 140

gaa ctt gat ttg cag gta cgc caa gaa ggc gac gtg ttg ggc acc cgc   480
Glu Leu Asp Leu Gln Val Arg Gln Glu Gly Asp Val Leu Gly Thr Arg
145                 150                 155                 160

cag tcc ggc agc gac acc aaa ctc cgt cac ctc tcg ttt atc agc gac   528
Gln Ser Gly Ser Asp Thr Lys Leu Arg His Leu Ser Phe Ile Ser Asp
                165                 170                 175

caa aaa atc atc gag cgt gcg ctt atc gac gcc acc gag ctg gtt gcc   576
Gln Lys Ile Ile Glu Arg Ala Leu Ile Asp Ala Thr Glu Leu Val Ala
            180                 185                 190
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gcc agc cgt tcc agg gcg ctt gag ctg gtc agc gac atc gca atg atc   624
Ala Ser Arg Ser Arg Ala Leu Glu Leu Val Ser Asp Ile Ala Met Ile
        195                 200                 205

aac cag gaa tac ctg gaa aag agc tgatattgat agggtttaag tca         671
Asn Gln Glu Tyr Leu Glu Lys Ser
    210                 215


<210> 1898
<211> 216
<212> PRT
<213> Corynebacterium glutamicum

<400> 1898
Ile Gly Glu Glu Val Leu Ala Gly Arg Gln Ala Tyr Val Val Cys Pro
  1               5                  10                  15

Arg Ile Glu Gly Glu Gly Gly Val Leu Glu Ile His Ala Tyr Leu Ser
             20                  25                  30

Glu Gln Val Tyr Pro Gly Leu Asn Val Gly Met Leu His Gly Arg Met
         35                  40                  45

Asp Thr Asp Leu Lys Asp Ser Val Met Gln Glu Phe Ala Gln Gly Glu
     50                  55                  60

Ile Asp Ile Leu Val Ala Thr Thr Val Ile Glu Val Gly Ile Asp Val
 65                  70                  75                  80

Ala Asn Ala Thr Val Met Leu Ile Arg Glu Ala Glu Arg Phe Gly Val
                 85                  90                  95

Ser Gln Ile His Gln Leu Arg Gly Arg Val Gly Arg Gly Gln His Asp
            100                 105                 110

Ser Leu Cys Leu Leu His Thr Thr Phe Asp Glu Asp Ser Pro Gln Gly
        115                 120                 125

Gln Arg Leu Ala Ala Ile Ser Thr Thr Thr Asp Gly Phe Gln Leu Ser
    130                 135                 140

Glu Leu Asp Leu Gln Val Arg Gln Glu Gly Asp Val Leu Gly Thr Arg
145                 150                 155                 160

Gln Ser Gly Ser Asp Thr Lys Leu Arg His Leu Ser Phe Ile Ser Asp
                165                 170                 175

Gln Lys Ile Ile Glu Arg Ala Leu Ile Asp Ala Thr Glu Leu Val Ala
            180                 185                 190

Ala Ser Arg Ser Arg Ala Leu Glu Leu Val Ser Asp Ile Ala Met Ile
        195                 200                 205

Asn Gln Glu Tyr Leu Glu Lys Ser
    210                 215


<210> 1899
<211> 164
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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(141)
<223> RXA00726

<400> 1899
cac gaa atg ggc ttc gcc cac gaa gtc gcc gac cag gtc gtg ttc atg 48
His Glu Met Gly Phe Ala His Glu Val Ala Asp Gln Val Val Phe Met
1 5 10 15

gcc gat gga gtt gtc gtt gaa gcc gga acc ccc gaa caa gtt ctg gac 96
Ala Asp Gly Val Val Val Glu Ala Gly Thr Pro Glu Gln Val Leu Asp
20 25 30

aat cca aag gaa cag cgc acc aaa gac ttc ctg tct tct ctg ctc 141
Asn Pro Lys Glu Gln Arg Thr Lys Asp Phe Leu Ser Ser Leu Leu
35 40 45

taacctttc gggtcttaaa aaa 164

<210> 1900
<211> 47
<212> PRT
<213> Corynebacterium glutamicum

<400> 1900
His Glu Met Gly Phe Ala His Glu Val Ala Asp Gln Val Val Phe Met
1 5 10 15

Ala Asp Gly Val Val Val Glu Ala Gly Thr Pro Glu Gln Val Leu Asp
20 25 30

Asn Pro Lys Glu Gln Arg Thr Lys Asp Phe Leu Ser Ser Leu Leu
35 40 45

<210> 1901
<211> 702
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(679)
<223> RXA00740

<400> 1901
gttataaata ttaaagtacg ctaaccatgg gtgcaggggg agacttctac agcagtcatg 60

gtccacacca cgactgctgt atatattaag gacgtaactc atg ttg aag aat aaa 115
Met Leu Lys Asn Lys
1 5

act ctt gcg ctg ctg gct gtc agt acg ctg atg ttt ggc tta tct gct 163
Thr Leu Ala Leu Leu Ala Val Ser Thr Leu Met Phe Gly Leu Ser Ala
10 15 20

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tgc tct agt gat gct gac ggc ccg gac agt agc ggt gct agt agt agc   211
Cys Ser Ser Asp Ala Asp Gly Pro Asp Ser Ser Gly Ala Ser Ser Ser
            25                  30                  35

agt act ggc tca tct tct gca tcg gct gac aca aca gat tct gca gct   259
Ser Thr Gly Ser Ser Ser Ala Ser Ala Asp Thr Thr Asp Ser Ala Ala
        40                  45                  50

gtt gat aag gat gct caa tta gac acc ttt atg cgt tct gct gtg gct   307
Val Asp Lys Asp Ala Gln Leu Asp Thr Phe Met Arg Ser Ala Val Ala
    55                  60                  65

gat gga tca tct gct gct gtg gct gtg gac aac gct gta ggt aag ggc   355
Asp Gly Ser Ser Ala Ala Val Ala Val Asp Asn Ala Val Gly Lys Gly
70                  75                  80                  85

ttt gat aaa gct gat gcg cag gcg gct gcg gag cgc ttg ggt gat ggt   403
Phe Asp Lys Ala Asp Ala Gln Ala Ala Ala Glu Arg Leu Gly Asp Gly
                90                  95                  100

ttc caa ttc gct gcg gat tac cag gct gtt ggc tat ttg gaa tct tgg   451
Phe Gln Phe Ala Ala Asp Tyr Gln Ala Val Gly Tyr Leu Glu Ser Trp
            105                 110                 115

tac ttt ggt ggc gcg cga agc gag aag ctt gac gag gtg cgt agt gat   499
Tyr Phe Gly Gly Ala Arg Ser Glu Lys Leu Asp Glu Val Arg Ser Asp
        120                 125                 130

gtc atc gct cat ttg tct gaa ttg gga ttt aca gat tta gag gct gaa   547
Val Ile Ala His Leu Ser Glu Leu Gly Phe Thr Asp Leu Glu Ala Glu
    135                 140                 145

tcc tcg gca tct cgt att aca tta ggt gat tac tgt gat ggg gtc cct   595
Ser Ser Ala Ser Arg Ile Thr Leu Gly Asp Tyr Cys Asp Gly Val Pro
150                 155                 160                 165

gag tat tgt gag ttg ttt ttt gat ggc gaa tct cct gac ttg tat gac   643
Glu Tyr Cys Glu Leu Phe Phe Asp Gly Glu Ser Pro Asp Leu Tyr Asp
                170                 175                 180

atg ggt acg gag ctt gac tcg tat aag ccc act gaa taaagctatt        689
Met Gly Thr Glu Leu Asp Ser Tyr Lys Pro Thr Glu
            185                 190

tcacttaaag cac                                                   702
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<210> 1902
<211> 193
<212> PRT
<213> Corynebacterium glutamicum

<400> 1902

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Met Leu Lys Asn Lys Thr Leu Ala Leu Leu Ala Val Ser Thr Leu Met
  1               5                  10                  15

Phe Gly Leu Ser Ala Cys Ser Ser Asp Ala Asp Gly Pro Asp Ser Ser
            20                  25                  30

Gly Ala Ser Ser Ser Ser Thr Gly Ser Ser Ser Ala Ser Ala Asp Thr
        35                  40                  45
```

```
Thr Asp Ser Ala Ala Val Asp Lys Asp Ala Gln Leu Asp Thr Phe Met
     50                  55                  60

Arg Ser Ala Val Ala Asp Gly Ser Ser Ala Ala Val Ala Val Asp Asn
 65                  70                  75                  80

Ala Val Gly Lys Gly Phe Asp Lys Ala Asp Ala Gln Ala Ala Ala Glu
                 85                  90                  95

Arg Leu Gly Asp Gly Phe Gln Phe Ala Ala Asp Tyr Gln Ala Val Gly
            100                 105                 110

Tyr Leu Glu Ser Trp Tyr Phe Gly Gly Ala Arg Ser Glu Lys Leu Asp
        115                 120                 125

Glu Val Arg Ser Asp Val Ile Ala His Leu Ser Glu Leu Gly Phe Thr
    130                 135                 140

Asp Leu Glu Ala Glu Ser Ser Ala Ser Arg Ile Thr Leu Gly Asp Tyr
145                 150                 155                 160

Cys Asp Gly Val Pro Glu Tyr Cys Glu Leu Phe Phe Asp Gly Glu Ser
                165                 170                 175

Pro Asp Leu Tyr Asp Met Gly Thr Glu Leu Asp Ser Tyr Lys Pro Thr
            180                 185                 190

Glu
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<210> 1903
<211> 1056
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1033)
<223> RXA00741

<400> 1903
tggtgatcac taggtccacc tcgtcttgca tggtggtcac ctcagtccag aacgcattga 60

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ttgacaccga tcaaatgttt gatggattat gatatttagc atg act gat tct ctg   115
                                            Met Thr Asp Ser Leu
                                              1               5

ctt gta tcc atc aga aaa ggc tta ata gaa gag cgt cca tta acg gag   163
Leu Val Ser Ile Arg Lys Gly Leu Ile Glu Glu Arg Pro Leu Thr Glu
                 10                  15                  20

ctt ctt cgg gcg tgt atc ttc ctt gga agt gat act aac tcg gac tct   211
Leu Leu Arg Ala Cys Ile Phe Leu Gly Ser Asp Thr Asn Ser Asp Ser
             25                  30                  35

tta caa gag tgg gcg aaa aat gaa tta aat ggt tat ggc tcc att gat   259
Leu Gln Glu Trp Ala Lys Asn Glu Leu Asn Gly Tyr Gly Ser Ile Asp
         40                  45                  50
```

```
ggt att ccg gaa tat cgc aaa ttg aaa gga cct cct gta ttc gcg aaa   307
Gly Ile Pro Glu Tyr Arg Lys Leu Lys Gly Pro Pro Val Phe Ala Lys
     55                  60                  65

att caa gct ggt aat tca ata atg tct aat atg gta ctg ggg cca cat   355
Ile Gln Ala Gly Asn Ser Ile Met Ser Asn Met Val Leu Gly Pro His
 70                  75                  80                  85

aat gtt cct gaa aga gct cgt aag tat ttc cct gaa gag ctg cat ttt   403
Asn Val Pro Glu Arg Ala Arg Lys Tyr Phe Pro Glu Glu Leu His Phe
                 90                  95                 100

gat cag ccg att caa acg cta att gaa tgg tcg act agg cag gat ggg   451
Asp Gln Pro Ile Gln Thr Leu Ile Glu Trp Ser Thr Arg Gln Asp Gly
            105                 110                 115

att aat tta tcg ccc ccg aat tta ctt cgg gtc cgc gat ctt cat aat   499
Ile Asn Leu Ser Pro Pro Asn Leu Leu Arg Val Arg Asp Leu His Asn
        120                 125                 130

gat cag tac gcg cca tta aat caa att ttg aat tta aat gtt tac tta   547
Asp Gln Tyr Ala Pro Leu Asn Gln Ile Leu Asn Leu Asn Val Tyr Leu
    135                 140                 145

gat aac tct tat ttt tcg gga att gtg gac cgc atc cga act cta atg   595
Asp Asn Ser Tyr Phe Ser Gly Ile Val Asp Arg Ile Arg Thr Leu Met
150                 155                 160                 165

act tcc atg att gcc gac ctc aca cac gca act cct ctg gat gaa cta   643
Thr Ser Met Ile Ala Asp Leu Thr His Ala Thr Pro Leu Asp Glu Leu
                170                 175                 180

cca agc agc gaa aag gtt aat gcc acg gtc atg aag cac att gaa aat   691
Pro Ser Ser Glu Lys Val Asn Ala Thr Val Met Lys His Ile Glu Asn
            185                 190                 195

aac tac gaa act aca atc act caa gcc aat gga gct gta gcc att ggt   739
Asn Tyr Glu Thr Thr Ile Thr Gln Ala Asn Gly Ala Val Ala Ile Gly
        200                 205                 210

aac agc gct aaa gct gtg cag aag gga ttg tcc gtg gat gac cta ctg   787
Asn Ser Ala Lys Ala Val Gln Lys Gly Leu Ser Val Asp Asp Leu Leu
    215                 220                 225

aag att atg cag acc att aat cct gaa aag ttc gac tta ggg gaa gct   835
Lys Ile Met Gln Thr Ile Asn Pro Glu Lys Phe Asp Leu Gly Glu Ala
230                 235                 240                 245

aga gct gaa gcc gaa gaa agc att caa tcc atc gcg gat gag ttg aag   883
Arg Ala Glu Ala Glu Glu Ser Ile Gln Ser Ile Ala Asp Glu Leu Lys
                250                 255                 260

aag gag tct ccg aat aaa ggt ttt atc cag aat gct ttt gaa aag ttg   931
Lys Glu Ser Pro Asn Lys Gly Phe Ile Gln Asn Ala Phe Glu Lys Leu
            265                 270                 275

aag gaa ctc agc ata aaa gcc ggc gat aaa gcc ttc act aca atg tta   979
Lys Glu Leu Ser Ile Lys Ala Gly Asp Lys Ala Phe Thr Thr Met Leu
        280                 285                 290

aat ctt gta ggt aaa cag ata atc gaa aac atc cca caa ctg gtt tca   1027
```

```
Asn Leu Val Gly Lys Gln Ile Ile Glu Asn Ile Pro Gln Leu Val Ser
    295                 300                 305

ggt ggc tagagaaatt caaggccgtc agc                                    1056
Gly Gly
310
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<210> 1904
<211> 311
<212> PRT
<213> Corynebacterium glutamicum

<400> 1904

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Met Thr Asp Ser Leu Leu Val Ser Ile Arg Lys Gly Leu Ile Glu Glu
  1               5                  10                  15

Arg Pro Leu Thr Glu Leu Leu Arg Ala Cys Ile Phe Leu Gly Ser Asp
             20                  25                  30

Thr Asn Ser Asp Ser Leu Gln Glu Trp Ala Lys Asn Glu Leu Asn Gly
         35                  40                  45

Tyr Gly Ser Ile Asp Gly Ile Pro Glu Tyr Arg Lys Leu Lys Gly Pro
     50                  55                  60

Pro Val Phe Ala Lys Ile Gln Ala Gly Asn Ser Ile Met Ser Asn Met
 65                  70                  75                  80

Val Leu Gly Pro His Asn Val Pro Glu Arg Ala Arg Lys Tyr Phe Pro
                 85                  90                  95

Glu Glu Leu His Phe Asp Gln Pro Ile Gln Thr Leu Ile Glu Trp Ser
            100                 105                 110

Thr Arg Gln Asp Gly Ile Asn Leu Ser Pro Pro Asn Leu Leu Arg Val
        115                 120                 125

Arg Asp Leu His Asn Asp Gln Tyr Ala Pro Leu Asn Gln Ile Leu Asn
    130                 135                 140

Leu Asn Val Tyr Leu Asp Asn Ser Tyr Phe Ser Gly Ile Val Asp Arg
145                 150                 155                 160

Ile Arg Thr Leu Met Thr Ser Met Ile Ala Asp Leu Thr His Ala Thr
                165                 170                 175

Pro Leu Asp Glu Leu Pro Ser Ser Glu Lys Val Asn Ala Thr Val Met
            180                 185                 190

Lys His Ile Glu Asn Asn Tyr Glu Thr Thr Ile Thr Gln Ala Asn Gly
        195                 200                 205

Ala Val Ala Ile Gly Asn Ser Ala Lys Ala Val Gln Lys Gly Leu Ser
    210                 215                 220

Val Asp Asp Leu Leu Lys Ile Met Gln Thr Ile Asn Pro Glu Lys Phe
225                 230                 235                 240

Asp Leu Gly Glu Ala Arg Ala Glu Ala Glu Glu Ser Ile Gln Ser Ile
                245                 250                 255
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Ala Asp Glu Leu Lys Lys Glu Ser Pro Asn Lys Gly Phe Ile Gln Asn
            260                 265                 270

Ala Phe Glu Lys Leu Lys Glu Leu Ser Ile Lys Ala Gly Asp Lys Ala
        275                 280                 285

Phe Thr Thr Met Leu Asn Leu Val Gly Lys Gln Ile Ile Glu Asn Ile
    290                 295                 300

Pro Gln Leu Val Ser Gly Gly
305                 310


<210> 1905
<211> 1773
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1750)
<223> RXA00742

<400> 1905
agaggggttt tttagtgaaa atgataaaac cacttttaca gatggacaca tagatattag 60

taatgatgct tctggagcta agcgtagctt tgggggtcgg gtg aat gtt cag att   115
                                          Val Asn Val Gln Ile
                                            1               5

aaa ggg cga aag gtt aat gcc aag gct gcc gac tta aat agc tat ccg   163
Lys Gly Arg Lys Val Asn Ala Lys Ala Ala Asp Leu Asn Ser Tyr Pro
                10                  15                  20

gtc tca gta gtt gat cta cga ggc ttc gtg aca ctg gct ggt ctc tta   211
Val Ser Val Val Asp Leu Arg Gly Phe Val Thr Leu Ala Gly Leu Leu
             25                  30                  35

ttt ttt gtg gtt gat att gat aag aaa tca aat aag aaa tat cca aag   259
Phe Phe Val Val Asp Ile Asp Lys Lys Ser Asn Lys Lys Tyr Pro Lys
         40                  45                  50

tat gtt ctt ttg aaa ccg ttt tat att cat gat cta ctg agt aaa gcg   307
Tyr Val Leu Leu Lys Pro Phe Tyr Ile His Asp Leu Leu Ser Lys Ala
     55                  60                  65

aag ccg ggc caa aag aca att agc gtc cgc tta aaa cgg tta cca tct   355
Lys Pro Gly Gln Lys Thr Ile Ser Val Arg Leu Lys Arg Leu Pro Ser
 70                  75                  80                  85

gat gaa gat cga atg gaa gcc ata atc gca tta gcg ctc gca tcg agg   403
Asp Glu Asp Arg Met Glu Ala Ile Ile Ala Leu Ala Leu Ala Ser Arg
                90                  95                 100

caa gaa aag ata gtc gag aac ccc agt aac tat ctc tat gaa aat atg   451
Gln Glu Lys Ile Val Glu Asn Pro Ser Asn Tyr Leu Tyr Glu Asn Met
            105                 110                 115

gaa tca att act gtt aaa tcg gct gaa ccc ctt aat agg gat aag ctg   499
Glu Ser Ile Thr Val Lys Ser Ala Glu Pro Leu Asn Arg Asp Lys Leu
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        120                 125                 130

gct gta tat gat ggt agt tcg cca gac cat tcg atc att att cgt act   547
Ala Val Tyr Asp Gly Ser Ser Pro Asp His Ser Ile Ile Ile Arg Thr
    135                 140                 145

ggg gat gga att gaa cag ttc gtc aat gcc acc gta gaa ata ata ccc   595
Gly Asp Gly Ile Glu Gln Phe Val Asn Ala Thr Val Glu Ile Ile Pro
150                 155                 160                 165

ccg aat atg cag ttt cat caa gcc aat tat aat gtt tcg tgt aat ggg   643
Pro Asn Met Gln Phe His Gln Ala Asn Tyr Asn Val Ser Cys Asn Gly
                170                 175                 180

gtc gtc tat gac aat gtt ttg cat cga aac att gat gat gag cac att   691
Val Val Tyr Asp Asn Val Leu His Arg Asn Ile Asp Asp Glu His Ile
            185                 190                 195

gaa ttg aaa atc gga aag ggg att act ctc cgc cta caa aag ctc gcc   739
Glu Leu Lys Ile Gly Lys Gly Ile Thr Leu Arg Leu Gln Lys Leu Ala
        200                 205                 210

att gat gct ccg ggg agc gtt acg gtt gag ttt caa gat agt ctt cct   787
Ile Asp Ala Pro Gly Ser Val Thr Val Glu Phe Gln Asp Ser Leu Pro
    215                 220                 225

gaa cgg tta aaa gac att gag ttc ttc cta gga gtg ctt cag gcg aat   835
Glu Arg Leu Lys Asp Ile Glu Phe Phe Leu Gly Val Leu Gln Ala Asn
230                 235                 240                 245

acg ttt ttt att aat gaa gaa cct gtt gtg ttg aag att aac tcg aac   883
Thr Phe Phe Ile Asn Glu Glu Pro Val Val Leu Lys Ile Asn Ser Asn
                250                 255                 260

cgg act gtg gct gac ctt aag gat gaa gcg ggt gtt ctt cgt cag ttg   931
Arg Thr Val Ala Asp Leu Lys Asp Glu Ala Gly Val Leu Arg Gln Leu
            265                 270                 275

gta gaa ata gct aac cat ttc aat att gat ccg tcc ctt att cga att   979
Val Glu Ile Ala Asn His Phe Asn Ile Asp Pro Ser Leu Ile Arg Ile
        280                 285                 290

ggt gag att aca gaa aaa cag ttc tgg cag ttg gat att gtg tat cga  1027
Gly Glu Ile Thr Glu Lys Gln Phe Trp Gln Leu Asp Ile Val Tyr Arg
    295                 300                 305

aca gcc gtt aag gga gaa tac gta aag aat tta gag gtt aaa gat gag  1075
Thr Ala Val Lys Gly Glu Tyr Val Lys Asn Leu Glu Val Lys Asp Glu
310                 315                 320                 325

act aga ctt ata ttg cag cct ttt ggt cgt tgg aat ctt gcg ttg ata  1123
Thr Arg Leu Ile Leu Gln Pro Phe Gly Arg Trp Asn Leu Ala Leu Ile
                330                 335                 340

gct cac cct ggt gat gtt gca ggg gag tgg act tat cat gaa gta att  1171
Ala His Pro Gly Asp Val Ala Gly Glu Trp Thr Tyr His Glu Val Ile
            345                 350                 355

tcc aag cgt cat cat ttt gct atg aca cct tca acg gat cgg agc gac  1219
Ser Lys Arg His His Phe Ala Met Thr Pro Ser Thr Asp Arg Ser Asp
        360                 365                 370
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tcc tca atc gag cga gtg acg ccg tac gag ctc att gat aat cga tgg   1267
Ser Ser Ile Glu Arg Val Thr Pro Tyr Glu Leu Ile Asp Asn Arg Trp
    375                 380                 385

ctt cca tca gta ttg aat ctg cat ttg gat aag ctt gtt gat ttc tat   1315
Leu Pro Ser Val Leu Asn Leu His Leu Asp Lys Leu Val Asp Phe Tyr
390                 395                 400                 405

tca gcg ctt gaa gaa act gtt gat gtt gat aat ctc gcc aca tgg atg   1363
Ser Ala Leu Glu Glu Thr Val Asp Val Asp Asn Leu Ala Thr Trp Met
                410                 415                 420

gtg ctt cgc cta att aag gca gct gat tct gag cag agc agg aaa act   1411
Val Leu Arg Leu Ile Lys Ala Ala Asp Ser Glu Gln Ser Arg Lys Thr
            425                 430                 435

gca ttt ctt ata gca gct caa gct ctc aat gat tgg ctc gtg gaa cga   1459
Ala Phe Leu Ile Ala Ala Gln Ala Leu Asn Asp Trp Leu Val Glu Arg
        440                 445                 450

gat cga gaa gag tcg cca att tac agg ctt aat ggt tgg caa att ttg   1507
Asp Arg Glu Glu Ser Pro Ile Tyr Arg Leu Asn Gly Trp Gln Ile Leu
    455                 460                 465

tat cgc caa act gga tta ctg gat tca caa aga aca gaa att cga tct   1555
Tyr Arg Gln Thr Gly Leu Leu Asp Ser Gln Arg Thr Glu Ile Arg Ser
470                 475                 480                 485

ttt agg cat aat ctt gat caa aca atg cac cca gac aac tat agc gag   1603
Phe Arg His Asn Leu Asp Gln Thr Met His Pro Asp Asn Tyr Ser Glu
                490                 495                 500

att atg att ggt tgc gct ttg ctt ctt gac gat aga gaa gag gcg aat   1651
Ile Met Ile Gly Cys Ala Leu Leu Leu Asp Asp Arg Glu Glu Ala Asn
            505                 510                 515

ttt ttg ctt act cag ctt tcg gtt gat cga cgc gca gtt ttt aat gaa   1699
Phe Leu Leu Thr Gln Leu Ser Val Asp Arg Arg Ala Val Phe Asn Glu
        520                 525                 530

tgg ccg ata gct caa ttg atg acg ggt gcc cta aaa gaa gag att gaa   1747
Trp Pro Ile Ala Gln Leu Met Thr Gly Ala Leu Lys Glu Glu Ile Glu
    535                 540                 545

aaa tgagttctga gatcttgatt taa                                    1773
Lys
550
```

<210> 1906
<211> 550
<212> PRT
<213> Corynebacterium glutamicum

<400> 1906

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Val Asn Val Gln Ile Lys Gly Arg Lys Val Asn Ala Lys Ala Ala Asp
  1               5                  10                  15

Leu Asn Ser Tyr Pro Val Ser Val Val Asp Leu Arg Gly Phe Val Thr
             20                  25                  30
```

```
Leu Ala Gly Leu Leu Phe Phe Val Val Asp Ile Asp Lys Lys Ser Asn
         35                  40                  45

Lys Lys Tyr Pro Lys Tyr Val Leu Leu Lys Pro Phe Tyr Ile His Asp
     50                  55                  60

Leu Leu Ser Lys Ala Lys Pro Gly Gln Lys Thr Ile Ser Val Arg Leu
 65                  70                  75                  80

Lys Arg Leu Pro Ser Asp Glu Asp Arg Met Glu Ala Ile Ile Ala Leu
                 85                  90                  95

Ala Leu Ala Ser Arg Gln Glu Lys Ile Val Glu Asn Pro Ser Asn Tyr
            100                 105                 110

Leu Tyr Glu Asn Met Glu Ser Ile Thr Val Lys Ser Ala Glu Pro Leu
        115                 120                 125

Asn Arg Asp Lys Leu Ala Val Tyr Asp Gly Ser Ser Pro Asp His Ser
    130                 135                 140

Ile Ile Ile Arg Thr Gly Asp Gly Ile Glu Gln Phe Val Asn Ala Thr
145                 150                 155                 160

Val Glu Ile Ile Pro Pro Asn Met Gln Phe His Gln Ala Asn Tyr Asn
                165                 170                 175

Val Ser Cys Asn Gly Val Val Tyr Asp Asn Val Leu His Arg Asn Ile
            180                 185                 190

Asp Asp Glu His Ile Glu Leu Lys Ile Gly Lys Gly Ile Thr Leu Arg
        195                 200                 205

Leu Gln Lys Leu Ala Ile Asp Ala Pro Gly Ser Val Thr Val Glu Phe
    210                 215                 220

Gln Asp Ser Leu Pro Glu Arg Leu Lys Asp Ile Glu Phe Phe Leu Gly
225                 230                 235                 240

Val Leu Gln Ala Asn Thr Phe Phe Ile Asn Glu Glu Pro Val Val Leu
                245                 250                 255

Lys Ile Asn Ser Asn Arg Thr Val Ala Asp Leu Lys Asp Glu Ala Gly
            260                 265                 270

Val Leu Arg Gln Leu Val Glu Ile Ala Asn His Phe Asn Ile Asp Pro
        275                 280                 285

Ser Leu Ile Arg Ile Gly Glu Ile Thr Glu Lys Gln Phe Trp Gln Leu
    290                 295                 300

Asp Ile Val Tyr Arg Thr Ala Val Lys Gly Glu Tyr Val Lys Asn Leu
305                 310                 315                 320

Glu Val Lys Asp Glu Thr Arg Leu Ile Leu Gln Pro Phe Gly Arg Trp
                325                 330                 335

Asn Leu Ala Leu Ile Ala His Pro Gly Asp Val Ala Gly Glu Trp Thr
            340                 345                 350
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```
Tyr His Glu Val Ile Ser Lys Arg His His Phe Ala Met Thr Pro Ser
        355                 360                 365

Thr Asp Arg Ser Asp Ser Ser Ile Glu Arg Val Thr Pro Tyr Glu Leu
    370                 375                 380

Ile Asp Asn Arg Trp Leu Pro Ser Val Leu Asn Leu His Leu Asp Lys
385                 390                 395                 400

Leu Val Asp Phe Tyr Ser Ala Leu Glu Glu Thr Val Asp Val Asp Asn
                405                 410                 415

Leu Ala Thr Trp Met Val Leu Arg Leu Ile Lys Ala Ala Asp Ser Glu
            420                 425                 430

Gln Ser Arg Lys Thr Ala Phe Leu Ile Ala Ala Gln Ala Leu Asn Asp
        435                 440                 445

Trp Leu Val Glu Arg Asp Arg Glu Glu Ser Pro Ile Tyr Arg Leu Asn
    450                 455                 460

Gly Trp Gln Ile Leu Tyr Arg Gln Thr Gly Leu Leu Asp Ser Gln Arg
465                 470                 475                 480

Thr Glu Ile Arg Ser Phe Arg His Asn Leu Asp Gln Thr Met His Pro
                485                 490                 495

Asp Asn Tyr Ser Glu Ile Met Ile Gly Cys Ala Leu Leu Leu Asp Asp
            500                 505                 510

Arg Glu Glu Ala Asn Phe Leu Leu Thr Gln Leu Ser Val Asp Arg Arg
        515                 520                 525

Ala Val Phe Asn Glu Trp Pro Ile Ala Gln Leu Met Thr Gly Ala Leu
    530                 535                 540

Lys Glu Glu Ile Glu Lys
545                 550
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Application Filed Electronically

<210> 1907
<211> 546
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(523)
<223> RXA00743

<400> 1907
attttggcgt agtgtttcgg gttttatagg ttgagattga ataccaaga caaggatgga 60

catcatgtca gcgcatctac cttctcatca tgatgagtta gtg cag cac tta gtt 115
                                              Val Gln His Leu Val
                                                1   5

ctt gcg gat gta aag tat cgg gag ctc agt gcg tta tcg gtc aaa att 163
Leu Ala Asp Val Lys Tyr Arg Glu Leu Ser Ala Leu Ser Val Lys Ile
                10   15   20

```
gag gaa cca tca gat cgt cct gag ttt aaa ctt gga gtt act gtt aac   211
Glu Glu Pro Ser Asp Arg Pro Glu Phe Lys Leu Gly Val Thr Val Asn
             25                  30                  35

gac aag agt aaa gac gaa gaa ggt gtg ccg cga atc att gag gtt tca   259
Asp Lys Ser Lys Asp Glu Glu Gly Val Pro Arg Ile Ile Glu Val Ser
         40                  45                  50

ttg agg gtg tcc atc gag gtt ccc gac gga aag ata acg gta gag cct   307
Leu Arg Val Ser Ile Glu Val Pro Asp Gly Lys Ile Thr Val Glu Pro
     55                  60                  65

gaa gca atc tat ttg att cct gag aat aag gtt tat tta acg gaa tct   355
Glu Ala Ile Tyr Leu Ile Pro Glu Asn Lys Val Tyr Leu Thr Glu Ser
 70                  75                  80                  85

gat gca atg gtg gat tat ttt aac aac cat gcg att ttt act ctg gtg   403
Asp Ala Met Val Asp Tyr Phe Asn Asn His Ala Ile Phe Thr Leu Val
                 90                  95                 100

cca tat gca cga cag gcc gtg tct gat tta ggg cag cgt gca ttc cac   451
Pro Tyr Ala Arg Gln Ala Val Ser Asp Leu Gly Gln Arg Ala Phe His
            105                 110                 115

acg cag atc ctc atg cct gcg tta ggt cct ggt gat ttg gtt ttt agt   499
Thr Gln Ile Leu Met Pro Ala Leu Gly Pro Gly Asp Leu Val Phe Ser
        120                 125                 130

aaa tcg acg gcc tca cga gaa tgg tagagaatta cctgatagtt gca         546
Lys Ser Thr Ala Ser Arg Glu Trp
    135                 140
```

Do not add any new matter to the disclosure

<210> 1908
<211> 141
<212> PRT
<213> Corynebacterium glutamicum

<400> 1908

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Val Gln His Leu Val Leu Ala Asp Val Lys Tyr Arg Glu Leu Ser Ala
  1               5                  10                  15

Leu Ser Val Lys Ile Glu Glu Pro Ser Asp Arg Pro Glu Phe Lys Leu
             20                  25                  30

Gly Val Thr Val Asn Asp Lys Ser Lys Asp Glu Glu Gly Val Pro Arg
         35                  40                  45

Ile Ile Glu Val Ser Leu Arg Val Ser Ile Glu Val Pro Asp Gly Lys
     50                  55                  60

Ile Thr Val Glu Pro Glu Ala Ile Tyr Leu Ile Pro Glu Asn Lys Val
 65                  70                  75                  80

Tyr Leu Thr Glu Ser Asp Ala Met Val Asp Tyr Phe Asn Asn His Ala
                 85                  90                  95

Ile Phe Thr Leu Val Pro Tyr Ala Arg Gln Ala Val Ser Asp Leu Gly
            100                 105                 110

Gln Arg Ala Phe His Thr Gln Ile Leu Met Pro Ala Leu Gly Pro Gly
```

```
        115                 120                 125

Asp Leu Val Phe Ser Lys Ser Thr Ala Ser Arg Glu Trp
    130                 135                 140


<210> 1909
<211> 657
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(634)
<223> RXA00745

<400> 1909
tttgacgtgg gatggccaca ccggtgacgg ggtcaatgtg cagaatctgt gcagtggtga 60

gttcagcatt gttttccgca tcagataacg cggtgggcga gtg gct tat ctg tac   115
                                            Val Ala Tyr Leu Tyr
                                              1               5

gga tct gcc gat ggg atg ctt aat aca gat ggt ttt aat atg ttt ccg   163
Gly Ser Ala Asp Gly Met Leu Asn Thr Asp Gly Phe Asn Met Phe Pro
                10                  15                  20

cgt gcg tcg tac acc att ctt ggc cct atg gat gct gac gcg gtc ggt   211
Arg Ala Ser Tyr Thr Ile Leu Gly Pro Met Asp Ala Asp Ala Val Gly
            25                  30                  35

gtg tac caa cag cta ctg aac agc acg att ccc atg gat ttg gca cgt   259
Val Tyr Gln Gln Leu Leu Asn Ser Thr Ile Pro Met Asp Leu Ala Arg
        40                  45                  50

ctt gta acc acg cat aat tcc ggt gca agt tat ctt cgc cgc ggt gct   307
Leu Val Thr Thr His Asn Ser Gly Ala Ser Tyr Leu Arg Arg Gly Ala
    55                  60                  65

acc aac gta gtt ttt gaa acg aat ctt gcc ctc ggt gtg aat ccg tat   355
Thr Asn Val Val Phe Glu Thr Asn Leu Ala Leu Gly Val Asn Pro Tyr
70                  75                  80                  85

atg aag aaa cgc cga gca aca gaa gca caa cgt ggt aag aag cgt ttt   403
Met Lys Lys Arg Arg Ala Thr Glu Ala Gln Arg Gly Lys Lys Arg Phe
                90                  95                  100

aaa cga gac agt cat tac ggc ggt ggc act gtg acc aca ggt act gct   451
Lys Arg Asp Ser His Tyr Gly Gly Gly Thr Val Thr Thr Gly Thr Ala
            105                 110                 115

gat ttg gat gtg gtg gcg atg cag gcg cgg gca gag cac cgg gaa gaa   499
Asp Leu Asp Val Val Ala Met Gln Ala Arg Ala Glu His Arg Glu Glu
        120                 125                 130

agg ttg gga gaa aaa tct acc cgc aag aaa gag gag ctt gct gca gta   547
Arg Leu Gly Glu Lys Ser Thr Arg Lys Lys Glu Glu Leu Ala Ala Val
    135                 140                 145

gag gcg aaa gag tta gct gcg aag aag ggt ccg cag act gtg gaa gaa   595
Glu Ala Lys Glu Leu Ala Ala Lys Lys Gly Pro Gln Thr Val Glu Glu
```

150 155 160 165

ggt ctt gct gcg gtg gag aag aaa cac ctg gcg aag cgg taggcgacgt 644
Gly Leu Ala Ala Val Glu Lys Lys His Leu Ala Lys Arg
170 175

ggttggcggt ggg 657

<210> 1910
<211> 178
<212> PRT
<213> Corynebacterium glutamicum

<400> 1910
Val Ala Tyr Leu Tyr Gly Ser Ala Asp Gly Met Leu Asn Thr Asp Gly
1 5 10 15

Phe Asn Met Phe Pro Arg Ala Ser Tyr Thr Ile Leu Gly Pro Met Asp
20 25 30

Ala Asp Ala Val Gly Val Tyr Gln Gln Leu Leu Asn Ser Thr Ile Pro
35 40 45

Met Asp Leu Ala Arg Leu Val Thr Thr His Asn Ser Gly Ala Ser Tyr
50 55 60

Leu Arg Arg Gly Ala Thr Asn Val Val Phe Glu Thr Asn Leu Ala Leu
65 70 75 80

Gly Val Asn Pro Tyr Met Lys Lys Arg Arg Ala Thr Glu Ala Gln Arg
85 90 95

Gly Lys Lys Arg Phe Lys Arg Asp Ser His Tyr Gly Gly Gly Thr Val
100 105 110

Thr Thr Gly Thr Ala Asp Leu Asp Val Val Ala Met Gln Ala Arg Ala
115 120 125

Glu His Arg Glu Glu Arg Leu Gly Glu Lys Ser Thr Arg Lys Lys Glu
130 135 140

Glu Leu Ala Ala Val Glu Ala Lys Glu Leu Ala Ala Lys Lys Gly Pro
145 150 155 160

Gln Thr Val Glu Glu Gly Leu Ala Ala Val Glu Lys Lys His Leu Ala
165 170 175

Lys Arg

<210> 1911
<211> 1314
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1291)
<223> RXA00746

<400> 1911
aaactacgtt ggtagcaccg cggcgaagat aacttgcacc ggaattatgc gtggttacaa 60

gacgtgccaa atccatggga atcgtgctgt tcagtagctg ttg gta cac acc gac 115
Leu Val His Thr Asp
1 5

cgc gtc agc atc cat agg gcc aag aat ggt gta cga cgc acg cgg aaa 163
Arg Val Ser Ile His Arg Ala Lys Asn Gly Val Arg Arg Thr Arg Lys
10 15 20

cat att aaa acc atc tgt att aag cat ccc atc ggc aga tcc gta cag 211
His Ile Lys Thr Ile Cys Ile Lys His Pro Ile Gly Arg Ser Val Gln
25 30 35

ata agc cac tcg ccc acc gcg tta tct gat gcg gaa aac aat gct gaa 259
Ile Ser His Ser Pro Thr Ala Leu Ser Asp Ala Glu Asn Asn Ala Glu
40 45 50

ctc acc act gca cag att ctg cac att gac ccc gtc acc ggt gtg gcc 307
Leu Thr Thr Ala Gln Ile Leu His Ile Asp Pro Val Thr Gly Val Ala
55 60 65

atc cca cgt caa aac att ctg ctg ggt gag gat ttt cag act atg gcc 355
Ile Pro Arg Gln Asn Ile Leu Leu Gly Glu Asp Phe Gln Thr Met Ala
70 75 80 85

agc tct ttt agt caa atc cgc cat gga tgg ggt atc acc cag ctc atc 403
Ser Ser Phe Ser Gln Ile Arg His Gly Trp Gly Ile Thr Gln Leu Ile
90 95 100

gga caa gac ccc aac aga aac caa cca atc cgc tct gct gat acg tgg 451
Gly Gln Asp Pro Asn Arg Asn Gln Pro Ile Arg Ser Ala Asp Thr Trp
105 110 115

aca gtg act gga tcg act gga ctc acc ggc ttt aat act gct acg cat 499
Thr Val Thr Gly Ser Thr Gly Leu Thr Gly Phe Asn Thr Ala Thr His
120 125 130

aat aca gat gac aca gac gcc act gcc gca tat acc atg ccg gca agc 547
Asn Thr Asp Asp Thr Asp Ala Thr Ala Ala Tyr Thr Met Pro Ala Ser
135 140 145

gat cct gcc gta gga cta tgc gca ctg gaa tcc aac aaa gac gca ccg 595
Asp Pro Ala Val Gly Leu Cys Ala Leu Glu Ser Asn Lys Asp Ala Pro
150 155 160 165

gtg gat gaa ttt cgc gat ctc agc ctc agt gct tta cgt acc gct acg 643
Val Asp Glu Phe Arg Asp Leu Ser Leu Ser Ala Leu Arg Thr Ala Thr
170 175 180

gtc atg tca agc tct ggc tcc gcc gtg att act atg cat gat cct atg 691
Val Met Ser Ser Ser Gly Ser Ala Val Ile Thr Met His Asp Pro Met
185 190 195

gtc atg agc acc act ggc gca ttg gaa gca cgt gca tac gtt gac ggc 739
Val Met Ser Thr Thr Gly Ala Leu Glu Ala Arg Ala Tyr Val Asp Gly
200 205 210

gaa gtc atc aac cag cac gat ctt gac tca ctg cgt gac cag cta ggt 787

```
Glu Val Ile Asn Gln His Asp Leu Asp Ser Leu Arg Asp Gln Leu Gly
    215                 220                 225

att act aca gac agc gca gat acc acc cct gcc cta cct gct gat ccc   835
Ile Thr Thr Asp Ser Ala Asp Thr Thr Pro Ala Leu Pro Ala Asp Pro
230                 235                 240                 245

ttg gca gca ttg ggc ttg agc aca cca act aca tca gct ctt gtc cca   883
Leu Ala Ala Leu Gly Leu Ser Thr Pro Thr Thr Ser Ala Leu Val Pro
                250                 255                 260

ggt ctt gcc gag ctg gac tgc ctc aac act gat caa gct cgc acc tgg   931
Gly Leu Ala Glu Leu Asp Cys Leu Asn Thr Asp Gln Ala Arg Thr Trp
            265                 270                 275

cat gac cgt gac aac agc att ggc act ggt aaa cca gct att ctt gcc   979
His Asp Arg Asp Asn Ser Ile Gly Thr Gly Lys Pro Ala Ile Leu Ala
        280                 285                 290

gtg att aac gcc gag ctc gct gat gat tac acc ctg cag atc ctc aaa   1027
Val Ile Asn Ala Glu Leu Ala Asp Asp Tyr Thr Leu Gln Ile Leu Lys
    295                 300                 305

aat agc act gcg acc ccc acc gac tcc acc gac tcc agc gat act gct   1075
Asn Ser Thr Ala Thr Pro Thr Asp Ser Thr Asp Ser Ser Asp Thr Ala
310                 315                 320                 325

gaa cgc ttc gta gcg cag cta cct gcg gaa aca gcc ttt gtg ctt att   1123
Glu Arg Phe Val Ala Gln Leu Pro Ala Glu Thr Ala Phe Val Leu Ile
                330                 335                 340

gat ccg gac atc ggc gct gtg acc gat ctg ttc ttt atc aac agc ata   1171
Asp Pro Asp Ile Gly Ala Val Thr Asp Leu Phe Phe Ile Asn Ser Ile
            345                 350                 355

aat cag gat ctc ccc gca ccg aca acc cag atc aac tca gta gcg gta   1219
Asn Gln Asp Leu Pro Ala Pro Thr Thr Gln Ile Asn Ser Val Ala Val
        360                 365                 370

gat caa cgt gac ccc aac atc atc tac gcg acc ttt gcc aat gat gac   1267
Asp Gln Arg Asp Pro Asn Ile Ile Tyr Ala Thr Phe Ala Asn Asp Asp
    375                 380                 385

cgc gtg tac cag ctc atg ctg ggt taaccgcgac ccgtttttat ctg        1314
Arg Val Tyr Gln Leu Met Leu Gly
390                 395
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<210> 1912
<211> 397
<212> PRT
<213> Corynebacterium glutamicum

<400> 1912

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Leu Val His Thr Asp Arg Val Ser Ile His Arg Ala Lys Asn Gly Val
  1               5                  10                  15

Arg Arg Thr Arg Lys His Ile Lys Thr Ile Cys Ile Lys His Pro Ile
             20                  25                  30

Gly Arg Ser Val Gln Ile Ser His Ser Pro Thr Ala Leu Ser Asp Ala
```

```
          35                  40                  45

Glu Asn Asn Ala Glu Leu Thr Thr Ala Gln Ile Leu His Ile Asp Pro
     50                  55                  60

Val Thr Gly Val Ala Ile Pro Arg Gln Asn Ile Leu Leu Gly Glu Asp
 65                  70                  75                  80

Phe Gln Thr Met Ala Ser Ser Phe Ser Gln Ile Arg His Gly Trp Gly
                 85                  90                  95

Ile Thr Gln Leu Ile Gly Gln Asp Pro Asn Arg Asn Gln Pro Ile Arg
            100                 105                 110

Ser Ala Asp Thr Trp Thr Val Thr Gly Ser Thr Gly Leu Thr Gly Phe
        115                 120                 125

Asn Thr Ala Thr His Asn Thr Asp Asp Thr Asp Ala Thr Ala Ala Tyr
    130                 135                 140

Thr Met Pro Ala Ser Asp Pro Ala Val Gly Leu Cys Ala Leu Glu Ser
145                 150                 155                 160

Asn Lys Asp Ala Pro Val Asp Glu Phe Arg Asp Leu Ser Leu Ser Ala
                165                 170                 175

Leu Arg Thr Ala Thr Val Met Ser Ser Ser Gly Ser Ala Val Ile Thr
            180                 185                 190

Met His Asp Pro Met Val Met Ser Thr Thr Gly Ala Leu Glu Ala Arg
        195                 200                 205

Ala Tyr Val Asp Gly Glu Val Ile Asn Gln His Asp Leu Asp Ser Leu
    210                 215                 220

Arg Asp Gln Leu Gly Ile Thr Thr Asp Ser Ala Asp Thr Thr Pro Ala
225                 230                 235                 240

Leu Pro Ala Asp Pro Leu Ala Ala Leu Gly Leu Ser Thr Pro Thr Thr
                245                 250                 255

Ser Ala Leu Val Pro Gly Leu Ala Glu Leu Asp Cys Leu Asn Thr Asp
            260                 265                 270

Gln Ala Arg Thr Trp His Asp Arg Asp Asn Ser Ile Gly Thr Gly Lys
        275                 280                 285

Pro Ala Ile Leu Ala Val Ile Asn Ala Glu Leu Ala Asp Asp Tyr Thr
    290                 295                 300

Leu Gln Ile Leu Lys Asn Ser Thr Ala Thr Pro Thr Asp Ser Thr Asp
305                 310                 315                 320

Ser Ser Asp Thr Ala Glu Arg Phe Val Ala Gln Leu Pro Ala Glu Thr
                325                 330                 335

Ala Phe Val Leu Ile Asp Pro Asp Ile Gly Ala Val Thr Asp Leu Phe
            340                 345                 350

Phe Ile Asn Ser Ile Asn Gln Asp Leu Pro Ala Pro Thr Thr Gln Ile
        355                 360                 365
```

```
Asn Ser Val Ala Val Asp Gln Arg Asp Pro Asn Ile Ile Tyr Ala Thr
    370                 375                 380

Phe Ala Asn Asp Asp Arg Val Tyr Gln Leu Met Leu Gly
385                 390                 395
```

<210> 1913
<211> 711
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(688)
<223> RXA00747

<400> 1913

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tgtgctgatc cgcgccgtgc caactcgcac tgggtcgcac tgggtcgcac aaccgcatac 60

acatacacac aattaatcac cctcaacacg aagatttatc atg aca ttt ttg cac   115
                                            Met Thr Phe Leu His
                                              1               5

cgt tcc gcc agt ttc cac cct cgt acc cac gat cac ctc agc gag ctc   163
Arg Ser Ala Ser Phe His Pro Arg Thr His Asp His Leu Ser Glu Leu
                 10                  15                  20

ggt ctt gat cct tat aag ctc tct caa gac atc ccc act gtt att tat   211
Gly Leu Asp Pro Tyr Lys Leu Ser Gln Asp Ile Pro Thr Val Ile Tyr
             25                  30                  35

gaa gtc cag ccg cac agt gtg ttc att tta aaa ttc aac act gcc gat   259
Glu Val Gln Pro His Ser Val Phe Ile Leu Lys Phe Asn Thr Ala Asp
         40                  45                  50

gtt cgg gtc tat cag gaa cac tcc gat ctc ttt gtg cga cat gct gtg   307
Val Arg Val Tyr Gln Glu His Ser Asp Leu Phe Val Arg His Ala Val
     55                  60                  65

ctt gtt gat cca gaa cag cgt aaa cat gag cat gac cag ctc ctt aaa   355
Leu Val Asp Pro Glu Gln Arg Lys His Glu His Asp Gln Leu Leu Lys
 70                  75                  80                  85

gag att ctc gac ctc gat gcc cct cgt gtc aac gat gat att agt ggt   403
Glu Ile Leu Asp Leu Asp Ala Pro Arg Val Asn Asp Asp Ile Ser Gly
                 90                  95                 100

cgc acg aca gtg ttt ctc cac gat aaa aca gtt gtt acg cac agt ggt   451
Arg Thr Thr Val Phe Leu His Asp Lys Thr Val Val Thr His Ser Gly
            105                 110                 115

ggc ccc att gcg att att ccg cac aat ccc gat gtc gcc agc gcc gct   499
Gly Pro Ile Ala Ile Ile Pro His Asn Pro Asp Val Ala Ser Ala Ala
        120                 125                 130

gcg tca gct aat aaa cac aaa caa tct gtg atg aca aca tcc agg cat   547
Ala Ser Ala Asn Lys His Lys Gln Ser Val Met Thr Thr Ser Arg His
    135                 140                 145
```

```
cct tat gcg cag atg tct ctc agc gac atg ctg aaa caa ggc ttc acg   595
Pro Tyr Ala Gln Met Ser Leu Ser Asp Met Leu Lys Gln Gly Phe Thr
150                 155                 160                 165

ctc aca cct cta gag ttc ccc tac tgc gct gtt gat gac ccc gac agc   643
Leu Thr Pro Leu Glu Phe Pro Tyr Cys Ala Val Asp Asp Pro Asp Ser
                170                 175                 180

tca cgc cac aca atg cac gtc atc aac gtt cga gat cat aca gtg       688
Ser Arg His Thr Met His Val Ile Asn Val Arg Asp His Thr Val
            185                 190                 195

tgaactaccg cgccgctaga gat                                        711


<210> 1914
<211> 196
<212> PRT
<213> Corynebacterium glutamicum

<400> 1914
Met Thr Phe Leu His Arg Ser Ala Ser Phe His Pro Arg Thr His Asp
  1               5                  10                  15

His Leu Ser Glu Leu Gly Leu Asp Pro Tyr Lys Leu Ser Gln Asp Ile
             20                  25                  30

Pro Thr Val Ile Tyr Glu Val Gln Pro His Ser Val Phe Ile Leu Lys
         35                  40                  45

Phe Asn Thr Ala Asp Val Arg Val Tyr Gln Glu His Ser Asp Leu Phe
     50                  55                  60

Val Arg His Ala Val Leu Val Asp Pro Glu Gln Arg Lys His Glu His
 65                  70                  75                  80

Asp Gln Leu Leu Lys Glu Ile Leu Asp Leu Asp Ala Pro Arg Val Asn
                 85                  90                  95

Asp Asp Ile Ser Gly Arg Thr Thr Val Phe Leu His Asp Lys Thr Val
            100                 105                 110

Val Thr His Ser Gly Gly Pro Ile Ala Ile Ile Pro His Asn Pro Asp
        115                 120                 125

Val Ala Ser Ala Ala Ala Ser Ala Asn Lys His Lys Gln Ser Val Met
    130                 135                 140

Thr Thr Ser Arg His Pro Tyr Ala Gln Met Ser Leu Ser Asp Met Leu
145                 150                 155                 160

Lys Gln Gly Phe Thr Leu Thr Pro Leu Glu Phe Pro Tyr Cys Ala Val
                165                 170                 175

Asp Asp Pro Asp Ser Ser Arg His Thr Met His Val Ile Asn Val Arg
            180                 185                 190

Asp His Thr Val
        195
```

<210> 1915
<211> 567
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(544)
<223> RXA00748

<400> 1915
aagccttatt ctcctcttaa ctaccatgag gtaaccatct aaagtagatg gttgcaacaa 60

cttttcatta catcaacatg tttaaaaaag gacactgatt atg act tac ttc gca 115
Met Thr Tyr Phe Ala
1 5

ctc gtt gct cgc aat tac gct gag aca ggt gtc tct gtt gaa ttc cat 163
Leu Val Ala Arg Asn Tyr Ala Glu Thr Gly Val Ser Val Glu Phe His
10 15 20

gag gtc gat gat gac gca gat aac tca aat ggc ccc aac aac aca agc 211
Glu Val Asp Asp Asp Ala Asp Asn Ser Asn Gly Pro Asn Asn Thr Ser
25 30 35

aat tta cct cta aaa ctt ctt cga gat cac tct ttt gat gcc act gtt 259
Asn Leu Pro Leu Lys Leu Leu Arg Asp His Ser Phe Asp Ala Thr Val
40 45 50

gtc tat ggt gac ctg gtg ctt cac acc tca gca cat ctc aga gat acg 307
Val Tyr Gly Asp Leu Val Leu His Thr Ser Ala His Leu Arg Asp Thr
55 60 65

gct atc gcc aac tca gac aac cgt ccg cga gta gtg acc aca gct caa 355
Ala Ile Ala Asn Ser Asp Asn Arg Pro Arg Val Val Thr Thr Ala Gln
70 75 80 85

aaa ttc ttt gat tac atc cgc tta gcc acc aga cac ggt gct atc cac 403
Lys Phe Phe Asp Tyr Ile Arg Leu Ala Thr Arg His Gly Ala Ile His
90 95 100

gac atg atc aat aac gcg cca gat acc ggc act gac atc gtt gtt att 451
Asp Met Ile Asn Asn Ala Pro Asp Thr Gly Thr Asp Ile Val Val Ile
105 110 115

acg gcc act aat gat gct ctt att agt gat gaa tca gaa tac tat gac 499
Thr Ala Thr Asn Asp Ala Leu Ile Ser Asp Glu Ser Glu Tyr Tyr Asp
120 125 130

gag ctt ttt cat att ctc gaa tcc gca cag ggt gtg att ctt aaa 544
Glu Leu Phe His Ile Leu Glu Ser Ala Gln Gly Val Ile Leu Lys
135 140 145

tgattgatta attgatatga tta 567

<210> 1916
<211> 148
<212> PRT
<213> Corynebacterium glutamicum

<400> 1916
Met Thr Tyr Phe Ala Leu Val Ala Arg Asn Tyr Ala Glu Thr Gly Val
1 5 10 15

Ser Val Glu Phe His Glu Val Asp Asp Asp Ala Asp Asn Ser Asn Gly
20 25 30

Pro Asn Asn Thr Ser Asn Leu Pro Leu Lys Leu Leu Arg Asp His Ser
35 40 45

Phe Asp Ala Thr Val Val Tyr Gly Asp Leu Val Leu His Thr Ser Ala
50 55 60

His Leu Arg Asp Thr Ala Ile Ala Asn Ser Asp Asn Arg Pro Arg Val
65 70 75 80

Val Thr Thr Ala Gln Lys Phe Phe Asp Tyr Ile Arg Leu Ala Thr Arg
85 90 95

His Gly Ala Ile His Asp Met Ile Asn Asn Ala Pro Asp Thr Gly Thr
100 105 110

Asp Ile Val Val Ile Thr Ala Thr Asn Asp Ala Leu Ile Ser Asp Glu
115 120 125

Ser Glu Tyr Tyr Asp Glu Leu Phe His Ile Leu Glu Ser Ala Gln Gly
130 135 140

Val Ile Leu Lys
145

<210> 1917
<211> 822
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(799)
<223> RXA00749

<400> 1917
cgtttcgatc atttgtaaca ttcttattac aagactggaa ataaaggtga gtcaatcata 60

cagtcagatg tggtcatcgg caaaacagaa aggaatcccg atg tta cga aaa aca 115
Met Leu Arg Lys Thr
1 5

gtt acc ggt gga att gtt gct ctt att gcg act gcc act ctc atg aat 163
Val Thr Gly Gly Ile Val Ala Leu Ile Ala Thr Ala Thr Leu Met Asn
10 15 20

tct gtc tct tct gct gaa gag gta tcc gga gat gtc tca gca gta gat 211
Ser Val Ser Ser Ala Glu Glu Val Ser Gly Asp Val Ser Ala Val Asp
25 30 35

ctc gca ttt gca gaa ttc gaa cgt aca act gca gag gac gtg gcc aat 259
Leu Ala Phe Ala Glu Phe Glu Arg Thr Thr Ala Glu Asp Val Ala Asn
40 45 50

```
gga gtg cca gag gct ata gct aat gca gaa aaa att tcc aat ttc act   307
Gly Val Pro Glu Ala Ile Ala Asn Ala Glu Lys Ile Ser Asn Phe Thr
     55                  60                  65

ccg agc gaa cta gag ggc ttc aag agt ctt tta gct agt gat gca gtg   355
Pro Ser Glu Leu Glu Gly Phe Lys Ser Leu Leu Ala Ser Asp Ala Val
 70                  75                  80                  85

ctg agg tcg gtc tct gga gaa gaa att ctc cca gat aat gtt gaa gtg   403
Leu Arg Ser Val Ser Gly Glu Glu Ile Leu Pro Asp Asn Val Glu Val
                 90                  95                 100

gtt cag acg gac aac gta ggc gac gaa gat cca aat gtc att tct cca   451
Val Gln Thr Asp Asn Val Gly Asp Glu Asp Pro Asn Val Ile Ser Pro
            105                 110                 115

gca gcc tgg cag ggt tct gat tat att gag ggg tgt tta acg aat act   499
Ala Ala Trp Gln Gly Ser Asp Tyr Ile Glu Gly Cys Leu Thr Asn Thr
        120                 125                 130

ctc tac gga att gaa gtc cta aag gtt tgt act ggt gga acc tac tac   547
Leu Tyr Gly Ile Glu Val Leu Lys Val Cys Thr Gly Gly Thr Tyr Tyr
    135                 140                 145

tcc aat gta gga atc gct act tct gtc agc aat cct cgc agt tac gta   595
Ser Asn Val Gly Ile Ala Thr Ser Val Ser Asn Pro Arg Ser Tyr Val
150                 155                 160                 165

aag tat aac agt gct cca gga ttg gca gtg acg aca agc aat cca cgt   643
Lys Tyr Asn Ser Ala Pro Gly Leu Ala Val Thr Thr Ser Asn Pro Arg
                170                 175                 180

gga ggt ata gag ggt ggt ctt gcg gcc ttc tat ggt gat gtt aac ctt   691
Gly Gly Ile Glu Gly Gly Leu Ala Ala Phe Tyr Gly Asp Val Asn Leu
            185                 190                 195

gtt gct ttt cca aat att cca tgg gtg gga cca att agt tct tct gca   739
Val Ala Phe Pro Asn Ile Pro Trp Val Gly Pro Ile Ser Ser Ser Ala
        200                 205                 210

gga act cac cgc gtt gtc gct aga tca ttt ccg aat tca gtg gtg ctt   787
Gly Thr His Arg Val Val Ala Arg Ser Phe Pro Asn Ser Val Val Leu
    215                 220                 225

aac gtc tac tac taatcgtttt ttagtttgaa aca                        822
Asn Val Tyr Tyr
230
```

<210> 1918
<211> 233
<212> PRT
<213> Corynebacterium glutamicum

<400> 1918

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Met Leu Arg Lys Thr Val Thr Gly Gly Ile Val Ala Leu Ile Ala Thr
  1               5                  10                  15

Ala Thr Leu Met Asn Ser Val Ser Ser Ala Glu Glu Val Ser Gly Asp
             20                  25                  30
```

```
Val Ser Ala Val Asp Leu Ala Phe Ala Glu Phe Glu Arg Thr Thr Ala
         35                  40                  45

Glu Asp Val Ala Asn Gly Val Pro Glu Ala Ile Ala Asn Ala Glu Lys
     50                  55                  60

Ile Ser Asn Phe Thr Pro Ser Glu Leu Glu Gly Phe Lys Ser Leu Leu
 65                  70                  75                  80

Ala Ser Asp Ala Val Leu Arg Ser Val Ser Gly Glu Glu Ile Leu Pro
                 85                  90                  95

Asp Asn Val Glu Val Val Gln Thr Asp Asn Val Gly Asp Glu Asp Pro
            100                 105                 110

Asn Val Ile Ser Pro Ala Ala Trp Gln Gly Ser Asp Tyr Ile Glu Gly
        115                 120                 125

Cys Leu Thr Asn Thr Leu Tyr Gly Ile Glu Val Leu Lys Val Cys Thr
    130                 135                 140

Gly Gly Thr Tyr Tyr Ser Asn Val Gly Ile Ala Thr Ser Val Ser Asn
145                 150                 155                 160

Pro Arg Ser Tyr Val Lys Tyr Asn Ser Ala Pro Gly Leu Ala Val Thr
                165                 170                 175

Thr Ser Asn Pro Arg Gly Gly Ile Glu Gly Gly Leu Ala Ala Phe Tyr
            180                 185                 190

Gly Asp Val Asn Leu Val Ala Phe Pro Asn Ile Pro Trp Val Gly Pro
        195                 200                 205

Ile Ser Ser Ser Ala Gly Thr His Arg Val Val Ala Arg Ser Phe Pro
    210                 215                 220

Asn Ser Val Val Leu Asn Val Tyr Tyr
225                 230
```

Sequence Listing as filed with the application

<210> 1919
<211> 951
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(928)
<223> RXA00751

<400> 1919

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cgcagcaacc ccgtccatga gggcagggaa cgccacacat cctgtaccta tactgtgagg 60

tggcatagag tatctctaat ttagaaagtg gtgtagaagt atg ttg gta cgt tca   115
                                               Met Leu Val Arg Ser
                                                 1               5

cgc acg ttg gtt acc gct gca ctg tca tgt tca ctg ttg ttc gga gca   163
Arg Thr Leu Val Thr Ala Ala Leu Ser Cys Ser Leu Leu Phe Gly Ala
                10                  15                  20
```

```
acg gta aat ggc acg ggt gtt gcg att gca tat gaa aat gtg tct atg   211
Thr Val Asn Gly Thr Gly Val Ala Ile Ala Tyr Glu Asn Val Ser Met
            25                  30                  35

gct gct cag tat gaa cca cgg tat gaa tcc tta gaa acg cgt ctc ggt   259
Ala Ala Gln Tyr Glu Pro Arg Tyr Glu Ser Leu Glu Thr Arg Leu Gly
        40                  45                  50

tct agt gga gtc ttt ccc aag tcg gtt gaa cag tct gtt gaa aac ctt   307
Ser Ser Gly Val Phe Pro Lys Ser Val Glu Gln Ser Val Glu Asn Leu
    55                  60                  65

gct gaa tta cca gag gag act cga ttt tta ctt gag ggt gat tcg ttt   355
Ala Glu Leu Pro Glu Glu Thr Arg Phe Leu Leu Glu Gly Asp Ser Phe
70                  75                  80                  85

tca att att att gat gat ggt ctg ctc gct tct cga ttg gac cca aat   403
Ser Ile Ile Ile Asp Asp Gly Leu Leu Ala Ser Arg Leu Asp Pro Asn
                90                  95                  100

aca ggg gag att cga cat act ctt ggg gct tcg ggg atc agc tac acc   451
Thr Gly Glu Ile Arg His Thr Leu Gly Ala Ser Gly Ile Ser Tyr Thr
            105                 110                 115

cct ggt gaa atg aaa cga tct tat aca gat cga gtg act gtc aag gtg   499
Pro Gly Glu Met Lys Arg Ser Tyr Thr Asp Arg Val Thr Val Lys Val
        120                 125                 130

gtc tac cct gat ggg tca ttt gat aga gtg aca ccc cat tca gtg gtt   547
Val Tyr Pro Asp Gly Ser Phe Asp Arg Val Thr Pro His Ser Val Val
    135                 140                 145

tat gtg gct gac agt att tac tac ggc att gaa agc acg ggt tat cct   595
Tyr Val Ala Asp Ser Ile Tyr Tyr Gly Ile Glu Ser Thr Gly Tyr Pro
150                 155                 160                 165

aaa gtc cgc aat ggt cag act gtc aag atc cca ttg agg gtg acg gat   643
Lys Val Arg Asn Gly Gln Thr Val Lys Ile Pro Leu Arg Val Thr Asp
                170                 175                 180

ggt ggt aca gga gcg gtt ggt ggg gtc cca cag gga tcg aag gtg gtc   691
Gly Gly Thr Gly Ala Val Gly Gly Val Pro Gln Gly Ser Lys Val Val
            185                 190                 195

cga gat cgt tac ggc tca att gag aat gcg gag ttg atg ggt gca atc   739
Arg Asp Arg Tyr Gly Ser Ile Glu Asn Ala Glu Leu Met Gly Ala Ile
        200                 205                 210

att ctc ata gat gag aag act ggc gat ctc acc ttc acg gcg cct gat   787
Ile Leu Ile Asp Glu Lys Thr Gly Asp Leu Thr Phe Thr Ala Pro Asp
    215                 220                 225

gat cga acc ggt caa ctg tgg ttt cgt aca gaa gtg act ttc ccg gat   835
Asp Arg Thr Gly Gln Leu Trp Phe Arg Thr Glu Val Thr Phe Pro Asp
230                 235                 240                 245

ggt tcg gac tca gag gtt caa tat gtg atc gag gtg acg gat cag cct   883
Gly Ser Asp Ser Glu Val Gln Tyr Val Ile Glu Val Thr Asp Gln Pro
                250                 255                 260

gaa cct gtg gat gtc att cgt cct gcc gga tcg tct ctg agt tct       928
```

Glu Pro Val Asp Val Ile Arg Pro Ala Gly Ser Ser Leu Ser Ser
265 270 275

tgatttatgc ctgagactta agc 951

<210> 1920
<211> 276
<212> PRT
<213> Corynebacterium glutamicum

<400> 1920
Met Leu Val Arg Ser Arg Thr Leu Val Thr Ala Ala Leu Ser Cys Ser
1 5 10 15

Leu Leu Phe Gly Ala Thr Val Asn Gly Thr Gly Val Ala Ile Ala Tyr
20 25 30

Glu Asn Val Ser Met Ala Ala Gln Tyr Glu Pro Arg Tyr Glu Ser Leu
35 40 45

Glu Thr Arg Leu Gly Ser Ser Gly Val Phe Pro Lys Ser Val Glu Gln
50 55 60

Ser Val Glu Asn Leu Ala Glu Leu Pro Glu Glu Thr Arg Phe Leu Leu
65 70 75 80

Glu Gly Asp Ser Phe Ser Ile Ile Ile Asp Asp Gly Leu Leu Ala Ser
85 90 95

Arg Leu Asp Pro Asn Thr Gly Glu Ile Arg His Thr Leu Gly Ala Ser
100 105 110

Gly Ile Ser Tyr Thr Pro Gly Glu Met Lys Arg Ser Tyr Thr Asp Arg
115 120 125

Val Thr Val Lys Val Val Tyr Pro Asp Gly Ser Phe Asp Arg Val Thr
130 135 140

Pro His Ser Val Val Tyr Val Ala Asp Ser Ile Tyr Tyr Gly Ile Glu
145 150 155 160

Ser Thr Gly Tyr Pro Lys Val Arg Asn Gly Gln Thr Val Lys Ile Pro
165 170 175

Leu Arg Val Thr Asp Gly Gly Thr Gly Ala Val Gly Gly Val Pro Gln
180 185 190

Gly Ser Lys Val Val Arg Asp Arg Tyr Gly Ser Ile Glu Asn Ala Glu
195 200 205

Leu Met Gly Ala Ile Ile Leu Ile Asp Glu Lys Thr Gly Asp Leu Thr
210 215 220

Phe Thr Ala Pro Asp Asp Arg Thr Gly Gln Leu Trp Phe Arg Thr Glu
225 230 235 240

Val Thr Phe Pro Asp Gly Ser Asp Ser Glu Val Gln Tyr Val Ile Glu
245 250 255

Val Thr Asp Gln Pro Glu Pro Val Asp Val Ile Arg Pro Ala Gly Ser

260 265 270

Ser Leu Ser Ser
275

<210> 1921
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(529)
<223> RXA00752

<400> 1921
aaggtcagcc gtatttcggt cagtcagcaa ctaactacgc ttatcttccg tgtacgatag 60

accgtagtta acataaggaa tggaatagga gaattgcggc atg tat tcc gac aag 115
Met Tyr Ser Asp Lys
1 5

ctg att ctc ttg ttc ctt tct gag cag gat tca agc tat gaa tgc tgc 163
Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser Ser Tyr Glu Cys Cys
10 15 20

gta ggt tta tta gat ggc tca gat gga ctt gat tat att gaa aag ctt 211
Val Gly Leu Leu Asp Gly Ser Asp Gly Leu Asp Tyr Ile Glu Lys Leu
25 30 35

ctg aag ggt agg aag ctg aag aac cat ttt ctt gaa tgg gaa gat att 259
Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu Glu Trp Glu Asp Ile
40 45 50

aac aag gct gat gtt gct cgt gaa gaa ata tat aaa ggg caa ttg gtg 307
Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr Lys Gly Gln Leu Val
55 60 65

cat ctg gtg ttt gtg acg gct ctt tcc acg cct ggt gaa att tct ttt 355
His Leu Val Phe Val Thr Ala Leu Ser Thr Pro Gly Glu Ile Ser Phe
70 75 80 85

gtt ttt cca ggt caa tct ctt atg agt gca aca ctc gaa gaa gac ttt 403
Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr Leu Glu Glu Asp Phe
90 95 100

gct gcg ctt gtg ctc gaa gag gag cgc aca tca ttt aga cct gaa ctg 451
Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser Phe Arg Pro Glu Leu
105 110 115

tct cac ctg tgg tca ctc ccc gta ggg tgg gta gct ccg ggg ctt gag 499
Ser His Leu Trp Ser Leu Pro Val Gly Trp Val Ala Pro Gly Leu Glu
120 125 130

ggt ttc gtg gag cgt aat tcc gag gca gct tgaaccaccg ctttctgagc 549
Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
135 140

cgg 552

<210> 1922
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 1922
Met Tyr Ser Asp Lys Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser
1 5 10 15

Ser Tyr Glu Cys Cys Val Gly Leu Leu Asp Gly Ser Asp Gly Leu Asp
20 25 30

Tyr Ile Glu Lys Leu Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu
35 40 45

Glu Trp Glu Asp Ile Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr
50 55 60

Lys Gly Gln Leu Val His Leu Val Phe Val Thr Ala Leu Ser Thr Pro
65 70 75 80

Gly Glu Ile Ser Phe Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr
85 90 95

Leu Glu Glu Asp Phe Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser
100 105 110

Phe Arg Pro Glu Leu Ser His Leu Trp Ser Leu Pro Val Gly Trp Val
115 120 125

Ala Pro Gly Leu Glu Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
130 135 140

<210> 1923
<211> 1377
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1354)
<223> RXA00757

<400> 1923
caggtttagc gaattcaatt tctaccactg ctcgagggga atgtgctaat tcaagggttg 60

tgacctcgag caacttttta ttccgctcga tcaaaacaac gtg agt ttc ggc gtc 115
Val Ser Phe Gly Val
1 5

gtt aag cgc ccc gat gcg tgc tac gcg ctt ttt gcc atc ctg atc aag 163
Val Lys Arg Pro Asp Ala Cys Tyr Ala Leu Phe Ala Ile Leu Ile Lys
10 15 20

cgc aac cag gcg acc gcg gtt tct gcg cca atg gcg cgg cag cgt cag 211
Arg Asn Gln Ala Thr Ala Val Ser Ala Pro Met Ala Arg Gln Arg Gln
25 30 35

tgg gtt gtc cac gcc cgg cgt gga cac ttc gag cgt gta acc cgc tcc 259

```
Trp Val Val His Ala Arg Arg Gly His Phe Glu Arg Val Thr Arg Ser
         40                  45                  50

gaa gtt gag ctc tcc gcg ctg ctc ggc ggc gtc gaa aag ctc tcc gat   307
Glu Val Glu Leu Ser Ala Leu Leu Gly Gly Val Glu Lys Leu Ser Asp
     55                  60                  65

ttc ttg gct gaa tac ttc cag ctg gtc gag atc ggg gcg gga atc cga   355
Phe Leu Ala Glu Tyr Phe Gln Leu Val Glu Ile Gly Ala Gly Ile Arg
 70                  75                  80                  85

atc tac ctt gat ggc gac ggc gga ttt tgg acc tgc ttt ggt cac ttt   403
Ile Tyr Leu Asp Gly Asp Gly Gly Phe Trp Thr Cys Phe Gly His Phe
                 90                  95                 100

cag gcc ctc gag gtc gaa ttt gtg gga tgc ggc gag cgg ctc gat gag   451
Gln Ala Leu Glu Val Glu Phe Val Gly Cys Gly Glu Arg Leu Asp Glu
            105                 110                 115

cgc aga cag aat ttc agt ggt tgg aaa agc cat aaa gac aag gat aac   499
Arg Arg Gln Asn Phe Ser Gly Trp Lys Ser His Lys Asp Lys Asp Asn
        120                 125                 130

ctg ccg gca aaa atc atc ggg cta tta cac tgt gaa gcc atg cgt agg   547
Leu Pro Ala Lys Ile Ile Gly Leu Leu His Cys Glu Ala Met Arg Arg
    135                 140                 145

cgt atc ccc tct gtc ctt ggt gtt tct ctt ctg gct gcc ttt ttg gtg   595
Arg Ile Pro Ser Val Leu Gly Val Ser Leu Leu Ala Ala Phe Leu Val
150                 155                 160                 165

gcg tgc acc ccc tcc ccc aat ccg aat gcg gcg ttg gcc cag atg tat   643
Ala Cys Thr Pro Ser Pro Asn Pro Asn Ala Ala Leu Ala Gln Met Tyr
                170                 175                 180

cag gat gcg ctt ttt gat tcc cag gcg atg tca gag gcc gag cct gag   691
Gln Asp Ala Leu Phe Asp Ser Gln Ala Met Ser Glu Ala Glu Pro Glu
            185                 190                 195

ctt gcc act ttg cgc agt cag cac gca gat gaa tta ttg gcc gag att   739
Leu Ala Thr Leu Arg Ser Gln His Ala Asp Glu Leu Leu Ala Glu Ile
        200                 205                 210

cgg cgt att tgt ggc ttt gat gaa ggc cag gtt ccg gaa tcg tgc cag   787
Arg Arg Ile Cys Gly Phe Asp Glu Gly Gln Val Pro Glu Ser Cys Gln
    215                 220                 225

gta acg gtt cct gcg atc gct att ctg ccc acc gat gat cca gag aag   835
Val Thr Val Pro Ala Ile Ala Ile Leu Pro Thr Asp Asp Pro Glu Lys
230                 235                 240                 245

tat gtc aac gac agt cag gcg ttg atc ctt gat aat ttg gat gac att   883
Tyr Val Asn Asp Ser Gln Ala Leu Ile Leu Asp Asn Leu Asp Asp Ile
                250                 255                 260

ccg gaa gat tcc gtg gct tta gtg gtt gag caa tac atc gcg cag gcg   931
Pro Glu Asp Ser Val Ala Leu Val Val Glu Gln Tyr Ile Ala Gln Ala
            265                 270                 275

gaa ttt gct gaa gga tct gag gtg tcc gtt cct gtt gat ttg gag ctc   979
Glu Phe Ala Glu Gly Ser Glu Val Ser Val Pro Val Asp Leu Glu Leu
```

```
        280                 285                 290

acc gag gca gaa tta gct gct gcg aag gac ttg gcg gac cgc gag ttt   1027
Thr Glu Ala Glu Leu Ala Ala Ala Lys Asp Leu Ala Asp Arg Glu Phe
    295                 300                 305

tcc gcc gcg tgg tct ttg ggc gtg gct ttg gct cag ctt ccg gaa acc   1075
Ser Ala Ala Trp Ser Leu Gly Val Ala Leu Ala Gln Leu Pro Glu Thr
310                 315                 320                 325

gac cgc gag gag gtg gaa acg gcg atc agc aac cac cat gac cgc gcg   1123
Asp Arg Glu Glu Val Glu Thr Ala Ile Ser Asn His His Asp Arg Ala
                330                 335                 340

tcg cag ctg caa att att acc tcc ggc act acc cca gcg cca ggt tac   1171
Ser Gln Leu Gln Ile Ile Thr Ser Gly Thr Thr Pro Ala Pro Gly Tyr
            345                 350                 355

gtg agc gag ctg ccc gac ccc acc gac gag act tca gcg cga agc aac   1219
Val Ser Glu Leu Pro Asp Pro Thr Asp Glu Thr Ser Ala Arg Ser Asn
        360                 365                 370

att gaa acc gtc gaa aac aac gtc acc cag gcc tgg cat gca gct gca   1267
Ile Glu Thr Val Glu Asn Asn Val Thr Gln Ala Trp His Ala Ala Ala
    375                 380                 385

agc gcc gca acc acc gac gcc tgg cgt gtc ttc tgc gcg cac atc gcc   1315
Ser Ala Ala Thr Thr Asp Ala Trp Arg Val Phe Cys Ala His Ile Ala
390                 395                 400                 405

ggc gat acc gca cgc gaa tta acg ctt atc gac gtc tcc tagcagtttc    1364
Gly Asp Thr Ala Arg Glu Leu Thr Leu Ile Asp Val Ser
                410                 415

actgccaatt ttt                                                   1377


<210> 1924
<211> 418
<212> PRT
<213> Corynebacterium glutamicum

<400> 1924
Val Ser Phe Gly Val Val Lys Arg Pro Asp Ala Cys Tyr Ala Leu Phe
  1               5                  10                  15

Ala Ile Leu Ile Lys Arg Asn Gln Ala Thr Ala Val Ser Ala Pro Met
             20                  25                  30

Ala Arg Gln Arg Gln Trp Val Val His Ala Arg Arg Gly His Phe Glu
         35                  40                  45

Arg Val Thr Arg Ser Glu Val Glu Leu Ser Ala Leu Leu Gly Gly Val
     50                  55                  60

Glu Lys Leu Ser Asp Phe Leu Ala Glu Tyr Phe Gln Leu Val Glu Ile
 65                  70                  75                  80

Gly Ala Gly Ile Arg Ile Tyr Leu Asp Gly Asp Gly Gly Phe Trp Thr
                 85                  90                  95
```

Cys Phe Gly His Phe Gln Ala Leu Glu Val Glu Phe Val Gly Cys Gly
100 105 110

Glu Arg Leu Asp Glu Arg Arg Gln Asn Phe Ser Gly Trp Lys Ser His
115 120 125

Lys Asp Lys Asp Asn Leu Pro Ala Lys Ile Ile Gly Leu Leu His Cys
130 135 140

Glu Ala Met Arg Arg Arg Ile Pro Ser Val Leu Gly Val Ser Leu Leu
145 150 155 160

Ala Ala Phe Leu Val Ala Cys Thr Pro Ser Pro Asn Pro Asn Ala Ala
165 170 175

Leu Ala Gln Met Tyr Gln Asp Ala Leu Phe Asp Ser Gln Ala Met Ser
180 185 190

Glu Ala Glu Pro Glu Leu Ala Thr Leu Arg Ser Gln His Ala Asp Glu
195 200 205

Leu Leu Ala Glu Ile Arg Arg Ile Cys Gly Phe Asp Glu Gly Gln Val
210 215 220

Pro Glu Ser Cys Gln Val Thr Val Pro Ala Ile Ala Ile Leu Pro Thr
225 230 235 240

Asp Asp Pro Glu Lys Tyr Val Asn Asp Ser Gln Ala Leu Ile Leu Asp
245 250 255

Asn Leu Asp Asp Ile Pro Glu Asp Ser Val Ala Leu Val Val Glu Gln
260 265 270

Tyr Ile Ala Gln Ala Glu Phe Ala Glu Gly Ser Glu Val Ser Val Pro
275 280 285

Val Asp Leu Glu Leu Thr Glu Ala Glu Leu Ala Ala Ala Lys Asp Leu
290 295 300

Ala Asp Arg Glu Phe Ser Ala Ala Trp Ser Leu Gly Val Ala Leu Ala
305 310 315 320

Gln Leu Pro Glu Thr Asp Arg Glu Glu Val Glu Thr Ala Ile Ser Asn
325 330 335

His His Asp Arg Ala Ser Gln Leu Gln Ile Ile Thr Ser Gly Thr Thr
340 345 350

Pro Ala Pro Gly Tyr Val Ser Glu Leu Pro Asp Pro Thr Asp Glu Thr
355 360 365

Ser Ala Arg Ser Asn Ile Glu Thr Val Glu Asn Asn Val Thr Gln Ala
370 375 380

Trp His Ala Ala Ala Ser Ala Ala Thr Thr Asp Ala Trp Arg Val Phe
385 390 395 400

Cys Ala His Ile Ala Gly Asp Thr Ala Arg Glu Leu Thr Leu Ile Asp
405 410 415

Val Ser

<210> 1925
<211> 906
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(883)
<223> RXA00763

<400> 1925
agcgcgattt gagtgctttt aatacgatcg gaagtattca tgtccccagg ttagccccaa 60

gtttgaatct cttgcaggaa cgtggggtaa agatatagat gtg gaa aaa tcc aga 115
Val Glu Lys Ser Arg
1 5

aaa cga ctt gtg acc atc gca gca tcg aca att ggg gcc gtt gcg gtg 163
Lys Arg Leu Val Thr Ile Ala Ala Ser Thr Ile Gly Ala Val Ala Val
10 15 20

gct ggc ggc gct ttt tgg atc gtt gat gct tcc atc gct gcg cac gcg 211
Ala Gly Gly Ala Phe Trp Ile Val Asp Ala Ser Ile Ala Ala His Ala
25 30 35

gaa cgc aac ttg tct aaa gca gtt gcg gaa tcc gca gat ctt gaa aac 259
Glu Arg Asn Leu Ser Lys Ala Val Ala Glu Ser Ala Asp Leu Glu Asn
40 45 50

gac ccg cga gta ttc ctc ggc agc tcc att tac tcc acg gcg ttt ttt 307
Asp Pro Arg Val Phe Leu Gly Ser Ser Ile Tyr Ser Thr Ala Phe Phe
55 60 65

acc ggc aaa ctc gac tcc gta agc atc gac atg ctg gac gtg gaa atc 355
Thr Gly Lys Leu Asp Ser Val Ser Ile Asp Met Leu Asp Val Glu Ile
70 75 80 85

ccc ggc gtc ggc atg gtg aat gca cgc aca gag gta gaa agc gtg gaa 403
Pro Gly Val Gly Met Val Asn Ala Arg Thr Glu Val Glu Ser Val Glu
90 95 100

gtc tca cgg gat caa atc ctc tcc ggt gac ctc gac ggc acc act gcg 451
Val Ser Arg Asp Gln Ile Leu Ser Gly Asp Leu Asp Gly Thr Thr Ala
105 110 115

gaa acc ttc acg cgc aca tta cgc atg gac ggc gtc gca atc ggc gcg 499
Glu Thr Phe Thr Arg Thr Leu Arg Met Asp Gly Val Ala Ile Gly Ala
120 125 130

cag ctc gga atc acc gac ctc gac atc tcc cac ccc atc gac atc tcc 547
Gln Leu Gly Ile Thr Asp Leu Asp Ile Ser His Pro Ile Asp Ile Ser
135 140 145

ccc tcc ggc ggc atc acc tca gaa gcg ctc ctg aca gga acc cca cca 595
Pro Ser Gly Gly Ile Thr Ser Glu Ala Leu Leu Thr Gly Thr Pro Pro
150 155 160 165

gac atg gaa gac ccg gtc agt gtg ctg gtc acc ctt cgc cta gtc ggc 643

```
Asp Met Glu Asp Pro Val Ser Val Leu Val Thr Leu Arg Leu Val Gly
                170                 175                 180

tca gaa ttc cag atg ctg ccg tac gag ctt atc gac gca ccc tcc gga   691
Ser Glu Phe Gln Met Leu Pro Tyr Glu Leu Ile Asp Ala Pro Ser Gly
            185                 190                 195

ctc acc ctc gac gat gtc gcc ccc gac ttc acg tgg aaa atc gac acc   739
Leu Thr Leu Asp Asp Val Ala Pro Asp Phe Thr Trp Lys Ile Asp Thr
        200                 205                 210

ctg caa cta ccc ctc gca gat cgg gca atg gcg gtt tac cta tct ggt   787
Leu Gln Leu Pro Leu Ala Asp Arg Ala Met Ala Val Tyr Leu Ser Gly
    215                 220                 225

ggc tcc gtc cat ttc caa tct gaa gcc cgc aac gtc cag ctc acc acc   835
Gly Ser Val His Phe Gln Ser Glu Ala Arg Asn Val Gln Leu Thr Thr
230                 235                 240                 245

cgc gaa cta tca cca cta gct gca ccg gaa gaa aac tcc gat gaa tcc   883
Arg Glu Leu Ser Pro Leu Ala Ala Pro Glu Glu Asn Ser Asp Glu Ser
                250                 255                 260

tagatgccaa acgtgcgcac ccg                                        906


<210> 1926
<211> 261
<212> PRT
<213> Corynebacterium glutamicum

<400> 1926
Val Glu Lys Ser Arg Lys Arg Leu Val Thr Ile Ala Ala Ser Thr Ile
  1               5                  10                  15

Gly Ala Val Ala Val Ala Gly Gly Ala Phe Trp Ile Val Asp Ala Ser
             20                  25                  30

Ile Ala Ala His Ala Glu Arg Asn Leu Ser Lys Ala Val Ala Glu Ser
         35                  40                  45

Ala Asp Leu Glu Asn Asp Pro Arg Val Phe Leu Gly Ser Ser Ile Tyr
     50                  55                  60

Ser Thr Ala Phe Phe Thr Gly Lys Leu Asp Ser Val Ser Ile Asp Met
 65                  70                  75                  80

Leu Asp Val Glu Ile Pro Gly Val Gly Met Val Asn Ala Arg Thr Glu
                 85                  90                  95

Val Glu Ser Val Glu Val Ser Arg Asp Gln Ile Leu Ser Gly Asp Leu
            100                 105                 110

Asp Gly Thr Thr Ala Glu Thr Phe Thr Arg Thr Leu Arg Met Asp Gly
        115                 120                 125

Val Ala Ile Gly Ala Gln Leu Gly Ile Thr Asp Leu Asp Ile Ser His
    130                 135                 140

Pro Ile Asp Ile Ser Pro Ser Gly Gly Ile Thr Ser Glu Ala Leu Leu
145                 150                 155                 160
```

```
Thr Gly Thr Pro Pro Asp Met Glu Asp Pro Val Ser Val Leu Val Thr
                165                 170                 175

Leu Arg Leu Val Gly Ser Glu Phe Gln Met Leu Pro Tyr Glu Leu Ile
            180                 185                 190

Asp Ala Pro Ser Gly Leu Thr Leu Asp Asp Val Ala Pro Asp Phe Thr
        195                 200                 205

Trp Lys Ile Asp Thr Leu Gln Leu Pro Leu Ala Asp Arg Ala Met Ala
    210                 215                 220

Val Tyr Leu Ser Gly Gly Ser Val His Phe Gln Ser Glu Ala Arg Asn
225                 230                 235                 240

Val Gln Leu Thr Thr Arg Glu Leu Ser Pro Leu Ala Ala Pro Glu Glu
                245                 250                 255

Asn Ser Asp Glu Ser
            260
```

Sequence Listing - Page 2195 - 2195

<210> 1927
<211> 810
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(787)
<223> RXA00765

<400> 1927

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acggaaaagt ttctgcgtct gcgtggtcga ctcaggattc gcaatcagaa gaacatgcac 60

gttatctaag agtagtgcca aaacgctagt cttgagtgtc atg agc gaa aat tcc   115
                                            Met Ser Glu Asn Ser
                                              1               5

acc cct aat aat cca gtc gtc cca ggt gca ggc gca gac ggc cca tca   163
Thr Pro Asn Asn Pro Val Val Pro Gly Ala Gly Ala Asp Gly Pro Ser
                 10                  15                  20

ctg tcc gat tct gca agc atc agc gga tcc gac gca gta aac ctc gct   211
Leu Ser Asp Ser Ala Ser Ile Ser Gly Ser Asp Ala Val Asn Leu Ala
             25                  30                  35

gcc gaa caa tcc aag agc acc gct cac cgc aac atc cca ggc cta ggt   259
Ala Glu Gln Ser Lys Ser Thr Ala His Arg Asn Ile Pro Gly Leu Gly
         40                  45                  50

gac ctt cct atc cct gac gac acc gct aac ctc cgc gaa ggc ccc aac   307
Asp Leu Pro Ile Pro Asp Asp Thr Ala Asn Leu Arg Glu Gly Pro Asn
     55                  60                  65

ctc cac gac gga ctc ctc gcg ctc ctc cct ctc gtc ggc gtc tgg cgc   355
Leu His Asp Gly Leu Leu Ala Leu Leu Pro Leu Val Gly Val Trp Arg
 70                  75                  80                  85

ggc gaa ggc caa gcc gac acc gca gaa gac gga caa tac gca ttc ggc   403
```

```
Gly Glu Gly Gln Ala Asp Thr Ala Glu Asp Gly Gln Tyr Ala Phe Gly
                 90                  95                 100

cag caa atc acc ttc gcc cac gac ggt gaa aac tac ctc tcc ttc gaa   451
Gln Gln Ile Thr Phe Ala His Asp Gly Glu Asn Tyr Leu Ser Phe Glu
            105                 110                 115

tcc cgc atg tgg aaa ctc gac gaa gaa gga aac ccc acc ggc gtc gac   499
Ser Arg Met Trp Lys Leu Asp Glu Glu Gly Asn Pro Thr Gly Val Asp
        120                 125                 130

cag cgc gaa tcc ggc ttc tgg cgc atc aat ctc aaa gat gaa atc gaa   547
Gln Arg Glu Ser Gly Phe Trp Arg Ile Asn Leu Lys Asp Glu Ile Glu
    135                 140                 145

ttc gtc tgc acc cac gcc ggc gga gtt gta gaa atc tac tac ggc cag   595
Phe Val Cys Thr His Ala Gly Gly Val Val Glu Ile Tyr Tyr Gly Gln
150                 155                 160                 165

cca ctc aat gag cgc gcc tgg cag ctt gaa tcc gca tct acc atg gtc   643
Pro Leu Asn Glu Arg Ala Trp Gln Leu Glu Ser Ala Ser Thr Met Val
                170                 175                 180

acc gcc acc ggc cca tcc acc ctt gga cca gga aag cgt ctc tac gga   691
Thr Ala Thr Gly Pro Ser Thr Leu Gly Pro Gly Lys Arg Leu Tyr Gly
            185                 190                 195

ctg ctt cca acc aac gaa ctc ggc tgg gtt gat gag cgt ctc gtt ggc   739
Leu Leu Pro Thr Asn Glu Leu Gly Trp Val Asp Glu Arg Leu Val Gly
        200                 205                 210

gac gcc ctc aag cca cgc atg tcc gca cag ctc acc cgc gtg atc ggc   787
Asp Ala Leu Lys Pro Arg Met Ser Ala Gln Leu Thr Arg Val Ile Gly
    215                 220                 225

tagttttttc tagttcaccg tca                                        810


<210> 1928
<211> 229
<212> PRT
<213> Corynebacterium glutamicum

<400> 1928
Met Ser Glu Asn Ser Thr Pro Asn Asn Pro Val Val Pro Gly Ala Gly
  1               5                  10                  15

Ala Asp Gly Pro Ser Leu Ser Asp Ser Ala Ser Ile Ser Gly Ser Asp
             20                  25                  30

Ala Val Asn Leu Ala Ala Glu Gln Ser Lys Ser Thr Ala His Arg Asn
         35                  40                  45

Ile Pro Gly Leu Gly Asp Leu Pro Ile Pro Asp Asp Thr Ala Asn Leu
     50                  55                  60

Arg Glu Gly Pro Asn Leu His Asp Gly Leu Leu Ala Leu Leu Pro Leu
 65                  70                  75                  80

Val Gly Val Trp Arg Gly Glu Gly Gln Ala Asp Thr Ala Glu Asp Gly
                 85                  90                  95
```

```
Gln Tyr Ala Phe Gly Gln Gln Ile Thr Phe Ala His Asp Gly Glu Asn
            100                 105                 110

Tyr Leu Ser Phe Glu Ser Arg Met Trp Lys Leu Asp Glu Glu Gly Asn
        115                 120                 125

Pro Thr Gly Val Asp Gln Arg Glu Ser Gly Phe Trp Arg Ile Asn Leu
    130                 135                 140

Lys Asp Glu Ile Glu Phe Val Cys Thr His Ala Gly Gly Val Val Glu
145                 150                 155                 160

Ile Tyr Tyr Gly Gln Pro Leu Asn Glu Arg Ala Trp Gln Leu Glu Ser
                165                 170                 175

Ala Ser Thr Met Val Thr Ala Thr Gly Pro Ser Thr Leu Gly Pro Gly
            180                 185                 190

Lys Arg Leu Tyr Gly Leu Leu Pro Thr Asn Glu Leu Gly Trp Val Asp
        195                 200                 205

Glu Arg Leu Val Gly Asp Ala Leu Lys Pro Arg Met Ser Ala Gln Leu
    210                 215                 220

Thr Arg Val Ile Gly
225
```

<210> 1929
<211> 411
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(388)
<223> RXA00781

<400> 1929

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tttcttagga aataaaacag ggtgtctttg tgttcaaaag gtataaagga agagtagttc 60

cggttaattc caccgggatg agataccgag gagaacgcac atg agc gag aac aaa   115
                                               Met Ser Glu Asn Lys
                                                 1               5

aac att gag att gtc cac aat gaa gga cag aag cgc ttt gtt atc agc   163
Asn Ile Glu Ile Val His Asn Glu Gly Gln Lys Arg Phe Val Ile Ser
                10                  15                  20

gtt gat gga acg cca gct gga ttt gcc agc tat tta gac ggc ccg gat   211
Val Asp Gly Thr Pro Ala Gly Phe Ala Ser Tyr Leu Asp Gly Pro Asp
            25                  30                  35

atc cgc aac ttc aac cac act gtt att aag cct gaa ttc cgt gga cag   259
Ile Arg Asn Phe Asn His Thr Val Ile Lys Pro Glu Phe Arg Gly Gln
        40                  45                  50

gga ctg tct gcg cca ttg atc aag ttt gct ttg gat gat gca cgt gag   307
Gly Leu Ser Ala Pro Leu Ile Lys Phe Ala Leu Asp Asp Ala Arg Glu
    55                  60                  65
```

```
tcc ggt atc cgt att cat gat gct tgc tct gca gtc gct ggc ttc att   355
Ser Gly Ile Arg Ile His Asp Ala Cys Ser Ala Val Ala Gly Phe Ile
 70                  75                  80                  85

cag aag aac cct gag tat aag gat cta aag aac tagctggcac agggggtgg 408
Gln Lys Asn Pro Glu Tyr Lys Asp Leu Lys Asn
                90                  95

ttc                                                               411


<210> 1930
<211> 96
<212> PRT
<213> Corynebacterium glutamicum

<400> 1930
Met Ser Glu Asn Lys Asn Ile Glu Ile Val His Asn Glu Gly Gln Lys
  1               5                  10                  15

Arg Phe Val Ile Ser Val Asp Gly Thr Pro Ala Gly Phe Ala Ser Tyr
             20                  25                  30

Leu Asp Gly Pro Asp Ile Arg Asn Phe Asn His Thr Val Ile Lys Pro
         35                  40                  45

Glu Phe Arg Gly Gln Gly Leu Ser Ala Pro Leu Ile Lys Phe Ala Leu
     50                  55                  60

Asp Asp Ala Arg Glu Ser Gly Ile Arg Ile His Asp Ala Cys Ser Ala
 65                  70                  75                  80

Val Ala Gly Phe Ile Gln Lys Asn Pro Glu Tyr Lys Asp Leu Lys Asn
                85                  90                  95



<210> 1931
<211> 348
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(325)
<223> RXA00788

<400> 1931
cgcatccctc tagttttcca tcacctcaat gaacggcgct aactccggtt cattgcgcaa 60

ttgatccagc actgcttgca gtgaggcctc attagttggc atg gcc tcc tcc atc   115
                                            Met Ala Ser Ser Ile
                                              1               5

aac atc gga gtg ttc aac ctt gga aat gct gtt gct gcc tgg ctt gct   163
Asn Ile Gly Val Phe Asn Leu Gly Asn Ala Val Ala Ala Trp Leu Ala
                10                  15                  20
```

```
ggt gca acc atc acc act tcc ctt gga ctc aca tca gcc gga tta gtt   211
Gly Ala Thr Ile Thr Thr Ser Leu Gly Leu Thr Ser Ala Gly Leu Val
             25                  30                  35

ggc ggt ttg atg acg tcc ctc gga cta gtg ttg gcc atc gtg gct gtg   259
Gly Gly Leu Met Thr Ser Leu Gly Leu Val Leu Ala Ile Val Ala Val
         40                  45                  50

gtt ttg cgt cga aaa gcg caa ggc acc caa gcg acc atc agc gtt gtg   307
Val Leu Arg Arg Lys Ala Gln Gly Thr Gln Ala Thr Ile Ser Val Val
     55                  60                  65

gag cac cag ccc gcc caa taaataattt ctctcttcta att                348
Glu His Gln Pro Ala Gln
 70                  75
```

<210> 1932
<211> 75
<212> PRT
<213> Corynebacterium glutamicum

<400> 1932

```
Met Ala Ser Ser Ile Asn Ile Gly Val Phe Asn Leu Gly Asn Ala Val
  1               5                  10                  15

Ala Ala Trp Leu Ala Gly Ala Thr Ile Thr Thr Ser Leu Gly Leu Thr
             20                  25                  30

Ser Ala Gly Leu Val Gly Gly Leu Met Thr Ser Leu Gly Leu Val Leu
         35                  40                  45

Ala Ile Val Ala Val Val Leu Arg Arg Lys Ala Gln Gly Thr Gln Ala
     50                  55                  60

Thr Ile Ser Val Val Glu His Gln Pro Ala Gln
 65                  70                  75
```

<210> 1933
<211> 567
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(544)
<223> RXA00804

<400> 1933

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aatctagtgc aagttccagc gaaaaccttc caaaactgac caagtttaag aagattcgct 60

accctatgaa tcagttgtag gagtaagagg ggagttagag atg aag atc aga agt   115
                                              Met Lys Ile Arg Ser
                                                1               5

gca cgt gaa atc gcg gag tgg ttc gtt gcc tgg gga gat gaa ctc gat   163
Ala Arg Glu Ile Ala Glu Trp Phe Val Ala Trp Gly Asp Glu Leu Asp
                10                  15                  20

gct gaa gtc tcc cct ttg aaa ttg cag aag ctc ctt tat tac tcc cag   211
```

```
Ala Glu Val Ser Pro Leu Lys Leu Gln Lys Leu Leu Tyr Tyr Ser Gln
             25                  30                  35

ggt gag cat ata gct gca aca ggg cga aaa ctt ttc tcg gat aag att   259
Gly Glu His Ile Ala Ala Thr Gly Arg Lys Leu Phe Ser Asp Lys Ile
         40                  45                  50

ctg gcg tgg cag cac gga cct gtc act ccg ggc gtt tat tca gat aca   307
Leu Ala Trp Gln His Gly Pro Val Thr Pro Gly Val Tyr Ser Asp Thr
     55                  60                  65

aaa tca tac ggc cga aac cca att gat cct gat gag ttt gtg tca gat   355
Lys Ser Tyr Gly Arg Asn Pro Ile Asp Pro Asp Glu Phe Val Ser Asp
 70                  75                  80                  85

gaa ttt aac tgg gat gac tac tca gat gtg tca gat gag ctt gta acc   403
Glu Phe Asn Trp Asp Asp Tyr Ser Asp Val Ser Asp Glu Leu Val Thr
                 90                  95                 100

gta tgg cga aaa tac ggc atc tat tcg gcg tgg gca ctg agg gaa aaa   451
Val Trp Arg Lys Tyr Gly Ile Tyr Ser Ala Trp Ala Leu Arg Glu Lys
             105                 110                 115

act cac agt gaa tcg ccg tgg ctc gat gcc tgg gca caa ggg caa aat   499
Thr His Ser Glu Ser Pro Trp Leu Asp Ala Trp Ala Gln Gly Gln Asn
         120                 125                 130

att gaa att aca gat gct gcg ctg aaa gat ttc ttc ttg gtg cat       544
Ile Glu Ile Thr Asp Ala Ala Leu Lys Asp Phe Phe Leu Val His
     135                 140                 145

tagaaatttg aaaaagaaac gaa                                        567


<210> 1934
<211> 148
<212> PRT
<213> Corynebacterium glutamicum

<400> 1934
Met Lys Ile Arg Ser Ala Arg Glu Ile Ala Glu Trp Phe Val Ala Trp
  1               5                  10                  15

Gly Asp Glu Leu Asp Ala Glu Val Ser Pro Leu Lys Leu Gln Lys Leu
             20                  25                  30

Leu Tyr Tyr Ser Gln Gly Glu His Ile Ala Ala Thr Gly Arg Lys Leu
         35                  40                  45

Phe Ser Asp Lys Ile Leu Ala Trp Gln His Gly Pro Val Thr Pro Gly
     50                  55                  60

Val Tyr Ser Asp Thr Lys Ser Tyr Gly Arg Asn Pro Ile Asp Pro Asp
 65                  70                  75                  80

Glu Phe Val Ser Asp Glu Phe Asn Trp Asp Asp Tyr Ser Asp Val Ser
                 85                  90                  95

Asp Glu Leu Val Thr Val Trp Arg Lys Tyr Gly Ile Tyr Ser Ala Trp
            100                 105                 110
```

```
Ala Leu Arg Glu Lys Thr His Ser Glu Ser Pro Trp Leu Asp Ala Trp
        115                 120                 125

Ala Gln Gly Gln Asn Ile Glu Ile Thr Asp Ala Ala Leu Lys Asp Phe
    130                 135                 140

Phe Leu Val His
145
```

<210> 1935
<211> 1005
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(982)
<223> RXA00805

<400> 1935

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tgctccgctg acagtggtgc gcctgagcag cccaaaagag acaaagcgct ggttgagggc 60

atatggggaa agcgtgaaac tctgataggg tgccatatcc atg gca gaa agt ttt   115
                                            Met Ala Glu Ser Phe
                                              1               5

ata gag gtc tcg gcg ggg cat gcg gat cgg cgg ata gat aag ttt ttg   163
Ile Glu Val Ser Ala Gly His Ala Asp Arg Arg Ile Asp Lys Phe Leu
                10                  15                  20

cgg gca cag cta aag ggc gtg ccc gcg tcg ttg att ttc cgt caa atg   211
Arg Ala Gln Leu Lys Gly Val Pro Ala Ser Leu Ile Phe Arg Gln Met
            25                  30                  35

cgt aaa ggc gac att cgg gtg aat ggt cgt aaa gtg gat ccg aat tac   259
Arg Lys Gly Asp Ile Arg Val Asn Gly Arg Lys Val Asp Pro Asn Tyr
        40                  45                  50

cgg ttg caa gaa ggc gac cga att cga atg tgg cag atg gat ttg ctg   307
Arg Leu Gln Glu Gly Asp Arg Ile Arg Met Trp Gln Met Asp Leu Leu
    55                  60                  65

gca gat ttg ccg cca ccg gtc gtc gat aag cat att ttt aag gct gtc   355
Ala Asp Leu Pro Pro Pro Val Val Asp Lys His Ile Phe Lys Ala Val
70                  75                  80                  85

gca gac agc gtg ctt ttt gag gac gcc gaa tta ctg gtg atc aat aag   403
Ala Asp Ser Val Leu Phe Glu Asp Ala Glu Leu Leu Val Ile Asn Lys
                90                  95                  100

cca gct gga att cct gtg cac ggt ggc acg ggg cac ggc ggt ggc gtg   451
Pro Ala Gly Ile Pro Val His Gly Gly Thr Gly His Gly Gly Gly Val
            105                 110                 115

att gag gcg ctg cgg cag aag ttt ccg cag gaa cgc gac ctg gaa ttg   499
Ile Glu Ala Leu Arg Gln Lys Phe Pro Gln Glu Arg Asp Leu Glu Leu
        120                 125                 130

gtg cat cgt ttg gat cgg gac acc tca ggt ttg ttg ctg gtt tct aaa   547
Val His Arg Leu Asp Arg Asp Thr Ser Gly Leu Leu Leu Val Ser Lys
```

```
    135                 140                 145

acg aca tct gtg ttg cgc gag ttg cag gaa att ttg cga gac cgc gaa   595
Thr Thr Ser Val Leu Arg Glu Leu Gln Glu Ile Leu Arg Asp Arg Glu
150                 155                 160                 165

gag gag att ttt cgg ggg tat tta ctc aag gtc gag ggg gct tgg cct   643
Glu Glu Ile Phe Arg Gly Tyr Leu Leu Lys Val Glu Gly Ala Trp Pro
                170                 175                 180

ggc gat ttg cga caa att gat gtg ccg ttg aag cgg acg gag aca act   691
Gly Asp Leu Arg Gln Ile Asp Val Pro Leu Lys Arg Thr Glu Thr Thr
            185                 190                 195

gtt gtg cca cat tcg gat ggt ttg cgg gcg cgg acg tat ttt gag gtt   739
Val Val Pro His Ser Asp Gly Leu Arg Ala Arg Thr Tyr Phe Glu Val
        200                 205                 210

gta aag cgt ttg ccg ggt gcg acc ttg gtg aag gcg cag ttg gcg acc   787
Val Lys Arg Leu Pro Gly Ala Thr Leu Val Lys Ala Gln Leu Ala Thr
    215                 220                 225

ggg cgg aaa cat cag att cgg gtc cat gcg cag tat gcg ggt cac cct   835
Gly Arg Lys His Gln Ile Arg Val His Ala Gln Tyr Ala Gly His Pro
230                 235                 240                 245

att gtt ggc gat cca cga tac ggg tcg cgt ggg ggc aga gct gcg acg   883
Ile Val Gly Asp Pro Arg Tyr Gly Ser Arg Gly Gly Arg Ala Ala Thr
                250                 255                 260

atg cat ttg cat gcg gcg gaa ttg gtg gcg cct cgt ggg gcg ggg aag   931
Met His Leu His Ala Ala Glu Leu Val Ala Pro Arg Gly Ala Gly Lys
            265                 270                 275

cgt cag aaa ttc act gca ccg ttg ccg aag gag tgg ggt atg gga cgg   979
Arg Gln Lys Phe Thr Ala Pro Leu Pro Lys Glu Trp Gly Met Gly Arg
        280                 285                 290

gtc tgagtcgggc cttcgtggaa tcg                                    1005
Val
```

```
<210> 1936
<211> 294
<212> PRT
<213> Corynebacterium glutamicum

<400> 1936
Met Ala Glu Ser Phe Ile Glu Val Ser Ala Gly His Ala Asp Arg Arg
  1               5                  10                  15

Ile Asp Lys Phe Leu Arg Ala Gln Leu Lys Gly Val Pro Ala Ser Leu
             20                  25                  30

Ile Phe Arg Gln Met Arg Lys Gly Asp Ile Arg Val Asn Gly Arg Lys
         35                  40                  45

Val Asp Pro Asn Tyr Arg Leu Gln Glu Gly Asp Arg Ile Arg Met Trp
     50                  55                  60
```

Gln Met Asp Leu Leu Ala Asp Leu Pro Pro Pro Val Val Asp Lys His
65 70 75 80

Ile Phe Lys Ala Val Ala Asp Ser Val Leu Phe Glu Asp Ala Glu Leu
85 90 95

Leu Val Ile Asn Lys Pro Ala Gly Ile Pro Val His Gly Gly Thr Gly
100 105 110

His Gly Gly Gly Val Ile Glu Ala Leu Arg Gln Lys Phe Pro Gln Glu
115 120 125

Arg Asp Leu Glu Leu Val His Arg Leu Asp Arg Asp Thr Ser Gly Leu
130 135 140

Leu Leu Val Ser Lys Thr Thr Ser Val Leu Arg Glu Leu Gln Glu Ile
145 150 155 160

Leu Arg Asp Arg Glu Glu Glu Ile Phe Arg Gly Tyr Leu Leu Lys Val
165 170 175

Glu Gly Ala Trp Pro Gly Asp Leu Arg Gln Ile Asp Val Pro Leu Lys
180 185 190

Arg Thr Glu Thr Thr Val Val Pro His Ser Asp Gly Leu Arg Ala Arg
195 200 205

Thr Tyr Phe Glu Val Val Lys Arg Leu Pro Gly Ala Thr Leu Val Lys
210 215 220

Ala Gln Leu Ala Thr Gly Arg Lys His Gln Ile Arg Val His Ala Gln
225 230 235 240

Tyr Ala Gly His Pro Ile Val Gly Asp Pro Arg Tyr Gly Ser Arg Gly
245 250 255

Gly Arg Ala Ala Thr Met His Leu His Ala Ala Glu Leu Val Ala Pro
260 265 270

Arg Gly Ala Gly Lys Arg Gln Lys Phe Thr Ala Pro Leu Pro Lys Glu
275 280 285

Trp Gly Met Gly Arg Val
290

<210> 1937
<211> 701
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(678)
<223> RXA00808

<400> 1937
gct ggc ttc aat gag atg atg cgt ggc ctg cgt gaa cgt cag cgc gtc 48
Ala Gly Phe Asn Glu Met Met Arg Gly Leu Arg Glu Arg Gln Arg Val
1 5 10 15

```
cgt gac ctt ttc ggt cgc tac gtg ggc gct gaa gtg gcc aag cgt gcg   96
Arg Asp Leu Phe Gly Arg Tyr Val Gly Ala Glu Val Ala Lys Arg Ala
             20                  25                  30

ctg gag gaa cgc ccc act ctg ggt ggc gag gac cgt aag gtt gcc gtg   144
Leu Glu Glu Arg Pro Thr Leu Gly Gly Glu Asp Arg Lys Val Ala Val
         35                  40                  45

ttg ttt gtc gat gtc atc ggc tcc act acc ttt gcc gtc aac cac act   192
Leu Phe Val Asp Val Ile Gly Ser Thr Thr Phe Ala Val Asn His Thr
     50                  55                  60

cct gaa gag gtt gtg gag gcg ctc aat gag ttc ttc gag cac gtc gtg   240
Pro Glu Glu Val Val Glu Ala Leu Asn Glu Phe Phe Glu His Val Val
 65                  70                  75                  80

gag gtt gtg cac cgc aac aag ggt gtt atc aac aag ttc cag ggt gac   288
Glu Val Val His Arg Asn Lys Gly Val Ile Asn Lys Phe Gln Gly Asp
                 85                  90                  95

gcg gcg ttg gcg att ttc ggc gct ccc ctg ccc ctg tct gat gcc acc   336
Ala Ala Leu Ala Ile Phe Gly Ala Pro Leu Pro Leu Ser Asp Ala Thr
            100                 105                 110

ggt cat gcg ctt gcg gct gcc cgt gag ctc cgc gca gag ctg aaa gat   384
Gly His Ala Leu Ala Ala Ala Arg Glu Leu Arg Ala Glu Leu Lys Asp
        115                 120                 125

ctc cag ctc aag gcc gga att ggt gtg gct gct ggc cat gtc gtt gct   432
Leu Gln Leu Lys Ala Gly Ile Gly Val Ala Ala Gly His Val Val Ala
    130                 135                 140

ggt cat atc ggc ggt cac gcg agg ttt gag tac act gtg atc ggc gac   480
Gly His Ile Gly Gly His Ala Arg Phe Glu Tyr Thr Val Ile Gly Asp
145                 150                 155                 160

gcg gtg aac cag gct gcg cgc ctg acg gag atc gcg aaa acg acc cca   528
Ala Val Asn Gln Ala Ala Arg Leu Thr Glu Ile Ala Lys Thr Thr Pro
                165                 170                 175

ggc cgc acc gtc acc aac gct tcc acg ctg cgt gag gcc aac gag gcg   576
Gly Arg Thr Val Thr Asn Ala Ser Thr Leu Arg Glu Ala Asn Glu Ala
            180                 185                 190

gag cag gct cgc tgg acg ctc atg aag tcc gtg gag ctg cgc gga cgt   624
Glu Gln Ala Arg Trp Thr Leu Met Lys Ser Val Glu Leu Arg Gly Arg
        195                 200                 205

agc cag atg acg cag att gcg cgg cct att cgg ccg acg ttg gcg gat   672
Ser Gln Met Thr Gln Ile Ala Arg Pro Ile Arg Pro Thr Leu Ala Asp
    210                 215                 220

agg tcc taatacgctt ttcgacgcaa aaa                                701
Arg Ser
225
```

<210> 1938
<211> 226
<212> PRT
<213> Corynebacterium glutamicum

<400> 1938
Ala Gly Phe Asn Glu Met Met Arg Gly Leu Arg Glu Arg Gln Arg Val
1 5 10 15

Arg Asp Leu Phe Gly Arg Tyr Val Gly Ala Glu Val Ala Lys Arg Ala
20 25 30

Leu Glu Glu Arg Pro Thr Leu Gly Gly Glu Asp Arg Lys Val Ala Val
35 40 45

Leu Phe Val Asp Val Ile Gly Ser Thr Thr Phe Ala Val Asn His Thr
50 55 60

Pro Glu Glu Val Val Glu Ala Leu Asn Glu Phe Phe Glu His Val Val
65 70 75 80

Glu Val Val His Arg Asn Lys Gly Val Ile Asn Lys Phe Gln Gly Asp
85 90 95

Ala Ala Leu Ala Ile Phe Gly Ala Pro Leu Pro Leu Ser Asp Ala Thr
100 105 110

Gly His Ala Leu Ala Ala Ala Arg Glu Leu Arg Ala Glu Leu Lys Asp
115 120 125

Leu Gln Leu Lys Ala Gly Ile Gly Val Ala Ala Gly His Val Val Ala
130 135 140

Gly His Ile Gly Gly His Ala Arg Phe Glu Tyr Thr Val Ile Gly Asp
145 150 155 160

Ala Val Asn Gln Ala Ala Arg Leu Thr Glu Ile Ala Lys Thr Thr Pro
165 170 175

Gly Arg Thr Val Thr Asn Ala Ser Thr Leu Arg Glu Ala Asn Glu Ala
180 185 190

Glu Gln Ala Arg Trp Thr Leu Met Lys Ser Val Glu Leu Arg Gly Arg
195 200 205

Ser Gln Met Thr Gln Ile Ala Arg Pro Ile Arg Pro Thr Leu Ala Asp
210 215 220

Arg Ser
225

<210> 1939
<211> 1182
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1159)
<223> RXA00812

<400> 1939
ttcacaggtg agcgtatcgc gggcggttga gaggtgagtt atccacaggc cgcagagggg 60

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gtcgttgaaa gcacgtaagc ctcaggccac agtaggtgcc atg aac acc atc aca   115
                                            Met Asn Thr Ile Thr
                                              1               5

cac caa gca att ctc atc gca gtg gaa gat ccg gtc ctg cac cca gag   163
His Gln Ala Ile Leu Ile Ala Val Glu Asp Pro Val Leu His Pro Glu
                10                  15                  20

gcc atg cac gta gct gca gcc act ggt cgg ccg gtt att gaa aca aca   211
Ala Met His Val Ala Ala Ala Thr Gly Arg Pro Val Ile Glu Thr Thr
            25                  30                  35

aat ttg atg gac atc tcc agg cat ttt cac cgc aca tcg gca gtg ctc   259
Asn Leu Met Asp Ile Ser Arg His Phe His Arg Thr Ser Ala Val Leu
        40                  45                  50

att gat gcg tcg atg gcc tct caa tta tca cct ggg aaa cgc cgc gac   307
Ile Asp Ala Ser Met Ala Ser Gln Leu Ser Pro Gly Lys Arg Arg Asp
    55                  60                  65

agg gtg ttt ctt ctc gat tct gat cca ggg ccc tct gat tgg aaa acg   355
Arg Val Phe Leu Leu Asp Ser Asp Pro Gly Pro Ser Asp Trp Lys Thr
70                  75                  80                  85

gcg atg aaa atc cac gct gag caa gcc atg ttg ctt ccc gct cag gca   403
Ala Met Lys Ile His Ala Glu Gln Ala Met Leu Leu Pro Ala Gln Ala
                90                  95                  100

ggg gag ttg ctc agc gct tta ggc aga gat gac aaa caa ctg ccg gtg   451
Gly Glu Leu Leu Ser Ala Leu Gly Arg Asp Asp Lys Gln Leu Pro Val
            105                 110                 115

gct tcg ggc cat gtc atc ggt gtt gcc ggg gtg gtg gga gga aca ggc   499
Ala Ser Gly His Val Ile Gly Val Ala Gly Val Val Gly Gly Thr Gly
        120                 125                 130

gcg agc acg ttt gct gcg gcg ctc gca aag cgg cgt gcg gag tca gtc   547
Ala Ser Thr Phe Ala Ala Ala Leu Ala Lys Arg Arg Ala Glu Ser Val
    135                 140                 145

acc act gtg ctt atc gac gcc gac cct tcc tct ggc ggc atc gac ctg   595
Thr Thr Val Leu Ile Asp Ala Asp Pro Ser Ser Gly Gly Ile Asp Leu
150                 155                 160                 165

ttg cta gga atc gaa gat gtg ccc ggc gcg cgg tgg cct gat gtg ggg   643
Leu Leu Gly Ile Glu Asp Val Pro Gly Ala Arg Trp Pro Asp Val Gly
                170                 175                 180

ttg cgt cgc gga act gtc cag gct gct gat gtg ttg aaa gcg ctg ccg   691
Leu Arg Arg Gly Thr Val Gln Ala Ala Asp Val Leu Lys Ala Leu Pro
            185                 190                 195

agc act cct gat gag gtc gtg gtg ttg tct acg gcg cgg tct aat att   739
Ser Thr Pro Asp Glu Val Val Val Leu Ser Thr Ala Arg Ser Asn Ile
        200                 205                 210

ctg gat cct ttt gca tta tcc gag tct gat gtt tca gcg gcg att gat   787
Leu Asp Pro Phe Ala Leu Ser Glu Ser Asp Val Ser Ala Ala Ile Asp
    215                 220                 225

tgt ttc tta agc gcc gat agg tcg gtg gat gtg gtg gtg gat ctg cct   835
```

```
Cys Phe Leu Ser Ala Asp Arg Ser Val Asp Val Val Val Asp Leu Pro
230                 235                 240                 245

cat gcg aga gtg cat cca gat att gcg gag cgc tta tcc cac ctg gtg   883
His Ala Arg Val His Pro Asp Ile Ala Glu Arg Leu Ser His Leu Val
                250                 255                 260

tta gtc atc cct gca gag gtc cga gcg gtg gct gct gcc agg gct cgg   931
Leu Val Ile Pro Ala Glu Val Arg Ala Val Ala Ala Ala Arg Ala Arg
            265                 270                 275

tgt ctg gaa tta caa caa ttg cat gta tcc atc acg tgc gtg ttg agg   979
Cys Leu Glu Leu Gln Gln Leu His Val Ser Ile Thr Cys Val Leu Arg
        280                 285                 290

cat cgc ggg tgg tca ggt ttg gat gtt gca gaa gtg gaa gag att tta   1027
His Arg Gly Trp Ser Gly Leu Asp Val Ala Glu Val Glu Glu Ile Leu
    295                 300                 305

ggt gcg gat att acc gcg gag gtt ggc tcg atc cag cgg ctg gct aag   1075
Gly Ala Asp Ile Thr Ala Glu Val Gly Ser Ile Gln Arg Leu Ala Lys
310                 315                 320                 325

tcc gtg gag atg cat ggg ctg acc ggt tct ttg ccg agg gtt tta agc   1123
Ser Val Glu Met His Gly Leu Thr Gly Ser Leu Pro Arg Val Leu Ser
                330                 335                 340

tca gca tgc gac gcg gtc ctc ggg gag gtg gcg gca tgactgacat        1169
Ser Ala Cys Asp Ala Val Leu Gly Glu Val Ala Ala
            345                 350

tgatctggtg gtg                                                   1182


<210> 1940
<211> 353
<212> PRT
<213> Corynebacterium glutamicum

<400> 1940
Met Asn Thr Ile Thr His Gln Ala Ile Leu Ile Ala Val Glu Asp Pro
  1               5                  10                  15

Val Leu His Pro Glu Ala Met His Val Ala Ala Ala Thr Gly Arg Pro
             20                  25                  30

Val Ile Glu Thr Thr Asn Leu Met Asp Ile Ser Arg His Phe His Arg
         35                  40                  45

Thr Ser Ala Val Leu Ile Asp Ala Ser Met Ala Ser Gln Leu Ser Pro
     50                  55                  60

Gly Lys Arg Arg Asp Arg Val Phe Leu Leu Asp Ser Asp Pro Gly Pro
 65                  70                  75                  80

Ser Asp Trp Lys Thr Ala Met Lys Ile His Ala Glu Gln Ala Met Leu
                 85                  90                  95

Leu Pro Ala Gln Ala Gly Glu Leu Leu Ser Ala Leu Gly Arg Asp Asp
            100                 105                 110
```

```
Lys Gln Leu Pro Val Ala Ser Gly His Val Ile Gly Val Ala Gly Val
        115                 120                 125

Val Gly Gly Thr Gly Ala Ser Thr Phe Ala Ala Ala Leu Ala Lys Arg
    130                 135                 140

Arg Ala Glu Ser Val Thr Thr Val Leu Ile Asp Ala Asp Pro Ser Ser
145                 150                 155                 160

Gly Gly Ile Asp Leu Leu Leu Gly Ile Glu Asp Val Pro Gly Ala Arg
                165                 170                 175

Trp Pro Asp Val Gly Leu Arg Arg Gly Thr Val Gln Ala Ala Asp Val
            180                 185                 190

Leu Lys Ala Leu Pro Ser Thr Pro Asp Glu Val Val Val Leu Ser Thr
        195                 200                 205

Ala Arg Ser Asn Ile Leu Asp Pro Phe Ala Leu Ser Glu Ser Asp Val
    210                 215                 220

Ser Ala Ala Ile Asp Cys Phe Leu Ser Ala Asp Arg Ser Val Asp Val
225                 230                 235                 240

Val Val Asp Leu Pro His Ala Arg Val His Pro Asp Ile Ala Glu Arg
                245                 250                 255

Leu Ser His Leu Val Leu Val Ile Pro Ala Glu Val Arg Ala Val Ala
            260                 265                 270

Ala Ala Arg Ala Arg Cys Leu Glu Leu Gln Gln Leu His Val Ser Ile
        275                 280                 285

Thr Cys Val Leu Arg His Arg Gly Trp Ser Gly Leu Asp Val Ala Glu
    290                 295                 300

Val Glu Glu Ile Leu Gly Ala Asp Ile Thr Ala Glu Val Gly Ser Ile
305                 310                 315                 320

Gln Arg Leu Ala Lys Ser Val Glu Met His Gly Leu Thr Gly Ser Leu
                325                 330                 335

Pro Arg Val Leu Ser Ser Ala Cys Asp Ala Val Leu Gly Glu Val Ala
            340                 345                 350

Ala
```

<210> 1941
<211> 897
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(874)
<223> RXA00814

<400> 1941
gccgcaggct agctcaactc ggggtgctcc gcggaaatcc tgtgaccacg caggtggtgt 60

```
gggatttgga ccacggcatg cacgaaggga gcgaagaggc atg gtt tat gcc cta   115
                                            Met Val Tyr Ala Leu
                                              1               5

ggc ctt ctt agc gtg gcg gtg ttg atc tct ggt tca agg ggc ccc ggc   163
Gly Leu Leu Ser Val Ala Val Leu Ile Ser Gly Ser Arg Gly Pro Gly
                 10                  15                  20

gcg cgt acc agg cca cca aca cct ggg aat ggc gtc cat cta ttc gcc   211
Ala Arg Thr Arg Pro Pro Thr Pro Gly Asn Gly Val His Leu Phe Ala
             25                  30                  35

cta att gca cta ttt tgc ctg gcc aca gtg cta ttt atc gtc gtt gac   259
Leu Ile Ala Leu Phe Cys Leu Ala Thr Val Leu Phe Ile Val Val Asp
         40                  45                  50

gcc tac acg atg atc gcc ggc atc atc atc gcc aca act cta ttc tgg   307
Ala Tyr Thr Met Ile Ala Gly Ile Ile Ile Ala Thr Thr Leu Phe Trp
     55                  60                  65

tat ctc cgc cag aca cac gcc gca gcc caa cgc acc aaa caa tcc ctc   355
Tyr Leu Arg Gln Thr His Ala Ala Ala Gln Arg Thr Lys Gln Ser Leu
 70                  75                  80                  85

caa tta gcc agc ttc tta agc ctc tgc gca ggc aat tta cgc gcc ggg   403
Gln Leu Ala Ser Phe Leu Ser Leu Cys Ala Gly Asn Leu Arg Ala Gly
                 90                  95                 100

gtc acc atg gtc gac gcc atg gac tac gcg ctc gac aac acc acg ccg   451
Val Thr Met Val Asp Ala Met Asp Tyr Ala Leu Asp Asn Thr Thr Pro
             105                 110                 115

gac aaa ttc tta agc ccc acg ttg cag acc gca gcc agg cag gcg cgc   499
Asp Lys Phe Leu Ser Pro Thr Leu Gln Thr Ala Ala Arg Gln Ala Arg
         120                 125                 130

tcg ggc ggc agc ggg ccg cga gtg ctt atc gac gcc tcc ctc ccc gat   547
Ser Gly Gly Ser Gly Pro Arg Val Leu Ile Asp Ala Ser Leu Pro Asp
     135                 140                 145

ctt caa cgc ctc ggc cat ttg tgg gaa aca tca gaa cga cac ggc atc   595
Leu Gln Arg Leu Gly His Leu Trp Glu Thr Ser Glu Arg His Gly Ile
150                 155                 160                 165

ccg ctg gtc gcc ctc att gat caa atg agg tcc cgg att tca tcg aag   643
Pro Leu Val Ala Leu Ile Asp Gln Met Arg Ser Arg Ile Ser Ser Lys
                 170                 175                 180

caa cgc cac ggc gaa tcc acc cga gct gca ctc caa gga ccg caa gca   691
Gln Arg His Gly Glu Ser Thr Arg Ala Ala Leu Gln Gly Pro Gln Ala
             185                 190                 195

acc gca gtg atc ctt acc gtg ttg cca cta gca gga atg ctc atg ggc   739
Thr Ala Val Ile Leu Thr Val Leu Pro Leu Ala Gly Met Leu Met Gly
         200                 205                 210

aca gcc atg gga gca aac ccc ctt ggg cta ctc acc ggt ggt ggg atc   787
Thr Ala Met Gly Ala Asn Pro Leu Gly Leu Leu Thr Gly Gly Gly Ile
     215                 220                 225
```

```
ggt ggg ttc ctg ctt gtc atc ggt gtg ggc ctc gat gct gca ggg ttt   835
Gly Gly Phe Leu Leu Val Ile Gly Val Gly Leu Asp Ala Ala Gly Phe
230                 235                 240                 245

gtg ctc acc cac aaa att ctc cag agc gcg agc ccc tca tgattacagc   884
Val Leu Thr His Lys Ile Leu Gln Ser Ala Ser Pro Ser
                250                 255

actagttctt gca                                                   897
```

<210> 1942
<211> 258
<212> PRT
<213> Corynebacterium glutamicum

<400> 1942

```
Met Val Tyr Ala Leu Gly Leu Leu Ser Val Ala Val Leu Ile Ser Gly
  1               5                  10                  15

Ser Arg Gly Pro Gly Ala Arg Thr Arg Pro Pro Thr Pro Gly Asn Gly
             20                  25                  30

Val His Leu Phe Ala Leu Ile Ala Leu Phe Cys Leu Ala Thr Val Leu
         35                  40                  45

Phe Ile Val Val Asp Ala Tyr Thr Met Ile Ala Gly Ile Ile Ile Ala
     50                  55                  60

Thr Thr Leu Phe Trp Tyr Leu Arg Gln Thr His Ala Ala Ala Gln Arg
 65                  70                  75                  80

Thr Lys Gln Ser Leu Gln Leu Ala Ser Phe Leu Ser Leu Cys Ala Gly
                 85                  90                  95

Asn Leu Arg Ala Gly Val Thr Met Val Asp Ala Met Asp Tyr Ala Leu
            100                 105                 110

Asp Asn Thr Thr Pro Asp Lys Phe Leu Ser Pro Thr Leu Gln Thr Ala
        115                 120                 125

Ala Arg Gln Ala Arg Ser Gly Gly Ser Gly Pro Arg Val Leu Ile Asp
    130                 135                 140

Ala Ser Leu Pro Asp Leu Gln Arg Leu Gly His Leu Trp Glu Thr Ser
145                 150                 155                 160

Glu Arg His Gly Ile Pro Leu Val Ala Leu Ile Asp Gln Met Arg Ser
                165                 170                 175

Arg Ile Ser Ser Lys Gln Arg His Gly Glu Ser Thr Arg Ala Ala Leu
            180                 185                 190

Gln Gly Pro Gln Ala Thr Ala Val Ile Leu Thr Val Leu Pro Leu Ala
        195                 200                 205

Gly Met Leu Met Gly Thr Ala Met Gly Ala Asn Pro Leu Gly Leu Leu
    210                 215                 220

Thr Gly Gly Gly Ile Gly Gly Phe Leu Leu Val Ile Gly Val Gly Leu
225                 230                 235                 240
```

```
Asp Ala Ala Gly Phe Val Leu Thr His Lys Ile Leu Gln Ser Ala Ser
                245                 250                 255

Pro Ser
```

<210> 1943
<211> 696
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(673)
<223> RXA00815

<400> 1943

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ccggtggtgg gatcggtggg ttcctgcttg tcatcggtgt gggcctcgat gctgcagggt 60

ttgtgctcac ccacaaaatt ctccagagcg cgagcccctc atg att aca gca cta   115
                                              Met Ile Thr Ala Leu
                                                1               5

gtt ctt gca gca gtg gcc atg ttc ctc ggt tca ccc aac cct gga gtt   163
Val Leu Ala Ala Val Ala Met Phe Leu Gly Ser Pro Asn Pro Gly Val
               10                  15                  20

cgc ggt gga ttg ata agc ccc aaa tcc ggt aaa agc ctg cgt atc cga   211
Arg Gly Gly Leu Ile Ser Pro Lys Ser Gly Lys Ser Leu Arg Ile Arg
            25                  30                  35

gct ggc cca aaa aag ctg ggc aac gct gac cca gtg gat gtc tct gca   259
Ala Gly Pro Lys Lys Leu Gly Asn Ala Asp Pro Val Asp Val Ser Ala
         40                  45                  50

gat atc gaa ctg ttt tca gcg tgt ttg gat gcg ggt tta aac aca cgt   307
Asp Ile Glu Leu Phe Ser Ala Cys Leu Asp Ala Gly Leu Asn Thr Arg
     55                  60                  65

gat gca gcg cag gtg gtg gct cat gtt gca gcc att acg cac cgc gaa   355
Asp Ala Ala Gln Val Val Ala His Val Ala Ala Ile Thr His Arg Glu
 70                  75                  80                  85

ctg tgg aca cat gtg gtg gca ttg cta tcg att gga gtg agt gcc cct   403
Leu Trp Thr His Val Val Ala Leu Leu Ser Ile Gly Val Ser Ala Pro
               90                  95                 100

caa gca ttc gcc ctg atg gca gga gtt gat ggg ctg gat gaa cta gcc   451
Gln Ala Phe Ala Leu Met Ala Gly Val Asp Gly Leu Asp Glu Leu Ala
            105                 110                 115

aat tta gcc acc gtg tcg cac agg tcg ggc agt gca tta agt gat ggg   499
Asn Leu Ala Thr Val Ser His Arg Ser Gly Ser Ala Leu Ser Asp Gly
        120                 125                 130

tgc agg aac att tcc acc tcg ttg ttg gcc tct gct ggt gac aag cgc   547
Cys Arg Asn Ile Ser Thr Ser Leu Leu Ala Ser Ala Gly Asp Lys Arg
    135                 140                 145
```

```
acc gcc gca gca gaa cgc gca gga gtg ttc atc gcc ctg cca ctt gct   595
Thr Ala Ala Ala Glu Arg Ala Gly Val Phe Ile Ala Leu Pro Leu Ala
150                 155                 160                 165

ctg tgt ttc ctc ccc gca ttc atg att gtc ggg ctt gca cca gtg gtg   643
Leu Cys Phe Leu Pro Ala Phe Met Ile Val Gly Leu Ala Pro Val Val
                170                 175                 180

ctc agc ttg ggt acg caa ctt atc aat ttc tagaaaacac acacaggaga     693
Leu Ser Leu Gly Thr Gln Leu Ile Asn Phe
            185                 190

aaa                                                               696


<210> 1944
<211> 191
<212> PRT
<213> Corynebacterium glutamicum

<400> 1944
Met Ile Thr Ala Leu Val Leu Ala Ala Val Ala Met Phe Leu Gly Ser
  1               5                  10                  15

Pro Asn Pro Gly Val Arg Gly Gly Leu Ile Ser Pro Lys Ser Gly Lys
             20                  25                  30

Ser Leu Arg Ile Arg Ala Gly Pro Lys Lys Leu Gly Asn Ala Asp Pro
         35                  40                  45

Val Asp Val Ser Ala Asp Ile Glu Leu Phe Ser Ala Cys Leu Asp Ala
     50                  55                  60

Gly Leu Asn Thr Arg Asp Ala Ala Gln Val Val Ala His Val Ala Ala
 65                  70                  75                  80

Ile Thr His Arg Glu Leu Trp Thr His Val Val Ala Leu Leu Ser Ile
                85                  90                  95

Gly Val Ser Ala Pro Gln Ala Phe Ala Leu Met Ala Gly Val Asp Gly
            100                 105                 110

Leu Asp Glu Leu Ala Asn Leu Ala Thr Val Ser His Arg Ser Gly Ser
        115                 120                 125

Ala Leu Ser Asp Gly Cys Arg Asn Ile Ser Thr Ser Leu Leu Ala Ser
    130                 135                 140

Ala Gly Asp Lys Arg Thr Ala Ala Ala Glu Arg Ala Gly Val Phe Ile
145                 150                 155                 160

Ala Leu Pro Leu Ala Leu Cys Phe Leu Pro Ala Phe Met Ile Val Gly
                165                 170                 175

Leu Ala Pro Val Val Leu Ser Leu Gly Thr Gln Leu Ile Asn Phe
            180                 185                 190


<210> 1945
<211> 420
<212> DNA
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<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(397)
<223> RXA00816

<400> 1945
atgctcaccg caacagccac tatcccggca ccgattgggc aggtgagcgc gagtgcggtg 60

ttcccggtgg aaaactagct gtgcaaatga cgaaggctac atg acc atc gcc agc 115
Met Thr Ile Ala Ser
1 5

gct ggt gtc gcc tcc atc ctc att agc ctg ctg gtg gtg ctg gcc tgg 163
Ala Gly Val Ala Ser Ile Leu Ile Ser Leu Leu Val Val Leu Ala Trp
10 15 20

cag gcg gga aac ctc gtg gcc agg gaa caa gca cag gta gcg gcc gat 211
Gln Ala Gly Asn Leu Val Ala Arg Glu Gln Ala Gln Val Ala Ala Asp
25 30 35

gtt tca gct gtt gcc gga gcc tac gcc ttt gcc cgc ggg gaa cta ccc 259
Val Ser Ala Val Ala Gly Ala Tyr Ala Phe Ala Arg Gly Glu Leu Pro
40 45 50

gac gct gcc tgc gcc acc gcg aaa cac aca gcc gaa gca aac aac gca 307
Asp Ala Ala Cys Ala Thr Ala Lys His Thr Ala Glu Ala Asn Asn Ala
55 60 65

caa cta gaa aac tgc gca aca gaa ggg gag gat ctc acg ctc acc gtc 355
Gln Leu Glu Asn Cys Ala Thr Glu Gly Glu Asp Leu Thr Leu Thr Val
70 75 80 85

acc gtt cgt gga caa gaa gcc cac gca aaa gca gga cct tta 397
Thr Val Arg Gly Gln Glu Ala His Ala Lys Ala Gly Pro Leu
90 95

tgaggttccc aacaaggtca cca 420

<210> 1946
<211> 99
<212> PRT
<213> Corynebacterium glutamicum

<400> 1946
Met Thr Ile Ala Ser Ala Gly Val Ala Ser Ile Leu Ile Ser Leu Leu
1 5 10 15

Val Val Leu Ala Trp Gln Ala Gly Asn Leu Val Ala Arg Glu Gln Ala
20 25 30

Gln Val Ala Ala Asp Val Ser Ala Val Ala Gly Ala Tyr Ala Phe Ala
35 40 45

Arg Gly Glu Leu Pro Asp Ala Ala Cys Ala Thr Ala Lys His Thr Ala
50 55 60

Glu Ala Asn Asn Ala Gln Leu Glu Asn Cys Ala Thr Glu Gly Glu Asp
65 70 75 80

Leu Thr Leu Thr Val Thr Val Arg Gly Gln Glu Ala His Ala Lys Ala
85 90 95

Gly Pro Leu

<210> 1947
<211> 654
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(631)
<223> RXA00826

<400> 1947
tcggcgcgcg cgatctggtg ctcatcttgg tgtgtgctgc catttccgcg atcgctctaa 60

ccgtgtccat tcagactggt ttctttaagt tcttgggcac atg atc aca gtt tta 115
Met Ile Thr Val Leu
1 5

att gat gga caa tcc ggt gcg ggc aaa acc acc ttg gcg ggt gag tta 163
Ile Asp Gly Gln Ser Gly Ala Gly Lys Thr Thr Leu Ala Gly Glu Leu
10 15 20

gct gcc cgc acc ggg ttt cag ttg gtt cat ttg gat gac ttt tat cct 211
Ala Ala Arg Thr Gly Phe Gln Leu Val His Leu Asp Asp Phe Tyr Pro
25 30 35

ggt tgg act ggc ctt gaa gcg gca tcg gag att gtt gca cgc cat gtt 259
Gly Trp Thr Gly Leu Glu Ala Ala Ser Glu Ile Val Ala Arg His Val
40 45 50

ttg gac gcg gac aac ccc ggt ttc ttc acg tgg gat tgg cac aac aat 307
Leu Asp Ala Asp Asn Pro Gly Phe Phe Thr Trp Asp Trp His Asn Asn
55 60 65

tgc caa ggc gat tgg atc aag ttg gag cct ggt cga agt ctc att atc 355
Cys Gln Gly Asp Trp Ile Lys Leu Glu Pro Gly Arg Ser Leu Ile Ile
70 75 80 85

gaa ggc tct gga tca atc act gct gca aca aaa cgc aag gca tcg ctg 403
Glu Gly Ser Gly Ser Ile Thr Ala Ala Thr Lys Arg Lys Ala Ser Leu
90 95 100

ttg ggc gag ctg gtg acc gtt cgt atc act ggt cct gag gct tta aga 451
Leu Gly Glu Leu Val Thr Val Arg Ile Thr Gly Pro Glu Ala Leu Arg
105 110 115

aaa cag cgc gcc ctc aac cgc gat cct gat tac gca cca ttt tgg aaa 499
Lys Gln Arg Ala Leu Asn Arg Asp Pro Asp Tyr Ala Pro Phe Trp Lys
120 125 130

gtg tgg gcg cag cag gag caa cgc cat ttc tct tta ggc gtt gag gtg 547
Val Trp Ala Gln Gln Glu Gln Arg His Phe Ser Leu Gly Val Glu Val
135 140 145

```
gat cat gag att gtg cta ggt tct gat gag gct tcg gga cga ccc gaa   595
Asp His Glu Ile Val Leu Gly Ser Asp Glu Ala Ser Gly Arg Pro Glu
150                 155                 160                 165

gaa atc tat gac agc ctg gga acg gcc cag agt tct taagaaagtt        641
Glu Ile Tyr Asp Ser Leu Gly Thr Ala Gln Ser Ser
                170                 175

tgactagaga aca                                                   654
```

<210> 1948
<211> 177
<212> PRT
<213> Corynebacterium glutamicum

<400> 1948

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Met Ile Thr Val Leu Ile Asp Gly Gln Ser Gly Ala Gly Lys Thr Thr
  1               5                  10                  15

Leu Ala Gly Glu Leu Ala Ala Arg Thr Gly Phe Gln Leu Val His Leu
             20                  25                  30

Asp Asp Phe Tyr Pro Gly Trp Thr Gly Leu Glu Ala Ala Ser Glu Ile
         35                  40                  45

Val Ala Arg His Val Leu Asp Ala Asp Asn Pro Gly Phe Phe Thr Trp
     50                  55                  60

Asp Trp His Asn Asn Cys Gln Gly Asp Trp Ile Lys Leu Glu Pro Gly
 65                  70                  75                  80

Arg Ser Leu Ile Ile Glu Gly Ser Gly Ser Ile Thr Ala Ala Thr Lys
                 85                  90                  95

Arg Lys Ala Ser Leu Leu Gly Glu Leu Val Thr Val Arg Ile Thr Gly
            100                 105                 110

Pro Glu Ala Leu Arg Lys Gln Arg Ala Leu Asn Arg Asp Pro Asp Tyr
        115                 120                 125

Ala Pro Phe Trp Lys Val Trp Ala Gln Gln Glu Gln Arg His Phe Ser
    130                 135                 140

Leu Gly Val Glu Val Asp His Glu Ile Val Leu Gly Ser Asp Glu Ala
145                 150                 155                 160

Ser Gly Arg Pro Glu Glu Ile Tyr Asp Ser Leu Gly Thr Ala Gln Ser
                165                 170                 175

Ser
```

<210> 1949
<211> 846
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(823)
<223> RXA00830

<400> 1949
tgatggtggc tcgattgtat tcgagggcag ccccgcggaa ctcatcaaaa ctgatactcc 60

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aacaggacgc caccttaaag cttatgtaga ttagtttctt atg gaa aac cct ggt   115
                                            Met Glu Asn Pro Gly
                                              1               5

gat ctc ggc gct atg cca cag tac ggt ttt gag cat att tcg atg ctc   163
Asp Leu Gly Ala Met Pro Gln Tyr Gly Phe Glu His Ile Ser Met Leu
                 10                  15                  20

atc acc gct gtg gtt tta gcg att ctt gtc gtc ccc att gct cgt cga   211
Ile Thr Ala Val Val Leu Ala Ile Leu Val Val Pro Ile Ala Arg Arg
             25                  30                  35

ttc aac ttc gca ccg gca ttt ggc tgg gtg cta ctc atc gca aca ctt   259
Phe Asn Phe Ala Pro Ala Phe Gly Trp Val Leu Leu Ile Ala Thr Leu
         40                  45                  50

ctg tcg aac ctg tgg aat ttt atg ccc ggc tat tac acg ctg gac caa   307
Leu Ser Asn Leu Trp Asn Phe Met Pro Gly Tyr Tyr Thr Leu Asp Gln
     55                  60                  65

tct tgg cca ttc cac ttc tca gat gca ttg cgc att att gct gcc atc   355
Ser Trp Pro Phe His Phe Ser Asp Ala Leu Arg Ile Ile Ala Ala Ile
 70                  75                  80                  85

gca ttg att aat cgc gcg cgg tgg gca gtt tca gtg act att ttg tgg   403
Ala Leu Ile Asn Arg Ala Arg Trp Ala Val Ser Val Thr Ile Leu Trp
                 90                  95                 100

ggc acc acg atc aac ctg atg tca ctg ctc act cca gat gtt cag tat   451
Gly Thr Thr Ile Asn Leu Met Ser Leu Leu Thr Pro Asp Val Gln Tyr
             105                 110                 115

tta cag gtt ccc tgg ctg gag ttt tta atg tac tgg ttt atg cac att   499
Leu Gln Val Pro Trp Leu Glu Phe Leu Met Tyr Trp Phe Met His Ile
         120                 125                 130

tct gtg ttc cta gca gct ata att ctc att ttc gct ttt gga gaa aag   547
Ser Val Phe Leu Ala Ala Ile Ile Leu Ile Phe Ala Phe Gly Glu Lys
     135                 140                 145

cca ggg ctg tcc gga gtg gtt atg tcc gtt gca gtg gcg att agc tgg   595
Pro Gly Leu Ser Gly Val Val Met Ser Val Ala Val Ala Ile Ser Trp
150                 155                 160                 165

ggc atc atg tgc ctc atg gtc aac gca ttt ttg gga acc aac tac ggg   643
Gly Ile Met Cys Leu Met Val Asn Ala Phe Leu Gly Thr Asn Tyr Gly
                 170                 175                 180

tac ctc tcc aca gaa cca gaa tca gcg tca att ctg gat ttg ttg gga   691
Tyr Leu Ser Thr Glu Pro Glu Ser Ala Ser Ile Leu Asp Leu Leu Gly
             185                 190                 195

gga tgg ccg ttc tac atc gtc gcg gaa gta tta ctc ctg tgt gca gtg   739
Gly Trp Pro Phe Tyr Ile Val Ala Glu Val Leu Leu Leu Cys Ala Val
         200                 205                 210
```

```
tgg gct ttg tgg tct tat ctg att gat aag ctg cct atc acg tat cgc   787
Trp Ala Leu Trp Ser Tyr Leu Ile Asp Lys Leu Pro Ile Thr Tyr Arg
    215                 220                 225

cct gct tac cgt ccg aaa act cgg aag gcc gct gcg taaccgccct        833
Pro Ala Tyr Arg Pro Lys Thr Arg Lys Ala Ala Ala
230                 235                 240

ctacctcgag aaa                                                   846
```

<210> 1950
<211> 241
<212> PRT
<213> Corynebacterium glutamicum

<400> 1950

```
Met Glu Asn Pro Gly Asp Leu Gly Ala Met Pro Gln Tyr Gly Phe Glu
  1               5                  10                  15

His Ile Ser Met Leu Ile Thr Ala Val Val Leu Ala Ile Leu Val Val
             20                  25                  30

Pro Ile Ala Arg Arg Phe Asn Phe Ala Pro Ala Phe Gly Trp Val Leu
         35                  40                  45

Leu Ile Ala Thr Leu Leu Ser Asn Leu Trp Asn Phe Met Pro Gly Tyr
     50                  55                  60

Tyr Thr Leu Asp Gln Ser Trp Pro Phe His Phe Ser Asp Ala Leu Arg
 65                  70                  75                  80

Ile Ile Ala Ala Ile Ala Leu Ile Asn Arg Ala Arg Trp Ala Val Ser
                 85                  90                  95

Val Thr Ile Leu Trp Gly Thr Thr Ile Asn Leu Met Ser Leu Leu Thr
            100                 105                 110

Pro Asp Val Gln Tyr Leu Gln Val Pro Trp Leu Glu Phe Leu Met Tyr
        115                 120                 125

Trp Phe Met His Ile Ser Val Phe Leu Ala Ala Ile Ile Leu Ile Phe
    130                 135                 140

Ala Phe Gly Glu Lys Pro Gly Leu Ser Gly Val Val Met Ser Val Ala
145                 150                 155                 160

Val Ala Ile Ser Trp Gly Ile Met Cys Leu Met Val Asn Ala Phe Leu
                165                 170                 175

Gly Thr Asn Tyr Gly Tyr Leu Ser Thr Glu Pro Glu Ser Ala Ser Ile
            180                 185                 190

Leu Asp Leu Leu Gly Gly Trp Pro Phe Tyr Ile Val Ala Glu Val Leu
        195                 200                 205

Leu Leu Cys Ala Val Trp Ala Leu Trp Ser Tyr Leu Ile Asp Lys Leu
    210                 215                 220

Pro Ile Thr Tyr Arg Pro Ala Tyr Arg Pro Lys Thr Arg Lys Ala Ala
```

225 230 235 240

Ala

<210> 1951
<211> 726
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(703)
<223> RXA00853

<400> 1951
ttggatccag ttgagaaatt tcagccccca tcccccacat gaacgctgtt caaaacatcc 60

agcttgcttg ttgaacactg ttcaggtgta tgatttttttc atg cct aca tcc tct 115
Met Pro Thr Ser Ser
1 5

tct cct gca act gtg act ccg cta aag aag cag tct tca cgt aaa cag 163
Ser Pro Ala Thr Val Thr Pro Leu Lys Lys Gln Ser Ser Arg Lys Gln
10 15 20

ctc caa gac atc gcg ctt att gca gtt ttt gca gca ctg atc att gtg 211
Leu Gln Asp Ile Ala Leu Ile Ala Val Phe Ala Ala Leu Ile Ile Val
25 30 35

ctt gct ttt gtt tcc atc cca gtt ggc aca gcg gga gtg cct att gtt 259
Leu Ala Phe Val Ser Ile Pro Val Gly Thr Ala Gly Val Pro Ile Val
40 45 50

ttg cag aat gcc tcc atc gtt ttg gct ggc ctg att ctt ggt ggt cga 307
Leu Gln Asn Ala Ser Ile Val Leu Ala Gly Leu Ile Leu Gly Gly Arg
55 60 65

cgt ggt ttt ctc act gct ttg ctg ttc ctg gca ctc ggc ctg att ggc 355
Arg Gly Phe Leu Thr Ala Leu Leu Phe Leu Ala Leu Gly Leu Ile Gly
70 75 80 85

ctg cct gtc ctt gca ggt ggt cgt acc act ttg gcc gca ctt gct ggc 403
Leu Pro Val Leu Ala Gly Gly Arg Thr Thr Leu Ala Ala Leu Ala Gly
90 95 100

cca aca gct ggc tac atc gtg ggt tac ctc att tcc cca ctt gtt gca 451
Pro Thr Ala Gly Tyr Ile Val Gly Tyr Leu Ile Ser Pro Leu Val Ala
105 110 115

ggc atc atc gct tac ctc gca cct aaa aag cgt ggc gct gga atg ttc 499
Gly Ile Ile Ala Tyr Leu Ala Pro Lys Lys Arg Gly Ala Gly Met Phe
120 125 130

atc gtt tta ggc ctg gcg ggt ctc gcg ggt ctg atc acc caa tac gct 547
Ile Val Leu Gly Leu Ala Gly Leu Ala Gly Leu Ile Thr Gln Tyr Ala
135 140 145

tgc ggc atc gtg ggt ctc gtc ctt cgt gcg ggt cta agc ttg agt gaa 595
Cys Gly Ile Val Gly Leu Val Leu Arg Ala Gly Leu Ser Leu Ser Glu

```
150                 155                 160                 165

gca aca att gct caa ggt gcc ttt gtg ctg cca gat ttg gcc aag atc   643
Ala Thr Ile Ala Gln Gly Ala Phe Val Leu Pro Asp Leu Ala Lys Ile
                170                 175                 180

acc gtc atg gtc ata atc gcc gct gga gtt cat gca gca ttc cct gac   691
Thr Val Met Val Ile Ile Ala Ala Gly Val His Ala Ala Phe Pro Asp
            185                 190                 195

atc cgt aag aaa tagttccaac ccacttttcc tca                         726
Ile Arg Lys Lys
        200


<210> 1952
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 1952
Met Pro Thr Ser Ser Ser Pro Ala Thr Val Thr Pro Leu Lys Lys Gln
  1               5                  10                  15

Ser Ser Arg Lys Gln Leu Gln Asp Ile Ala Leu Ile Ala Val Phe Ala
             20                  25                  30

Ala Leu Ile Ile Val Leu Ala Phe Val Ser Ile Pro Val Gly Thr Ala
         35                  40                  45

Gly Val Pro Ile Val Leu Gln Asn Ala Ser Ile Val Leu Ala Gly Leu
     50                  55                  60

Ile Leu Gly Gly Arg Arg Gly Phe Leu Thr Ala Leu Leu Phe Leu Ala
 65                  70                  75                  80

Leu Gly Leu Ile Gly Leu Pro Val Leu Ala Gly Gly Arg Thr Thr Leu
                 85                  90                  95

Ala Ala Leu Ala Gly Pro Thr Ala Gly Tyr Ile Val Gly Tyr Leu Ile
            100                 105                 110

Ser Pro Leu Val Ala Gly Ile Ile Ala Tyr Leu Ala Pro Lys Lys Arg
        115                 120                 125

Gly Ala Gly Met Phe Ile Val Leu Gly Leu Ala Gly Leu Ala Gly Leu
    130                 135                 140

Ile Thr Gln Tyr Ala Cys Gly Ile Val Gly Leu Val Leu Arg Ala Gly
145                 150                 155                 160

Leu Ser Leu Ser Glu Ala Thr Ile Ala Gln Gly Ala Phe Val Leu Pro
                165                 170                 175

Asp Leu Ala Lys Ile Thr Val Met Val Ile Ile Ala Ala Gly Val His
            180                 185                 190

Ala Ala Phe Pro Asp Ile Arg Lys Lys
        195                 200
```

<210> 1953
<211> 426
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(426)
<223> RXA00861

<400> 1953

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atg gct cct cac aag gtc atg ctg att acc act ggt act cag ggt gag   48
Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
  1               5                  10                  15

cct atg gct gcg ctg tct cgc atg gcg cgt cgt gag cac cga cag atc   96
Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
             20                  25                  30

act gtc cgt gat gga gac ttg att atc ctt tct tcc tcc ctg gtt cca   144
Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
         35                  40                  45

ggt aac gaa gaa gca gtg ttc ggt gtc atc aac atg ctg gct cag atc   192
Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
     50                  55                  60

ggt gca act gtt gtt acc ggt cgc gac gcc aag gtg cac acc tcg ggc   240
Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
 65                  70                  75                  80

cac ggc tac tcc gga gag ctg ttg ttc ttg tac aac gcc gct cgt ccg   288
His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
                 85                  90                  95

aag aac gct atg cct gtc cac ggc gag tgg cgc cac ctg cgc gcc aac   336
Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn
            100                 105                 110

aag gaa ctg gct atc tcc act ggt gtt aac cgc gac aac gtt gtg ctt   384
Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu
        115                 120                 125

gca caa aac ggt gtt gtg gtt gat atg gtc aac ggt cgc gca           426
Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
    130                 135                 140
```

<210> 1954
<211> 142
<212> PRT
<213> Corynebacterium glutamicum

<400> 1954

```
Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
  1               5                  10                  15

Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
             20                  25                  30

Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
```

```
         35                  40                  45

Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
     50                  55                  60

Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
 65                  70                  75                  80

His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
                 85                  90                  95

Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn
            100                 105                 110

Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu
        115                 120                 125

Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
    130                 135                 140
```

20040219 20040219 20040219 20040219 20040219

<210> 1955
<211> 680
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(664)
<223> RXA00862

<400> 1955
aggtagttcc ttggcgcttg tggtttccgc ctctttactt ttaagtgctt gtgatggaag 60

```
cggctcaacg cctacaacct ctgctagtcc tgctccagtt gtg aca gaa act gaa   115
                                              Val Thr Glu Thr Glu
                                                1               5

acc gct aac ccg gtc acc aca act cgc acg cct tca gat gct gcc ccg   163
Thr Ala Asn Pro Val Thr Thr Thr Arg Thr Pro Ser Asp Ala Ala Pro
                10                  15                  20

tcg cct acc act tca gag ccc act ggt tca gag tcc acc aac tcc cct   211
Ser Pro Thr Thr Ser Glu Pro Thr Gly Ser Glu Ser Thr Asn Ser Pro
            25                  30                  35

tcc ccc act gct ttg ccg ccg ttg ggt tcc ccg tcg atg gat cag aag   259
Ser Pro Thr Ala Leu Pro Pro Leu Gly Ser Pro Ser Met Asp Gln Lys
        40                  45                  50

cag cag gct caa gtt ggt gac tcc gat atg tcg atc gct ggc atc cgc   307
Gln Gln Ala Gln Val Gly Asp Ser Asp Met Ser Ile Ala Gly Ile Arg
    55                  60                  65

gtt gcc gag cac gaa acg ttc aca cga gtt gtt ttt gat atc gcc ggt   355
Val Ala Glu His Glu Thr Phe Thr Arg Val Val Phe Asp Ile Ala Gly
70                  75                  80                  85

aat ggc caa cct ggt tgg tgg gtc gat tgg gcc act gat cca att cag   403
Asn Gly Gln Pro Gly Trp Trp Val Asp Trp Ala Thr Asp Pro Ile Gln
                90                  95                 100
```

```
cag gcg tca ggt ctt cca gtt gag atg gct ggt gat tcc ttc ctc aac   451
Gln Ala Ser Gly Leu Pro Val Glu Met Ala Gly Asp Ser Phe Leu Asn
            105                 110                 115

gtc aat att caa ggc act gga tat cct gat cag gtt gtc gtt cca ggt   499
Val Asn Ile Gln Gly Thr Gly Tyr Pro Asp Gln Val Val Val Pro Gly
        120                 125                 130

atc gat acc gga tca tat cct ggt gca ggc att gtt gaa gac atc aac   547
Ile Asp Thr Gly Ser Tyr Pro Gly Ala Gly Ile Val Glu Asp Ile Asn
    135                 140                 145

ttc acc agt att ttt gaa gcc cgt tcc caa gtt ctc att ggt gta tct   595
Phe Thr Ser Ile Phe Glu Ala Arg Ser Gln Val Leu Ile Gly Val Ser
150                 155                 160                 165

ggt caa ccc cga aat tac tcg gtc tca ttg ctg cag gaa cca acc agg   643
Gly Gln Pro Arg Asn Tyr Ser Val Ser Leu Leu Gln Glu Pro Thr Arg
                170                 175                 180

ctt gtg gtg gac atc gtt cac tagcgctgga acgccg                    680
Leu Val Val Asp Ile Val His
            185
```

Sequence Listing.ST25.txt

<210> 1956
<211> 188
<212> PRT
<213> Corynebacterium glutamicum

<400> 1956

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Val Thr Glu Thr Glu Thr Ala Asn Pro Val Thr Thr Thr Arg Thr Pro
  1               5                  10                  15

Ser Asp Ala Ala Pro Ser Pro Thr Thr Ser Glu Pro Thr Gly Ser Glu
             20                  25                  30

Ser Thr Asn Ser Pro Ser Pro Thr Ala Leu Pro Pro Leu Gly Ser Pro
         35                  40                  45

Ser Met Asp Gln Lys Gln Gln Ala Gln Val Gly Asp Ser Asp Met Ser
     50                  55                  60

Ile Ala Gly Ile Arg Val Ala Glu His Glu Thr Phe Thr Arg Val Val
 65                  70                  75                  80

Phe Asp Ile Ala Gly Asn Gly Gln Pro Gly Trp Trp Val Asp Trp Ala
                 85                  90                  95

Thr Asp Pro Ile Gln Gln Ala Ser Gly Leu Pro Val Glu Met Ala Gly
            100                 105                 110

Asp Ser Phe Leu Asn Val Asn Ile Gln Gly Thr Gly Tyr Pro Asp Gln
        115                 120                 125

Val Val Val Pro Gly Ile Asp Thr Gly Ser Tyr Pro Gly Ala Gly Ile
    130                 135                 140

Val Glu Asp Ile Asn Phe Thr Ser Ile Phe Glu Ala Arg Ser Gln Val
145                 150                 155                 160
```

```
Leu Ile Gly Val Ser Gly Gln Pro Arg Asn Tyr Ser Val Ser Leu Leu
                165                 170                 175

Gln Glu Pro Thr Arg Leu Val Val Asp Ile Val His
            180                 185


<210> 1957
<211> 1212
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1189)
<223> RXA00874

<400> 1957
agctgttccc taccattgct gaacgggagt ggattgtcac tttagcccct cacggattct 60

tctggtttga tctcaccgcc gatgaaaagg acgatatgga atg agc att ggc caa   115
                                          Met Ser Ile Gly Gln
                                            1               5

cac atc atc acc gag cgt ttc tac ggc gcc aag tcc cac acc atc gac   163
His Ile Ile Thr Glu Arg Phe Tyr Gly Ala Lys Ser His Thr Ile Asp
                10                  15                  20

aac gta gat att gtg ttg tcc cgc gaa tgt ggc gag aac act ttg gct   211
Asn Val Asp Ile Val Leu Ser Arg Glu Cys Gly Glu Asn Thr Leu Ala
            25                  30                  35

gta gtg cgc atc aac aat gcg ctg tat cag ttg ttg gtc aat gat gat   259
Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu Leu Val Asn Asp Asp
        40                  45                  50

ggc aaa gat gtt ctc aac gac cac gta gaa gag gtc ggt gcg agt ttc   307
Gly Lys Asp Val Leu Asn Asp His Val Glu Glu Val Gly Ala Ser Phe
    55                  60                  65

gga gca tgg act ggc agc tct gct ttt ccc att ggc cct ttc act cca   355
Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile Gly Pro Phe Thr Pro
70                  75                  80                  85

ctc ggc aca gaa caa tcc aat agc tct ttc atc acc gcc gac aat aaa   403
Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile Thr Ala Asp Asn Lys
                90                  95                  100

gcg atc gtg aaa tac ttc cgc aaa tta gaa tcc ggg caa aac ccc gat   451
Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser Gly Gln Asn Pro Asp
            105                 110                 115

gtg gag cta att tct aaa att tcc tcc tgc ccc aac atc gcg ccc atc   499
Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro Asn Ile Ala Pro Ile
        120                 125                 130

ctg ggt ttt tcc tcc gct gag atc tcc ggg gct aac tac acc ctg gtc   547
Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala Asn Tyr Thr Leu Val
    135                 140                 145
```

```
atg gcg cag cag tac gtt cca ggt ttg gat ggc tgg tca cac gcg ctg   595
Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly Trp Ser His Ala Leu
150                 155                 160                 165

act act acc tct ggc agc ttt gca gag gat gca gaa aag atc ggc gaa   643
Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala Glu Lys Ile Gly Glu
                170                 175                 180

gcc acc cgc aat gtt cac act gct ctt gca tcg gcc ttc cct act cgg   691
Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser Ala Phe Pro Thr Arg
            185                 190                 195

gta gtt ccc gta gaa gca ctc gcc gat gcg ctc act acc cgc ctt aat   739
Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu Thr Thr Arg Leu Asn
        200                 205                 210

gaa cta atc tcc caa gca ccc gaa atc gcc cgc ttc aaa gaa gca gcc   787
Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg Phe Lys Glu Ala Ala
    215                 220                 225

atc gac ctc tac caa tcg ttg gaa ggc gaa gcc cac atc caa cgc atc   835
Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala His Ile Gln Arg Ile
230                 235                 240                 245

cac ggt gac ctc cac ttg ggg cag ctc atc aaa acc ccc gaa cgc tac   883
His Gly Asp Leu His Leu Gly Gln Leu Ile Lys Thr Pro Glu Arg Tyr
                250                 255                 260

atc ctc atc gat ttc gaa ggc gaa cct gcc cgc cca ctt aat caa cga   931
Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg Pro Leu Asn Gln Arg
            265                 270                 275

cgc ctc ccc gac tct ccc ctg aaa gat ctc gcc ggc atc atc aga tcc   979
Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala Gly Ile Ile Arg Ser
        280                 285                 290

atc gac tac gca gcc tac ttc gac ggc gaa cac acc caa tgg gcc aac   1027
Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His Thr Gln Trp Ala Asn
    295                 300                 305

gaa gcc acc gcg cta ttc ctc gac ggc tac gga tca att gaa gac caa   1075
Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly Ser Ile Glu Asp Gln
310                 315                 320                 325

gaa ctc ctc aat gcc tac att ctg gac aag gcg ttg tac gag gtt gcc   1123
Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala Leu Tyr Glu Val Ala
                330                 335                 340

tat gaa ata aac aac cgc ccc gac tgg gtg aaa atc cca ctc gag gcg   1171
Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys Ile Pro Leu Glu Ala
            345                 350                 355

gtc gaa agg ctt cta gac tagttagtta ctctgcgtca aac                1212
Val Glu Arg Leu Leu Asp
        360
```

<210> 1958
<211> 363
<212> PRT
<213> Corynebacterium glutamicum

<400> 1958

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Met Ser Ile Gly Gln His Ile Ile Thr Glu Arg Phe Tyr Gly Ala Lys
  1               5                  10                  15

Ser His Thr Ile Asp Asn Val Asp Ile Val Leu Ser Arg Glu Cys Gly
             20                  25                  30

Glu Asn Thr Leu Ala Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu
         35                  40                  45

Leu Val Asn Asp Asp Gly Lys Asp Val Leu Asn Asp His Val Glu Glu
     50                  55                  60

Val Gly Ala Ser Phe Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile
 65                  70                  75                  80

Gly Pro Phe Thr Pro Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile
                 85                  90                  95

Thr Ala Asp Asn Lys Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser
            100                 105                 110

Gly Gln Asn Pro Asp Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro
        115                 120                 125

Asn Ile Ala Pro Ile Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala
    130                 135                 140

Asn Tyr Thr Leu Val Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly
145                 150                 155                 160

Trp Ser His Ala Leu Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala
                165                 170                 175

Glu Lys Ile Gly Glu Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser
            180                 185                 190

Ala Phe Pro Thr Arg Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu
        195                 200                 205

Thr Thr Arg Leu Asn Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg
    210                 215                 220

Phe Lys Glu Ala Ala Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala
225                 230                 235                 240

His Ile Gln Arg Ile His Gly Asp Leu His Leu Gly Gln Leu Ile Lys
                245                 250                 255

Thr Pro Glu Arg Tyr Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg
            260                 265                 270

Pro Leu Asn Gln Arg Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala
        275                 280                 285

Gly Ile Ile Arg Ser Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His
    290                 295                 300

Thr Gln Trp Ala Asn Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly
305                 310                 315                 320
```

```
Ser Ile Glu Asp Gln Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala
               325                 330                 335

Leu Tyr Glu Val Ala Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys
            340                 345                 350

Ile Pro Leu Glu Ala Val Glu Arg Leu Leu Asp
        355                 360


<210> 1959
<211> 1878
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1855)
<223> RXA00876

<400> 1959
ttgactatct cgaattaggt gagggctggg agccagaaat tttgtgctct gatgctgttg 60

aaattttaga aaatctcatc aaggaactaa ggggaattcc atg aca ttg aaa att   115
                                          Met Thr Leu Lys Ile
                                            1               5

gat ccc tcg tcc atc agt agt gct gtg tct cgc ttg aat gag ctt cag   163
Asp Pro Ser Ser Ile Ser Ser Ala Val Ser Arg Leu Asn Glu Leu Gln
                10                  15                  20

cat caa gct att act gca tct caa gtg gga atg aaa tca aca att cta   211
His Gln Ala Ile Thr Ala Ser Gln Val Gly Met Lys Ser Thr Ile Leu
            25                  30                  35

tcc gcg ttt tcg ccc gtc tct gga ctc gat caa ttg ggt tcc ggt cac   259
Ser Ala Phe Ser Pro Val Ser Gly Leu Asp Gln Leu Gly Ser Gly His
        40                  45                  50

ggg aat gtg att aat ggt ggg gca ggc gca gca aac tct gtg ctg aat   307
Gly Asn Val Ile Asn Gly Gly Ala Gly Ala Ala Asn Ser Val Leu Asn
    55                  60                  65

tcc tat gcc gaa caa atc gag tgg ttg tct gcg gct ttg cag gct tct   355
Ser Tyr Ala Glu Gln Ile Glu Trp Leu Ser Ala Ala Leu Gln Ala Ser
70                  75                  80                  85

ggt gcg gct ttg act ggc cag gat gaa tta ttc gct agg ggt atg gat   403
Gly Ala Ala Leu Thr Gly Gln Asp Glu Leu Phe Ala Arg Gly Met Asp
                90                  95                  100

gta gcg gat acc ggt ggc agg gtt gta gaa gag tca gta atg ttc ccg   451
Val Ala Asp Thr Gly Gly Arg Val Val Glu Glu Ser Val Met Phe Pro
            105                 110                 115

gcg cgg ccg gca cct cgg ttt gag tct ttc gtt ttt aat cca cca gct   499
Ala Arg Pro Ala Pro Arg Phe Glu Ser Phe Val Phe Asn Pro Pro Ala
        120                 125                 130

gtt agt cct tcg ttg tcg ttg gat gcg ttg tgt agt cag ttt tcc gga   547
```

```
Val Ser Pro Ser Leu Ser Leu Asp Ala Leu Cys Ser Gln Phe Ser Gly
    135                 140                 145

acc aac tcg ggg gcg gtt ttg gag gcg cag ggg tct tgg ggc tct atg   595
Thr Asn Ser Gly Ala Val Leu Glu Ala Gln Gly Ser Trp Gly Ser Met
150                 155                 160                 165

gcg tcg gct att agc aat gtg tcg gct tcg ttg tcg tcg att gct ggt   643
Ala Ser Ala Ile Ser Asn Val Ser Ala Ser Leu Ser Ser Ile Ala Gly
                170                 175                 180

gag att ttg gcg gag aac tca ggc gaa acg ttt gag cag gct gct gct   691
Glu Ile Leu Ala Glu Asn Ser Gly Glu Thr Phe Glu Gln Ala Ala Ala
            185                 190                 195

cgg att aat gag gtg gcg gct gcg ggg gcg acg ttt gct gcg aat gcg   739
Arg Ile Asn Glu Val Ala Ala Ala Gly Ala Thr Phe Ala Ala Asn Ala
        200                 205                 210

aaa atg atg ggg gcg tcg gtg ggg acg ctg aat cgg att tat atg ggg   787
Lys Met Met Gly Ala Ser Val Gly Thr Leu Asn Arg Ile Tyr Met Gly
    215                 220                 225

cat cgc atg cag gtg ttt atg gct gcg acg tcg att aag gcg att ttg   835
His Arg Met Gln Val Phe Met Ala Ala Thr Ser Ile Lys Ala Ile Leu
230                 235                 240                 245

gat ccg gtg cag agg ctt gct gcg gag agg gcg ttt ttg gcg tcg ttt   883
Asp Pro Val Gln Arg Leu Ala Ala Glu Arg Ala Phe Leu Ala Ser Phe
                250                 255                 260

cag gct act ttt cag gcg gat gtg ttg acg ggt atg cct cct gtg agc   931
Gln Ala Thr Phe Gln Ala Asp Val Leu Thr Gly Met Pro Pro Val Ser
            265                 270                 275

aat ttg atg cag atg aag ggg gcg aat ggt tct gcg ggg gaa att gct   979
Asn Leu Met Gln Met Lys Gly Ala Asn Gly Ser Ala Gly Glu Ile Ala
        280                 285                 290

ctg ggg atg gat gag att gct ggc agt ggg cag gca tgg tct gcg gcg   1027
Leu Gly Met Asp Glu Ile Ala Gly Ser Gly Gln Ala Trp Ser Ala Ala
    295                 300                 305

ggg ttg act ccg tcg ggg gct gcg cag ggt ggt gtc gcc aat gcg ggc   1075
Gly Leu Thr Pro Ser Gly Ala Ala Gln Gly Gly Val Ala Asn Ala Gly
310                 315                 320                 325

agt atc gcg ccg gat gca gcg gtt caa ggt gct gcg ggg cag agt ggg   1123
Ser Ile Ala Pro Asp Ala Ala Val Gln Gly Ala Ala Gly Gln Ser Gly
                330                 335                 340

gtt gga agt ttt ggc act gtc act gat cag ttg gat ggc atc aat att   1171
Val Gly Ser Phe Gly Thr Val Thr Asp Gln Leu Asp Gly Ile Asn Ile
            345                 350                 355

ggg gat atg ttg acc tct gct gcc tca gct ggg cag agc ctt gcg aat   1219
Gly Asp Met Leu Thr Ser Ala Ala Ser Ala Gly Gln Ser Leu Ala Asn
        360                 365                 370

ggt ttg gcg atg cct act tct acg cct aat tcg gcg tcc ggt gcg att   1267
Gly Leu Ala Met Pro Thr Ser Thr Pro Asn Ser Ala Ser Gly Ala Ile
```

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    375                 380                 385

cct tcc tcg atg tct gcg gca tcg ccg ctt ggt gcg ttt ggc agc ggt   1315
Pro Ser Ser Met Ser Ala Ala Ser Pro Leu Gly Ala Phe Gly Ser Gly
390                 395                 400                 405

gca ggg ttg ggc gca cag ggt ggc tcg att gga tct tcg gca cct gga   1363
Ala Gly Leu Gly Ala Gln Gly Gly Ser Ile Gly Ser Ser Ala Pro Gly
                410                 415                 420

gcg atc agt agt cga gcg gcc gga tcc gca ggt ggt tcg gta ccg gga   1411
Ala Ile Ser Ser Arg Ala Ala Gly Ser Ala Gly Gly Ser Val Pro Gly
            425                 430                 435

atg act ggt ggt cct ggc gcg ccg ggg att acc tcg gat tcg ttg atg   1459
Met Thr Gly Gly Pro Gly Ala Pro Gly Ile Thr Ser Asp Ser Leu Met
        440                 445                 450

gga gct cga act cat ggt gct tct tcc gcg gga gct gtc gct ccg atg   1507
Gly Ala Arg Thr His Gly Ala Ser Ser Ala Gly Ala Val Ala Pro Met
    455                 460                 465

atg ggt ggt gct ggc gga atg tct ggt ggc gtc gtt ggt gca ggt ggt   1555
Met Gly Gly Ala Gly Gly Met Ser Gly Gly Val Val Gly Ala Gly Gly
470                 475                 480                 485

act ggt tct cag agc aag tat gcg cgc cag act gga tcg tcg gtt gga   1603
Thr Gly Ser Gln Ser Lys Tyr Ala Arg Gln Thr Gly Ser Ser Val Gly
                490                 495                 500

tct agt tcg cag tcg ggt tct ggc ctg ggg atg gtg gga tca ggg agt   1651
Ser Ser Ser Gln Ser Gly Ser Gly Leu Gly Met Val Gly Ser Gly Ser
            505                 510                 515

ggg aag ccg tcg ata agc aat ttt ggg cgc ggc atg atg ccg atg atg   1699
Gly Lys Pro Ser Ile Ser Asn Phe Gly Arg Gly Met Met Pro Met Met
        520                 525                 530

ccc atg atg ccc atg gga ggc gcc ggc ggt ggg cag aag aat acc ggc   1747
Pro Met Met Pro Met Gly Gly Ala Gly Gly Gly Gln Lys Asn Thr Gly
    535                 540                 545

aag gtg aaa acg gtg acg tct gcg gtg gag gaa gac cgc aat ttg gcg   1795
Lys Val Lys Thr Val Thr Ser Ala Val Glu Glu Asp Arg Asn Leu Ala
550                 555                 560                 565

gcg ctg ctg ggt gat cgg ggg ccg gtt gtt ccg ggt gtg att ggt gac   1843
Ala Leu Leu Gly Asp Arg Gly Pro Val Val Pro Gly Val Ile Gly Asp
                570                 575                 580

tgg gtg agg ggc taacgcaaca atgtgtctaa gct                        1878
Trp Val Arg Gly
            585
```

<210> 1960
<211> 585
<212> PRT
<213> Corynebacterium glutamicum

<400> 1960

```
Met Thr Leu Lys Ile Asp Pro Ser Ser Ile Ser Ser Ala Val Ser Arg
 1               5                  10                  15

Leu Asn Glu Leu Gln His Gln Ala Ile Thr Ala Ser Gln Val Gly Met
            20                  25                  30

Lys Ser Thr Ile Leu Ser Ala Phe Ser Pro Val Ser Gly Leu Asp Gln
        35                  40                  45

Leu Gly Ser Gly His Gly Asn Val Ile Asn Gly Gly Ala Gly Ala Ala
    50                  55                  60

Asn Ser Val Leu Asn Ser Tyr Ala Glu Gln Ile Glu Trp Leu Ser Ala
65                  70                  75                  80

Ala Leu Gln Ala Ser Gly Ala Ala Leu Thr Gly Gln Asp Glu Leu Phe
                85                  90                  95

Ala Arg Gly Met Asp Val Ala Asp Thr Gly Gly Arg Val Val Glu Glu
            100                 105                 110

Ser Val Met Phe Pro Ala Arg Pro Ala Pro Arg Phe Glu Ser Phe Val
        115                 120                 125

Phe Asn Pro Pro Ala Val Ser Pro Ser Leu Ser Leu Asp Ala Leu Cys
    130                 135                 140

Ser Gln Phe Ser Gly Thr Asn Ser Gly Ala Val Leu Glu Ala Gln Gly
145                 150                 155                 160

Ser Trp Gly Ser Met Ala Ser Ala Ile Ser Asn Val Ser Ala Ser Leu
                165                 170                 175

Ser Ser Ile Ala Gly Glu Ile Leu Ala Glu Asn Ser Gly Glu Thr Phe
            180                 185                 190

Glu Gln Ala Ala Ala Arg Ile Asn Glu Val Ala Ala Ala Gly Ala Thr
        195                 200                 205

Phe Ala Ala Asn Ala Lys Met Met Gly Ala Ser Val Gly Thr Leu Asn
    210                 215                 220

Arg Ile Tyr Met Gly His Arg Met Gln Val Phe Met Ala Ala Thr Ser
225                 230                 235                 240

Ile Lys Ala Ile Leu Asp Pro Val Gln Arg Leu Ala Ala Glu Arg Ala
                245                 250                 255

Phe Leu Ala Ser Phe Gln Ala Thr Phe Gln Ala Asp Val Leu Thr Gly
            260                 265                 270

Met Pro Pro Val Ser Asn Leu Met Gln Met Lys Gly Ala Asn Gly Ser
        275                 280                 285

Ala Gly Glu Ile Ala Leu Gly Met Asp Glu Ile Ala Gly Ser Gly Gln
    290                 295                 300

Ala Trp Ser Ala Ala Gly Leu Thr Pro Ser Gly Ala Ala Gln Gly Gly
305                 310                 315                 320

Val Ala Asn Ala Gly Ser Ile Ala Pro Asp Ala Ala Val Gln Gly Ala
```

325 330 335

Ala Gly Gln Ser Gly Val Gly Ser Phe Gly Thr Val Thr Asp Gln Leu
340 345 350

Asp Gly Ile Asn Ile Gly Asp Met Leu Thr Ser Ala Ala Ser Ala Gly
355 360 365

Gln Ser Leu Ala Asn Gly Leu Ala Met Pro Thr Ser Thr Pro Asn Ser
370 375 380

Ala Ser Gly Ala Ile Pro Ser Ser Met Ser Ala Ala Ser Pro Leu Gly
385 390 395 400

Ala Phe Gly Ser Gly Ala Gly Leu Gly Ala Gln Gly Gly Ser Ile Gly
405 410 415

Ser Ser Ala Pro Gly Ala Ile Ser Ser Arg Ala Ala Gly Ser Ala Gly
420 425 430

Gly Ser Val Pro Gly Met Thr Gly Gly Pro Gly Ala Pro Gly Ile Thr
435 440 445

Ser Asp Ser Leu Met Gly Ala Arg Thr His Gly Ala Ser Ser Ala Gly
450 455 460

Ala Val Ala Pro Met Met Gly Gly Ala Gly Gly Met Ser Gly Gly Val
465 470 475 480

Val Gly Ala Gly Gly Thr Gly Ser Gln Ser Lys Tyr Ala Arg Gln Thr
485 490 495

Gly Ser Ser Val Gly Ser Ser Ser Gln Ser Gly Ser Gly Leu Gly Met
500 505 510

Val Gly Ser Gly Ser Gly Lys Pro Ser Ile Ser Asn Phe Gly Arg Gly
515 520 525

Met Met Pro Met Met Pro Met Met Pro Met Gly Gly Ala Gly Gly Gly
530 535 540

Gln Lys Asn Thr Gly Lys Val Lys Thr Val Thr Ser Ala Val Glu Glu
545 550 555 560

Asp Arg Asn Leu Ala Ala Leu Leu Gly Asp Arg Gly Pro Val Val Pro
565 570 575

Gly Val Ile Gly Asp Trp Val Arg Gly
580 585

<210> 1961
<211> 501
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(478)
<223> RXA00881

<400> 1961
acctgaccga ggaagccgac gagctgaccc caacgctgaa ggtcaagcgc aacgttgttg 60

ttcgccgtta cgcagacgcc atcgaccaca tctacaaccg atg agt aac aca gag 115
Met Ser Asn Thr Glu
1 5

acc caa ttt gat tgg gat gga tcg aca tgg acc cgc acc gaa gtc ggc 163
Thr Gln Phe Asp Trp Asp Gly Ser Thr Trp Thr Arg Thr Glu Val Gly
10 15 20

gaa gca cca aca cgc ttc gct gtg ggc gtg atg gag gat ttc gcc tac 211
Glu Ala Pro Thr Arg Phe Ala Val Gly Val Met Glu Asp Phe Ala Tyr
25 30 35

att gca gcc act ggc acg gac ggg gat gaa gag ttc ttt act ttg ggc 259
Ile Ala Ala Thr Gly Thr Asp Gly Asp Glu Glu Phe Phe Thr Leu Gly
40 45 50

tca aat ccg ggt ctg acg ttt ggt gat ccc gag tgg ctt ttc gct cag 307
Ser Asn Pro Gly Leu Thr Phe Gly Asp Pro Glu Trp Leu Phe Ala Gln
55 60 65

gat aat ccg cag tat gtg gtg gag tgc att ggc cag cag gga acc gag 355
Asp Asn Pro Gln Tyr Val Val Glu Cys Ile Gly Gln Gln Gly Thr Glu
70 75 80 85

ccg gca gcc ctg aag gtt gta gat aaa tat ttg tcg cga cta tct gat 403
Pro Ala Ala Leu Lys Val Val Asp Lys Tyr Leu Ser Arg Leu Ser Asp
90 95 100

gag gag tca cgt ggc gaa ccc acg cgg att ctc aat gaa ttg gtc tcg 451
Glu Glu Ser Arg Gly Glu Pro Thr Arg Ile Leu Asn Glu Leu Val Ser
105 110 115

gcg atg gag ttg ccg gca ttg ccg tgg tgatttttct cgggctttag 498
Ala Met Glu Leu Pro Ala Leu Pro Trp
120 125

tga 501

<210> 1962
<211> 126
<212> PRT
<213> Corynebacterium glutamicum

<400> 1962
Met Ser Asn Thr Glu Thr Gln Phe Asp Trp Asp Gly Ser Thr Trp Thr
1 5 10 15

Arg Thr Glu Val Gly Glu Ala Pro Thr Arg Phe Ala Val Gly Val Met
20 25 30

Glu Asp Phe Ala Tyr Ile Ala Ala Thr Gly Thr Asp Gly Asp Glu Glu
35 40 45

Phe Phe Thr Leu Gly Ser Asn Pro Gly Leu Thr Phe Gly Asp Pro Glu
50 55 60

Trp Leu Phe Ala Gln Asp Asn Pro Gln Tyr Val Val Glu Cys Ile Gly

```
65                  70                  75                  80

Gln Gln Gly Thr Glu Pro Ala Ala Leu Lys Val Val Asp Lys Tyr Leu
                85                  90                  95

Ser Arg Leu Ser Asp Glu Glu Ser Arg Gly Glu Pro Thr Arg Ile Leu
            100                 105                 110

Asn Glu Leu Val Ser Ala Met Glu Leu Pro Ala Leu Pro Trp
        115                 120                 125


<210> 1963
<211> 801
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(778)
<223> RXA00882

<400> 1963
aaatagctga gaaattggct agaggacggc tagcaaaccg gatcaagacc ggctagaact 60

ttagctacga ggcaagaaaa ggaaggtgtg ttggaacgcg atg agc agt aca acc   115
                                              Met Ser Ser Thr Thr
                                                1               5

gca cag cta cgc cac cga gag ctg acc cag gag atc tac aac atc ggc   163
Ala Gln Leu Arg His Arg Glu Leu Thr Gln Glu Ile Tyr Asn Ile Gly
                10                  15                  20

gac gag gtc gct gaa tac att gag cac atc atg gaa gca gtc tcc gac   211
Asp Glu Val Ala Glu Tyr Ile Glu His Ile Met Glu Ala Val Ser Asp
            25                  30                  35

tgg gat ctg gag ctc gtg gaa gat tgc ctc gct gaa ttc gat gag atc   259
Trp Asp Leu Glu Leu Val Glu Asp Cys Leu Ala Glu Phe Asp Glu Ile
        40                  45                  50

atc act gaa gcc cgc gat gac tcc cgc act gtt gtg gct gaa ctt tca   307
Ile Thr Glu Ala Arg Asp Asp Ser Arg Thr Val Val Ala Glu Leu Ser
    55                  60                  65

ggc ctg cgt cac gca cta acc act ggt atc cgt cag ggc acc gtg agc   355
Gly Leu Arg His Ala Leu Thr Thr Gly Ile Arg Gln Gly Thr Val Ser
70                  75                  80                  85

gct aga gcc acg gtg gag gtg gac gtc gat aag ccg gaa cgc ctg acc   403
Ala Arg Ala Thr Val Glu Val Asp Val Asp Lys Pro Glu Arg Leu Thr
                90                  95                  100

gcc tcc gag ctg gag cgc gac ttc gat att gat gcc ggc ctc gtt gat   451
Ala Ser Glu Leu Glu Arg Asp Phe Asp Ile Asp Ala Gly Leu Val Asp
            105                 110                 115

gta cgc gat ctg tcg acc gcg ctc aat gcg cgc aca gac gct gtg gtt   499
Val Arg Asp Leu Ser Thr Ala Leu Asn Ala Arg Thr Asp Ala Val Val
        120                 125                 130
```

```
aag cgc ctg gag gcc act gtg gag tgg gtg ctg gcg gaa act gac aag   547
Lys Arg Leu Glu Ala Thr Val Glu Trp Val Leu Ala Glu Thr Asp Lys
    135                 140                 145

gtg gcc aac gat ctg gat tcc ctg tct ctg cca ctg ctt tat ggc cgc   595
Val Ala Asn Asp Leu Asp Ser Leu Ser Leu Pro Leu Leu Tyr Gly Arg
150                 155                 160                 165

gtt gca gcg gtg atc gaa agc gcc acc agc gca tgg atc aac gca gtg   643
Val Ala Ala Val Ile Glu Ser Ala Thr Ser Ala Trp Ile Asn Ala Val
                170                 175                 180

ggc acc gcc aat ccg gcg tat gtg cgc acc atg cga ggc agc aac ccg   691
Gly Thr Ala Asn Pro Ala Tyr Val Arg Thr Met Arg Gly Ser Asn Pro
            185                 190                 195

cca cgt ttc ctg ctt gag cgt gcg cgt atc gac gct gtc gtg gcc cgg   739
Pro Arg Phe Leu Leu Glu Arg Ala Arg Ile Asp Ala Val Val Ala Arg
        200                 205                 210

gtt gca gac aag ctt gcg caa aag cgc aac gct gtt tcc tagaaatctc   788
Val Ala Asp Lys Leu Ala Gln Lys Arg Asn Ala Val Ser
    215                 220                 225

ggtgcagcaa aaa                                                  801
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<210> 1964
<211> 226
<212> PRT
<213> Corynebacterium glutamicum

<400> 1964

```
Met Ser Ser Thr Thr Ala Gln Leu Arg His Arg Glu Leu Thr Gln Glu
  1               5                  10                  15

Ile Tyr Asn Ile Gly Asp Glu Val Ala Glu Tyr Ile Glu His Ile Met
             20                  25                  30

Glu Ala Val Ser Asp Trp Asp Leu Glu Leu Val Glu Asp Cys Leu Ala
         35                  40                  45

Glu Phe Asp Glu Ile Ile Thr Glu Ala Arg Asp Asp Ser Arg Thr Val
     50                  55                  60

Val Ala Glu Leu Ser Gly Leu Arg His Ala Leu Thr Thr Gly Ile Arg
 65                  70                  75                  80

Gln Gly Thr Val Ser Ala Arg Ala Thr Val Glu Val Asp Val Asp Lys
                 85                  90                  95

Pro Glu Arg Leu Thr Ala Ser Glu Leu Glu Arg Asp Phe Asp Ile Asp
            100                 105                 110

Ala Gly Leu Val Asp Val Arg Asp Leu Ser Thr Ala Leu Asn Ala Arg
        115                 120                 125

Thr Asp Ala Val Val Lys Arg Leu Glu Ala Thr Val Glu Trp Val Leu
    130                 135                 140

Ala Glu Thr Asp Lys Val Ala Asn Asp Leu Asp Ser Leu Ser Leu Pro
```

```
145                 150                 155                 160

Leu Leu Tyr Gly Arg Val Ala Ala Val Ile Glu Ser Ala Thr Ser Ala
                165                 170                 175

Trp Ile Asn Ala Val Gly Thr Ala Asn Pro Ala Tyr Val Arg Thr Met
            180                 185                 190

Arg Gly Ser Asn Pro Pro Arg Phe Leu Leu Glu Arg Ala Arg Ile Asp
        195                 200                 205

Ala Val Val Ala Arg Val Ala Asp Lys Leu Ala Gln Lys Arg Asn Ala
    210                 215                 220

Val Ser
225
```

<210> 1965
<211> 642
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(619)
<223> RXA00883

<400> 1965

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aatatacaca ccaaaaactg acatgcccca agcctagtgc ctgcccccta tacatgatta 60

attgatgtta aacatagcga attcctaaga acagggtaga gtg cag ggt atg aaa   115
                                              Val Gln Gly Met Lys
                                                1               5

cgg aag atg gtc gca gcg gcg ctg gca aca gcg ctt ctt ttt ggg gct   163
Arg Lys Met Val Ala Ala Ala Leu Ala Thr Ala Leu Leu Phe Gly Ala
                10                  15                  20

gca cct gcg cac gct tcc gaa ttg gta gag ccc acc aca gtt gca gag   211
Ala Pro Ala His Ala Ser Glu Leu Val Glu Pro Thr Thr Val Ala Glu
            25                  30                  35

tca gtg gca ctc gat ccc aac aaa gca atc aat att ctc acc cca gat   259
Ser Val Ala Leu Asp Pro Asn Lys Ala Ile Asn Ile Leu Thr Pro Asp
        40                  45                  50

ctc tgg gaa gac att gag gca aaa cca ggc gat atc gtc cac atc ccc   307
Leu Trp Glu Asp Ile Glu Ala Lys Pro Gly Asp Ile Val His Ile Pro
    55                  60                  65

tac cag ggc acc cga aac tac gag gac ctc acc gta gaa gtc gcg aaa   355
Tyr Gln Gly Thr Arg Asn Tyr Glu Asp Leu Thr Val Glu Val Ala Lys
70                  75                  80                  85

cct ttc gaa gat ttc caa atc ctc gtc gga ctc gac aac agc atc gtc   403
Pro Phe Glu Asp Phe Gln Ile Leu Val Gly Leu Asp Asn Ser Ile Val
                90                  95                  100

atc gca gtg cca aag aac tta agt ggc gca gca tca gtc gcc cca gtt   451
Ile Ala Val Pro Lys Asn Leu Ser Gly Ala Ala Ser Val Ala Pro Val
```

```
            105                 110                 115

ttc act gtc tct gac aaa aac ggt gag atc gac tct ttc acc atc aaa   499
Phe Thr Val Ser Asp Lys Asn Gly Glu Ile Asp Ser Phe Thr Ile Lys
        120                 125                 130

gta agc gtc gag cca cgc cgc caa agc gac gaa gaa aag cgc tcc gca   547
Val Ser Val Glu Pro Arg Arg Gln Ser Asp Glu Glu Lys Arg Ser Ala
    135                 140                 145

cta ttt gat gtc atc tct gag ctt gcc tac cgc atg cct cat ctg cca   595
Leu Phe Asp Val Ile Ser Glu Leu Ala Tyr Arg Met Pro His Leu Pro
150                 155                 160                 165

ttc gtg tca gag ttg ctg aag tac tagaacagta acgagaaaac ccc         642
Phe Val Ser Glu Leu Leu Lys Tyr
                170
```

<210> 1966
<211> 173
<212> PRT
<213> Corynebacterium glutamicum

<400> 1966

```
Val Gln Gly Met Lys Arg Lys Met Val Ala Ala Ala Leu Ala Thr Ala
  1               5                  10                  15

Leu Leu Phe Gly Ala Ala Pro Ala His Ala Ser Glu Leu Val Glu Pro
             20                  25                  30

Thr Thr Val Ala Glu Ser Val Ala Leu Asp Pro Asn Lys Ala Ile Asn
         35                  40                  45

Ile Leu Thr Pro Asp Leu Trp Glu Asp Ile Glu Ala Lys Pro Gly Asp
     50                  55                  60

Ile Val His Ile Pro Tyr Gln Gly Thr Arg Asn Tyr Glu Asp Leu Thr
 65                  70                  75                  80

Val Glu Val Ala Lys Pro Phe Glu Asp Phe Gln Ile Leu Val Gly Leu
                 85                  90                  95

Asp Asn Ser Ile Val Ile Ala Val Pro Lys Asn Leu Ser Gly Ala Ala
            100                 105                 110

Ser Val Ala Pro Val Phe Thr Val Ser Asp Lys Asn Gly Glu Ile Asp
        115                 120                 125

Ser Phe Thr Ile Lys Val Ser Val Glu Pro Arg Arg Gln Ser Asp Glu
    130                 135                 140

Glu Lys Arg Ser Ala Leu Phe Asp Val Ile Ser Glu Leu Ala Tyr Arg
145                 150                 155                 160

Met Pro His Leu Pro Phe Val Ser Glu Leu Leu Lys Tyr
                165                 170
```

<210> 1967
<211> 846

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(823)
<223> RXA00887

<400> 1967
aagaaatccg caaccatcgc agcgacaacg cttccgtgca tcgcgaaggc ggagaagaat 60

ccggtttctt tgacaagctc cgaaacaagt tccgcaaata atg tca ctg cca gta 115
Met Ser Leu Pro Val
1 5

ttt atc tct gat tcc gca gcc gga cca ggc gaa acc att gag ctc gcc 163
Phe Ile Ser Asp Ser Ala Ala Gly Pro Gly Glu Thr Ile Glu Leu Ala
10 15 20

ggt ccg gaa ggc cgg cac gcc gtc acc gtc aaa cgg atc cag gta ggc 211
Gly Pro Glu Gly Arg His Ala Val Thr Val Lys Arg Ile Gln Val Gly
25 30 35

gaa aag att tcg ctt atc gac ggc cgg ggt aca gcg cgc acc tgc acg 259
Glu Lys Ile Ser Leu Ile Asp Gly Arg Gly Thr Ala Arg Thr Cys Thr
40 45 50

gtc acc gcc ttg cag ggc aaa gac cgc ctg aac gct gtg gtg gat ttg 307
Val Thr Ala Leu Gln Gly Lys Asp Arg Leu Asn Ala Val Val Asp Leu
55 60 65

gtc gag gaa atc ccc gca ccg aac cca cag gtc acc atc gtg cag gct 355
Val Glu Glu Ile Pro Ala Pro Asn Pro Gln Val Thr Ile Val Gln Ala
70 75 80 85

atc ccc aaa tca gag cgt tcc gag ctg acc atc gac ctg ctc acc caa 403
Ile Pro Lys Ser Glu Arg Ser Glu Leu Thr Ile Asp Leu Leu Thr Gln
90 95 100

gct ggc gcc gat cgg att gtt gcg tgg caa gca tcg cgc tgc gta gca 451
Ala Gly Ala Asp Arg Ile Val Ala Trp Gln Ala Ser Arg Cys Val Ala
105 110 115

aaa tgg ggc ggc aag gaa gca aaa tca ctg gct aaa tgg cag gtg gct 499
Lys Trp Gly Gly Lys Glu Ala Lys Ser Leu Ala Lys Trp Gln Val Ala
120 125 130

gcg gaa gca gcc gcc aag caa tcg cgg cgc gca acg atc cct gaa att 547
Ala Glu Ala Ala Ala Lys Gln Ser Arg Arg Ala Thr Ile Pro Glu Ile
135 140 145

ctt ggc gta gtg ggg gag gag ggc gtc gaa aag ctt atc gac gaa tcc 595
Leu Gly Val Val Gly Glu Glu Gly Val Glu Lys Leu Ile Asp Glu Ser
150 155 160 165

gac ctg gcc atc atc ctg cac gaa gaa gca acc gcc gcg atc cgt gaa 643
Asp Leu Ala Ile Ile Leu His Glu Glu Ala Thr Ala Ala Ile Arg Glu
170 175 180

ctg gaa ttt tcc ggc aac gtc gtg gtg atc atc gga ccc gaa ggt ggc 691
Leu Glu Phe Ser Gly Asn Val Val Val Ile Ile Gly Pro Glu Gly Gly

```
            185                 190                 195

gtc gcg cca tcg gaa att tca cgc ttc gtc gac gct ggc gca cac acc   739
Val Ala Pro Ser Glu Ile Ser Arg Phe Val Asp Ala Gly Ala His Thr
        200                 205                 210

gtg aaa cta ggc cct gag gtg ttg cgc act gcc tcc gca ggc atg gtg   787
Val Lys Leu Gly Pro Glu Val Leu Arg Thr Ala Ser Ala Gly Met Val
    215                 220                 225

gcg ctc gca gct atc ggc gtg ctg tct gac cgc tgg taacatttct        833
Ala Leu Ala Ala Ile Gly Val Leu Ser Asp Arg Trp
230                 235                 240

ctgacataac ctt                                                   846
```

<210> 1968
<211> 241
<212> PRT
<213> Corynebacterium glutamicum

<400> 1968

```
Met Ser Leu Pro Val Phe Ile Ser Asp Ser Ala Ala Gly Pro Gly Glu
  1               5                  10                  15

Thr Ile Glu Leu Ala Gly Pro Glu Gly Arg His Ala Val Thr Val Lys
             20                  25                  30

Arg Ile Gln Val Gly Glu Lys Ile Ser Leu Ile Asp Gly Arg Gly Thr
         35                  40                  45

Ala Arg Thr Cys Thr Val Thr Ala Leu Gln Gly Lys Asp Arg Leu Asn
     50                  55                  60

Ala Val Val Asp Leu Val Glu Glu Ile Pro Ala Pro Asn Pro Gln Val
 65                  70                  75                  80

Thr Ile Val Gln Ala Ile Pro Lys Ser Glu Arg Ser Glu Leu Thr Ile
                 85                  90                  95

Asp Leu Leu Thr Gln Ala Gly Ala Asp Arg Ile Val Ala Trp Gln Ala
            100                 105                 110

Ser Arg Cys Val Ala Lys Trp Gly Gly Lys Glu Ala Lys Ser Leu Ala
        115                 120                 125

Lys Trp Gln Val Ala Ala Glu Ala Ala Ala Lys Gln Ser Arg Arg Ala
    130                 135                 140

Thr Ile Pro Glu Ile Leu Gly Val Val Gly Glu Glu Gly Val Glu Lys
145                 150                 155                 160

Leu Ile Asp Glu Ser Asp Leu Ala Ile Ile Leu His Glu Glu Ala Thr
                165                 170                 175

Ala Ala Ile Arg Glu Leu Glu Phe Ser Gly Asn Val Val Val Ile Ile
            180                 185                 190

Gly Pro Glu Gly Gly Val Ala Pro Ser Glu Ile Ser Arg Phe Val Asp
        195                 200                 205
```

```
Ala Gly Ala His Thr Val Lys Leu Gly Pro Glu Val Leu Arg Thr Ala
    210                 215                 220

Ser Ala Gly Met Val Ala Leu Ala Ala Ile Gly Val Leu Ser Asp Arg
225                 230                 235                 240

Trp
```

<210> 1969
<211> 711
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(688)
<223> RXA00889

<400> 1969

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tggtccgcca ccaactggtt ggacacattg tggatgcata cgaagactat gaagaacgcg 60

aggcccgcga attgaaacgc aaacgccagg agacacggcc atg agc att gag gta   115
                                              Met Ser Ile Glu Val
                                                1               5

ttc aac gaa tca gga tac gac ggc gtc aat gaa gaa atg ctc att gat   163
Phe Asn Glu Ser Gly Tyr Asp Gly Val Asn Glu Glu Met Leu Ile Asp
                10                  15                  20

gtc ctc tcc ttc gca ctc ggg gaa atg gac atc cac ccc gac gcc gaa   211
Val Leu Ser Phe Ala Leu Gly Glu Met Asp Ile His Pro Asp Ala Glu
            25                  30                  35

gca tcc atc cac atc gtc gac gtc gac acc atc gcc gat ctc cac gtg   259
Ala Ser Ile His Ile Val Asp Val Asp Thr Ile Ala Asp Leu His Val
        40                  45                  50

aaa tgg ctt gat ctt gaa ggc cca acc gac gtg atg agc ttc ccg atg   307
Lys Trp Leu Asp Leu Glu Gly Pro Thr Asp Val Met Ser Phe Pro Met
    55                  60                  65

gat gag ctc acc ccc ggc tac tcc cgc ccc gac ggc gcc acc ccc ggc   355
Asp Glu Leu Thr Pro Gly Tyr Ser Arg Pro Asp Gly Ala Thr Pro Gly
70                  75                  80                  85

ccc gcc atg ctg ggc gac att gtg ctg tgc cca gag ttc gcg gca aag   403
Pro Ala Met Leu Gly Asp Ile Val Leu Cys Pro Glu Phe Ala Ala Lys
                90                  95                  100

caa gcg acc aaa gca ggc cac gac tta gcc cac gag cta gct ttg ctg   451
Gln Ala Thr Lys Ala Gly His Asp Leu Ala His Glu Leu Ala Leu Leu
            105                 110                 115

acc gtg cac ggc agc ctg cac ctg ctt ggc tac gac cac gtc gat cca   499
Thr Val His Gly Ser Leu His Leu Leu Gly Tyr Asp His Val Asp Pro
        120                 125                 130

gcc gaa gag cgt gaa atg ttc gcc ctt caa aac gag ctg ctt gcc gat   547
```

```
Ala Glu Glu Arg Glu Met Phe Ala Leu Gln Asn Glu Leu Leu Ala Asp
    135                 140                 145

tgg tac gac aac gtc gaa gcc cgt ggc gtc acc tac cag cca aaa cca   595
Trp Tyr Asp Asn Val Glu Ala Arg Gly Val Thr Tyr Gln Pro Lys Pro
150                 155                 160                 165

tcc ggc gcc ggt gca ttc ccc acc gct gct gat cgt ctg gaa ttg gac   643
Ser Gly Ala Gly Ala Phe Pro Thr Ala Ala Asp Arg Leu Glu Leu Asp
                170                 175                 180

gaa aag atg gaa gcg gat gac tct ggc ttt gga ggc gtt gag tcc       688
Glu Lys Met Glu Ala Asp Asp Ser Gly Phe Gly Gly Val Glu Ser
            185                 190                 195

taggtggaat cctcagttat atg                                        711


<210> 1970
<211> 196
<212> PRT
<213> Corynebacterium glutamicum

<400> 1970
Met Ser Ile Glu Val Phe Asn Glu Ser Gly Tyr Asp Gly Val Asn Glu
  1               5                  10                  15

Glu Met Leu Ile Asp Val Leu Ser Phe Ala Leu Gly Glu Met Asp Ile
             20                  25                  30

His Pro Asp Ala Glu Ala Ser Ile His Ile Val Asp Val Asp Thr Ile
         35                  40                  45

Ala Asp Leu His Val Lys Trp Leu Asp Leu Glu Gly Pro Thr Asp Val
     50                  55                  60

Met Ser Phe Pro Met Asp Glu Leu Thr Pro Gly Tyr Ser Arg Pro Asp
 65                  70                  75                  80

Gly Ala Thr Pro Gly Pro Ala Met Leu Gly Asp Ile Val Leu Cys Pro
                 85                  90                  95

Glu Phe Ala Ala Lys Gln Ala Thr Lys Ala Gly His Asp Leu Ala His
            100                 105                 110

Glu Leu Ala Leu Leu Thr Val His Gly Ser Leu His Leu Leu Gly Tyr
        115                 120                 125

Asp His Val Asp Pro Ala Glu Glu Arg Glu Met Phe Ala Leu Gln Asn
    130                 135                 140

Glu Leu Leu Ala Asp Trp Tyr Asp Asn Val Glu Ala Arg Gly Val Thr
145                 150                 155                 160

Tyr Gln Pro Lys Pro Ser Gly Ala Gly Ala Phe Pro Thr Ala Ala Asp
                165                 170                 175

Arg Leu Glu Leu Asp Glu Lys Met Glu Ala Asp Asp Ser Gly Phe Gly
            180                 185                 190

Gly Val Glu Ser
```

195

<210> 1971
<211> 720
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(697)
<223> RXA00893

<400> 1971
acgccaacgc agagtgttta aagaaactgg cagttggaaa gctgcagttg atttagcctg 60

cgacgaactc aacgacctca aagcactgga ctaaatagct atg gtg gaa tcc caa 115
Met Val Glu Ser Gln
1 5

cac atc att ttc atc ccg gaa tcc caa caa aca ccc gac gag ttt acc 163
His Ile Ile Phe Ile Pro Glu Ser Gln Gln Thr Pro Asp Glu Phe Thr
10 15 20

gag gta gtc aac gag att ccc gcc gga atc aaa cca cgg atc gta ccg 211
Glu Val Val Asn Glu Ile Pro Ala Gly Ile Lys Pro Arg Ile Val Pro
25 30 35

tgg agc ggt agt gtt tcc gca ggt gtg cag gct gtg gaa tcc atc ctc 259
Trp Ser Gly Ser Val Ser Ala Gly Val Gln Ala Val Glu Ser Ile Leu
40 45 50

gac cgt gaa gaa atc cgg cgc gtc atc ctg gtc ggc gct gga acc gga 307
Asp Arg Glu Glu Ile Arg Arg Val Ile Leu Val Gly Ala Gly Thr Gly
55 60 65

gct gga gtg gcg ttg gaa att gcc aag aac caa ccc cgc cgc gtg gaa 355
Ala Gly Val Ala Leu Glu Ile Ala Lys Asn Gln Pro Arg Arg Val Glu
70 75 80 85

cgc ctc gtg ctg gat tca ccg ttg gtg acc ttt gat gag aaa caa ctc 403
Arg Leu Val Leu Asp Ser Pro Leu Val Thr Phe Asp Glu Lys Gln Leu
90 95 100

aaa ggc atg agc acc gca ctg aaa atg atg cca gga ttc ttc ttc cga 451
Lys Gly Met Ser Thr Ala Leu Lys Met Met Pro Gly Phe Phe Phe Arg
105 110 115

aag aag aac aag aaa gac ctc ctg cag cag gta gaa gaa gcc cgt act 499
Lys Lys Asn Lys Lys Asp Leu Leu Gln Gln Val Glu Glu Ala Arg Thr
120 125 130

gca gtt ccg atg gga ttt tcc gag att acc atg ccg acg tta atc atc 547
Ala Val Pro Met Gly Phe Ser Glu Ile Thr Met Pro Thr Leu Ile Ile
135 140 145

cga ggc tcc gct gcg aag gct gga att gat tct gac ttg gaa aaa caa 595
Arg Gly Ser Ala Ala Lys Ala Gly Ile Asp Ser Asp Leu Glu Lys Gln
150 155 160 165

atc ccg agc gct cgg gct acc acc att att ggt gcc aat tgg ctg act 643

```
Ile Pro Ser Ala Arg Ala Thr Thr Ile Ile Gly Ala Asn Trp Leu Thr
                170                 175                 180

tac aca acg cat gga cgc caa act ggt gct gcg att gcg gaa ttc ctc   691
Tyr Thr Thr His Gly Arg Gln Thr Gly Ala Ala Ile Ala Glu Phe Leu
            185                 190                 195

gcc caa tagaagggca cgcctaaacg cca                                 720
Ala Gln
```

<210> 1972
<211> 199
<212> PRT
<213> Corynebacterium glutamicum

<400> 1972

```
Met Val Glu Ser Gln His Ile Ile Phe Ile Pro Glu Ser Gln Gln Thr
  1               5                  10                  15

Pro Asp Glu Phe Thr Glu Val Val Asn Glu Ile Pro Ala Gly Ile Lys
             20                  25                  30

Pro Arg Ile Val Pro Trp Ser Gly Ser Val Ser Ala Gly Val Gln Ala
         35                  40                  45

Val Glu Ser Ile Leu Asp Arg Glu Glu Ile Arg Arg Val Ile Leu Val
     50                  55                  60

Gly Ala Gly Thr Gly Ala Gly Val Ala Leu Glu Ile Ala Lys Asn Gln
 65                  70                  75                  80

Pro Arg Arg Val Glu Arg Leu Val Leu Asp Ser Pro Leu Val Thr Phe
                 85                  90                  95

Asp Glu Lys Gln Leu Lys Gly Met Ser Thr Ala Leu Lys Met Met Pro
            100                 105                 110

Gly Phe Phe Phe Arg Lys Lys Asn Lys Lys Asp Leu Leu Gln Gln Val
        115                 120                 125

Glu Glu Ala Arg Thr Ala Val Pro Met Gly Phe Ser Glu Ile Thr Met
    130                 135                 140

Pro Thr Leu Ile Ile Arg Gly Ser Ala Ala Lys Ala Gly Ile Asp Ser
145                 150                 155                 160

Asp Leu Glu Lys Gln Ile Pro Ser Ala Arg Ala Thr Thr Ile Ile Gly
                165                 170                 175

Ala Asn Trp Leu Thr Tyr Thr Thr His Gly Arg Gln Thr Gly Ala Ala
            180                 185                 190

Ile Ala Glu Phe Leu Ala Gln
        195
```

<210> 1973
<211> 714
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(691)
<223> RXA00895

<400> 1973
gtcgcgccgg aaagatagac taagccacat gacttcggac atgcagaatt ctccacagca 60

ctcggccacg ccttcagaag aaaaacaagg cggactgccc atg cgc ggt ttg gcc 115
Met Arg Gly Leu Ala
1 5

atg att ttg atc gcc gtg gcc gta ttg ctc gca gcg tgg gca ctg tgg 163
Met Ile Leu Ile Ala Val Ala Val Leu Leu Ala Ala Trp Ala Leu Trp
10 15 20

tca atg cag ggc aaa gac gac acc tcc acc acc agc gcc gga caa acc 211
Ser Met Gln Gly Lys Asp Asp Thr Ser Thr Thr Ser Ala Gly Gln Thr
25 30 35

cag tcc acg gaa acc aac gcg gga act att gct gaa tct tct ggc tct 259
Gln Ser Thr Glu Thr Asn Ala Gly Thr Ile Ala Glu Ser Ser Gly Ser
40 45 50

tcg gat tcc gag cag gca tca gca gaa cct gga acc tcc gaa gaa acc 307
Ser Asp Ser Glu Gln Ala Ser Ala Glu Pro Gly Thr Ser Glu Glu Thr
55 60 65

tct gct gag cag cca gct gca gat ggc gaa gcc gct aat gct gct ggg 355
Ser Ala Glu Gln Pro Ala Ala Asp Gly Glu Ala Ala Asn Ala Ala Gly
70 75 80 85

gcc gct gct gct ggt ggc gct agt tcg gct aac ggc aac tcc acc cca 403
Ala Ala Ala Ala Gly Gly Ala Ser Ser Ala Asn Gly Asn Ser Thr Pro
90 95 100

gtg aac act ctg tac gtg ctc aac aac tcc acc gtc cca caa ctt gca 451
Val Asn Thr Leu Tyr Val Leu Asn Asn Ser Thr Val Pro Gln Leu Ala
105 110 115

gca cga gtg gca gac agc cta agc ggt gac tac caa aag gta gag tcc 499
Ala Arg Val Ala Asp Ser Leu Ser Gly Asp Tyr Gln Lys Val Glu Ser
120 125 130

gga aac ctt cca gac acc atc att ccg cag aac act gtg tac ttc acc 547
Gly Asn Leu Pro Asp Thr Ile Ile Pro Gln Asn Thr Val Tyr Phe Thr
135 140 145

gct gga aac acc gaa gct gaa aag gct gca cgt gaa ctc gct gac cgc 595
Ala Gly Asn Thr Glu Ala Glu Lys Ala Ala Arg Glu Leu Ala Asp Arg
150 155 160 165

gtc agt ggc gta gca atg gaa cgc agc gat gca ctg cca acc gaa aca 643
Val Ser Gly Val Ala Met Glu Arg Ser Asp Ala Leu Pro Thr Glu Thr
170 175 180

gaa ggc aaa gat gcc ctc gtt ttg gtg ctg gtc caa gac gta gcg ctg 691
Glu Gly Lys Asp Ala Leu Val Leu Val Leu Val Gln Asp Val Ala Leu
185 190 195

tagttttctc ggatttgttg gaa 714

<210> 1974
<211> 197
<212> PRT
<213> Corynebacterium glutamicum

<400> 1974

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Met Arg Gly Leu Ala Met Ile Leu Ile Ala Val Ala Val Leu Leu Ala
  1               5                  10                  15

Ala Trp Ala Leu Trp Ser Met Gln Gly Lys Asp Asp Thr Ser Thr Thr
             20                  25                  30

Ser Ala Gly Gln Thr Gln Ser Thr Glu Thr Asn Ala Gly Thr Ile Ala
         35                  40                  45

Glu Ser Ser Gly Ser Ser Asp Ser Glu Gln Ala Ser Ala Glu Pro Gly
     50                  55                  60

Thr Ser Glu Glu Thr Ser Ala Glu Gln Pro Ala Ala Asp Gly Glu Ala
 65                  70                  75                  80

Ala Asn Ala Ala Gly Ala Ala Ala Ala Gly Gly Ala Ser Ser Ala Asn
                 85                  90                  95

Gly Asn Ser Thr Pro Val Asn Thr Leu Tyr Val Leu Asn Asn Ser Thr
            100                 105                 110

Val Pro Gln Leu Ala Ala Arg Val Ala Asp Ser Leu Ser Gly Asp Tyr
        115                 120                 125

Gln Lys Val Glu Ser Gly Asn Leu Pro Asp Thr Ile Ile Pro Gln Asn
    130                 135                 140

Thr Val Tyr Phe Thr Ala Gly Asn Thr Glu Ala Glu Lys Ala Ala Arg
145                 150                 155                 160

Glu Leu Ala Asp Arg Val Ser Gly Val Ala Met Glu Arg Ser Asp Ala
                165                 170                 175

Leu Pro Thr Glu Thr Glu Gly Lys Asp Ala Leu Val Leu Val Leu Val
            180                 185                 190

Gln Asp Val Ala Leu
        195
```

<210> 1975
<211> 815
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (37)..(792)
<223> RXA00904

<400> 1975

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aagcagtgca gtaccaggct ggaagtgtgg acaacaatg att aat acc atc cgc    54
                                       Met Ile Asn Thr Ile Arg
                                         1               5

tcc gaa tgg acc aaa ctt gtc acc acc aaa tcc ttc tgg tgg aca acc   102
Ser Glu Trp Thr Lys Leu Val Thr Thr Lys Ser Phe Trp Trp Thr Thr
            10                  15                  20

gca cta att ctg gtc ttc agc ctg gga tac gca gcg ctc acc gga tca   150
Ala Leu Ile Leu Val Phe Ser Leu Gly Tyr Ala Ala Leu Thr Gly Ser
        25                  30                  35

ctc gcc acc ggc gaa agc ttt gca tca ctg ttc ctt ctc gca ggc agc   198
Leu Ala Thr Gly Glu Ser Phe Ala Ser Leu Phe Leu Leu Ala Gly Ser
    40                  45                  50

aca gtc acc ggc ctt tac ctc ctt ggc ttc gtg gtg atc atg atc caa   246
Thr Val Thr Gly Leu Tyr Leu Leu Gly Phe Val Val Ile Met Ile Gln
55                  60                  65                  70

tcc atc atg atg ttc acc acc gaa ttt cga ttc ggc tac caa acc caa   294
Ser Ile Met Met Phe Thr Thr Glu Phe Arg Phe Gly Tyr Gln Thr Gln
                75                  80                  85

acc ttc ctc gcc aca cca aaa cgc tgg gtt gtc gcc gtt tcc aaa tgg   342
Thr Phe Leu Ala Thr Pro Lys Arg Trp Val Val Ala Val Ser Lys Trp
            90                  95                  100

ttg ctg tac ctc gtg ttc gcc gta gtg ttg acc ttc atc acc gtg att   390
Leu Leu Tyr Leu Val Phe Ala Val Val Leu Thr Phe Ile Thr Val Ile
        105                 110                 115

ctg tgc ttc tat cta gcc aaa gcc ctg gca tca gac act gca agc tcc   438
Leu Cys Phe Tyr Leu Ala Lys Ala Leu Ala Ser Asp Thr Ala Ser Ser
    120                 125                 130

acc ctg gtg gtg tgg gaa gat acg caa gca cga cga atc atg tgg caa   486
Thr Leu Val Val Trp Glu Asp Thr Gln Ala Arg Arg Ile Met Trp Gln
135                 140                 145                 150

tac cca ctg gca gca gca cta ttg gta act ttc tgt tcc gga att gcg   534
Tyr Pro Leu Ala Ala Ala Leu Leu Val Thr Phe Cys Ser Gly Ile Ala
                155                 160                 165

ctc ctg ctg cgt caa act gca gga gca gtg gca ctg gtg ctt atg tgg   582
Leu Leu Leu Arg Gln Thr Ala Gly Ala Val Ala Leu Val Leu Met Trp
            170                 175                 180

cac ttc gct atc gaa aac ctc ctg tct ttc ttg cca cgc atc ggc gaa   630
His Phe Ala Ile Glu Asn Leu Leu Ser Phe Leu Pro Arg Ile Gly Glu
        185                 190                 195

tac gtc ggc aag tat ggt ccc ttc acc aac ctc tac gca ttc atc acc   678
Tyr Val Gly Lys Tyr Gly Pro Phe Thr Asn Leu Tyr Ala Phe Ile Thr
    200                 205                 210

gac tat caa tca att gat cca gga tgg tcc acc acc atg gga gcg gtg   726
Asp Tyr Gln Ser Ile Asp Pro Gly Trp Ser Thr Thr Met Gly Ala Val
215                 220                 225                 230

tac ttc gga gcg tgg gca ttc gtg ctg ttc gca ctc gga atc gtc gtc   774
```

Tyr Phe Gly Ala Trp Ala Phe Val Leu Phe Ala Leu Gly Ile Val Val
235 240 245

cta gaa aag aaa gac gcc taaaatgccc tctaaaatat cgc 815
Leu Glu Lys Lys Asp Ala
250

<210> 1976
<211> 252
<212> PRT
<213> Corynebacterium glutamicum

<400> 1976
Met Ile Asn Thr Ile Arg Ser Glu Trp Thr Lys Leu Val Thr Thr Lys
1 5 10 15

Ser Phe Trp Trp Thr Thr Ala Leu Ile Leu Val Phe Ser Leu Gly Tyr
20 25 30

Ala Ala Leu Thr Gly Ser Leu Ala Thr Gly Glu Ser Phe Ala Ser Leu
35 40 45

Phe Leu Leu Ala Gly Ser Thr Val Thr Gly Leu Tyr Leu Leu Gly Phe
50 55 60

Val Val Ile Met Ile Gln Ser Ile Met Met Phe Thr Thr Glu Phe Arg
65 70 75 80

Phe Gly Tyr Gln Thr Gln Thr Phe Leu Ala Thr Pro Lys Arg Trp Val
85 90 95

Val Ala Val Ser Lys Trp Leu Leu Tyr Leu Val Phe Ala Val Val Leu
100 105 110

Thr Phe Ile Thr Val Ile Leu Cys Phe Tyr Leu Ala Lys Ala Leu Ala
115 120 125

Ser Asp Thr Ala Ser Ser Thr Leu Val Val Trp Glu Asp Thr Gln Ala
130 135 140

Arg Arg Ile Met Trp Gln Tyr Pro Leu Ala Ala Ala Leu Leu Val Thr
145 150 155 160

Phe Cys Ser Gly Ile Ala Leu Leu Leu Arg Gln Thr Ala Gly Ala Val
165 170 175

Ala Leu Val Leu Met Trp His Phe Ala Ile Glu Asn Leu Leu Ser Phe
180 185 190

Leu Pro Arg Ile Gly Glu Tyr Val Gly Lys Tyr Gly Pro Phe Thr Asn
195 200 205

Leu Tyr Ala Phe Ile Thr Asp Tyr Gln Ser Ile Asp Pro Gly Trp Ser
210 215 220

Thr Thr Met Gly Ala Val Tyr Phe Gly Ala Trp Ala Phe Val Leu Phe
225 230 235 240

Ala Leu Gly Ile Val Val Leu Glu Lys Lys Asp Ala
245 250

<210> 1977
<211> 681
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(658)
<223> RXA00908

<400> 1977
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tccgcccaac atctttttca tgacgcaaag gaccgtgtca atg tct ctc tac acc   115
                                            Met Ser Leu Tyr Thr
                                              1               5

cgt act caa aat acc cgt cac tcc acc atc atc gag ttc cgc cgc gag   163
Arg Thr Gln Asn Thr Arg His Ser Thr Ile Ile Glu Phe Arg Arg Glu
                 10                  15                  20

cag act cgt aat cac acg atg gag cca atc cag tcc gag cca cgg atc   211
Gln Thr Arg Asn His Thr Met Glu Pro Ile Gln Ser Glu Pro Arg Ile
             25                  30                  35

tac gct gac gat cct ttc cgt gca cgc ttc gga cac caa ctc ccc cgc   259
Tyr Ala Asp Asp Pro Phe Arg Ala Arg Phe Gly His Gln Leu Pro Arg
         40                  45                  50

gga ctt cgc gaa gaa gca cgc ggc atg gaa tgg cgc acc ttc acc aac   307
Gly Leu Arg Glu Glu Ala Arg Gly Met Glu Trp Arg Thr Phe Thr Asn
     55                  60                  65

acc tac gca cca acc ggc aac ctg cgc atc agc aac ctc gag tcc gag   355
Thr Tyr Ala Pro Thr Gly Asn Leu Arg Ile Ser Asn Leu Glu Ser Glu
 70                  75                  80                  85

gca cgc cgc gga gga atg ttc cac ttc aac gca acc ctg atc aac aac   403
Ala Arg Arg Gly Gly Met Phe His Phe Asn Ala Thr Leu Ile Asn Asn
                 90                  95                 100

tgc cag ggc gag cgc acc acc acc gac gct cac atc atg gca acc ggc   451
Cys Gln Gly Glu Arg Thr Thr Thr Asp Ala His Ile Met Ala Thr Gly
            105                 110                 115

cca gtt tcc gca tgc acc aac ttg ctt gcc gac gcc ggc cgt cgc gtt   499
Pro Val Ser Ala Cys Thr Asn Leu Leu Ala Asp Ala Gly Arg Arg Val
        120                 125                 130

gaa atc ctc gaa ttc cac caa ttc gac atc ttt gaa gca acc gtc acc   547
Glu Ile Leu Glu Phe His Gln Phe Asp Ile Phe Glu Ala Thr Val Thr
    135                 140                 145

ttc atc tac acc tgc aac aac gtt tcc cgc acc tgg gca atg ggc ttc   595
Phe Ile Tyr Thr Cys Asn Asn Val Ser Arg Thr Trp Ala Met Gly Phe
150                 155                 160                 165

ggc ggt acc cct gag cag tcc gct gct tcc gca atg agc tcc gca gct   643
Gly Gly Thr Pro Glu Gln Ser Ala Ala Ser Ala Met Ser Ser Ala Ala
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                170                 175                 180

cac ttg ctc tac gga taggttgcaa taacattcat tcc                    681
His Leu Leu Tyr Gly
            185


<210> 1978
<211> 186
<212> PRT
<213> Corynebacterium glutamicum

<400> 1978
Met Ser Leu Tyr Thr Arg Thr Gln Asn Thr Arg His Ser Thr Ile Ile
  1               5                  10                  15

Glu Phe Arg Arg Glu Gln Thr Arg Asn His Thr Met Glu Pro Ile Gln
             20                  25                  30

Ser Glu Pro Arg Ile Tyr Ala Asp Asp Pro Phe Arg Ala Arg Phe Gly
         35                  40                  45

His Gln Leu Pro Arg Gly Leu Arg Glu Glu Ala Arg Gly Met Glu Trp
     50                  55                  60

Arg Thr Phe Thr Asn Thr Tyr Ala Pro Thr Gly Asn Leu Arg Ile Ser
 65                  70                  75                  80

Asn Leu Glu Ser Glu Ala Arg Arg Gly Gly Met Phe His Phe Asn Ala
                 85                  90                  95

Thr Leu Ile Asn Asn Cys Gln Gly Glu Arg Thr Thr Thr Asp Ala His
            100                 105                 110

Ile Met Ala Thr Gly Pro Val Ser Ala Cys Thr Asn Leu Leu Ala Asp
        115                 120                 125

Ala Gly Arg Arg Val Glu Ile Leu Glu Phe His Gln Phe Asp Ile Phe
    130                 135                 140

Glu Ala Thr Val Thr Phe Ile Tyr Thr Cys Asn Asn Val Ser Arg Thr
145                 150                 155                 160

Trp Ala Met Gly Phe Gly Gly Thr Pro Glu Gln Ser Ala Ala Ser Ala
                165                 170                 175

Met Ser Ser Ala Ala His Leu Leu Tyr Gly
            180                 185


<210> 1979
<211> 3714
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(3691)
<223> RXA00916

<400> 1979
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cctgtaactt gcgattaaaa actaacttaa ggatttacac atg aag aaa gtt ctc   115
                                            Met Lys Lys Val Leu
                                              1               5

gtt gtc ggc tgt ggt ggt tca ggt gcc aaa acg ctc gct tat atg atg   163
Val Val Gly Cys Gly Gly Ser Gly Ala Lys Thr Leu Ala Tyr Met Met
                10                  15                  20

gac cag ctc aag acc acc ctg gcg gat agt ctt ccc gag cgt tac cca   211
Asp Gln Leu Lys Thr Thr Leu Ala Asp Ser Leu Pro Glu Arg Tyr Pro
            25                  30                  35

aat cca aag gaa gca aaa ctt cct ggt gcg tgg cag ttc gtg tcg gtg   259
Asn Pro Lys Glu Ala Lys Leu Pro Gly Ala Trp Gln Phe Val Ser Val
        40                  45                  50

gat gtt ccg acc tcc cca gaa agc ccc ggc ccg aac ctt ccg aat gtt   307
Asp Val Pro Thr Ser Pro Glu Ser Pro Gly Pro Asn Leu Pro Asn Val
    55                  60                  65

cca gaa gcc ggt gga cgt tat att tcc tgt ggt tcc tcg gat cgc tat   355
Pro Glu Ala Gly Gly Arg Tyr Ile Ser Cys Gly Ser Ser Asp Arg Tyr
70                  75                  80                  85

gcc acc gtt gat act gcg gtg tcc aac cag ctc tcc tcc agg ggc gcg   403
Ala Thr Val Asp Thr Ala Val Ser Asn Gln Leu Ser Ser Arg Gly Ala
                90                  95                  100

ttg ggt ggc gtt tct tca tgg gcg ctt cga aac cct gat tct gaa acc   451
Leu Gly Gly Val Ser Ser Trp Ala Leu Arg Asn Pro Asp Ser Glu Thr
            105                 110                 115

acc cca att agt aaa ggt gcg ggc cag tac cgc tcc att ggc cgt atg   499
Thr Pro Ile Ser Lys Gly Ala Gly Gln Tyr Arg Ser Ile Gly Arg Met
        120                 125                 130

ttg atc ctg agc cga ctt cag gaa att cag gct gaa tta cgt aaa tca   547
Leu Ile Leu Ser Arg Leu Gln Glu Ile Gln Ala Glu Leu Arg Lys Ser
    135                 140                 145

tgg gat gtg ttg ttc agc ggt gag act gaa cgt gag ctc gct gac ctt   595
Trp Asp Val Leu Phe Ser Gly Glu Thr Glu Arg Glu Leu Ala Asp Leu
150                 155                 160                 165

cgt tct gca ctg tat ggc acg tct gtt tcc agt ggt gaa acc tct aaa   643
Arg Ser Ala Leu Tyr Gly Thr Ser Val Ser Ser Gly Glu Thr Ser Lys
                170                 175                 180

gag cag cca att atc ttc ggt gtc tcc tcc atg gct ggt ggc gcc ggt   691
Glu Gln Pro Ile Ile Phe Gly Val Ser Ser Met Ala Gly Gly Ala Gly
            185                 190                 195

gct tcg atg gct cta gat atc tgc cgc ctg ctc acc ggt ctt gaa ggc   739
Ala Ser Met Ala Leu Asp Ile Cys Arg Leu Leu Thr Gly Leu Glu Gly
        200                 205                 210

aac gca gtg ggt ctg agc tca ctg ttt atg gtg acc ccg gat atc ttc   787
Asn Ala Val Gly Leu Ser Ser Leu Phe Met Val Thr Pro Asp Ile Phe
    215                 220                 225
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tcc cag ctt tcc cca gac cag gtt gcc gga act aac cca aac gcg ctg   835
Ser Gln Leu Ser Pro Asp Gln Val Ala Gly Thr Asn Pro Asn Ala Leu
230                 235                 240                 245

gcc atg ttt gcc gag ctc gca gca gca cag atg ggt gca gct tcc gaa   883
Ala Met Phe Ala Glu Leu Ala Ala Ala Gln Met Gly Ala Ala Ser Glu
                250                 255                 260

gaa gat gcc cga ctg ttt aac gct ttg ggt gtt tct gtt ggc gat gac   931
Glu Asp Ala Arg Leu Phe Asn Ala Leu Gly Val Ser Val Gly Asp Asp
            265                 270                 275

tcc atc cca gtt gga cgt atc ttc cca gtg ggt att cgc tcc ggt gaa   979
Ser Ile Pro Val Gly Arg Ile Phe Pro Val Gly Ile Arg Ser Gly Glu
        280                 285                 290

aac ggc gct ctg ctt ggt gat ggc aag cca gat acc gtc tac cgc gca   1027
Asn Gly Ala Leu Leu Gly Asp Gly Lys Pro Asp Thr Val Tyr Arg Ala
    295                 300                 305

ctc ggc cgt ggc ctt gca gct ctg atg gct gat gaa gtg tcc atg gac   1075
Leu Gly Arg Gly Leu Ala Ala Leu Met Ala Asp Glu Val Ser Met Asp
310                 315                 320                 325

aac ttc gag caa ttc acc ctc ggc aac cgt ggt ggc gga agt gcc gat   1123
Asn Phe Glu Gln Phe Thr Leu Gly Asn Arg Gly Gly Gly Ser Ala Asp
                330                 335                 340

cag agc aag tac gca tgg ggt gca cag gaa gct aag aac att ccg tgg   1171
Gln Ser Lys Tyr Ala Trp Gly Ala Gln Glu Ala Lys Asn Ile Pro Trp
            345                 350                 355

ggc agc tac ggc tac tca caa cta tcc atg ggt cgt gat cgc tac gca   1219
Gly Ser Tyr Gly Tyr Ser Gln Leu Ser Met Gly Arg Asp Arg Tyr Ala
        360                 365                 370

gaa tac gcc gcc cag cga ctg gca cgc tct gcc gtg gat cgt ctg ctc   1267
Glu Tyr Ala Ala Gln Arg Leu Ala Arg Ser Ala Val Asp Arg Leu Leu
    375                 380                 385

aag gga cac ttt gat cca agc aat gat gcg gcc tct gac cag cag ctt   1315
Lys Gly His Phe Asp Pro Ser Asn Asp Ala Ala Ser Asp Gln Gln Leu
390                 395                 400                 405

caa aag cga ctc gag aac aac cgt cca tcg ctg atg ggc aac ctc agc   1363
Gln Lys Arg Leu Glu Asn Asn Arg Pro Ser Leu Met Gly Asn Leu Ser
                410                 415                 420

gac gtt ttg ccc gtc aac gcg ccg gca ggg gac tgg att ttc cat agt   1411
Asp Val Leu Pro Val Asn Ala Pro Ala Gly Asp Trp Ile Phe His Ser
            425                 430                 435

ttc aac cag atg att gaa aac tgg acc cag cgt atg aaa gca atc atc   1459
Phe Asn Gln Met Ile Glu Asn Trp Thr Gln Arg Met Lys Ala Ile Ile
        440                 445                 450

aag agc caa att cct gca gct aat ggc cag cgc gga agt gaa tgg ctc   1507
Lys Ser Gln Ile Pro Ala Ala Asn Gly Gln Arg Gly Ser Glu Trp Leu
    455                 460                 465
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ggg gat gtc cag cgt gct ttc caa tca tcc agc cag atg att gat aat   1555
Gly Asp Val Gln Arg Ala Phe Gln Ser Ser Ser Gln Met Ile Asp Asn
470                 475                 480                 485

gac tcc cgc cat gag ctc tac atg ggt gtc gcc gac tgg gcc agt gct   1603
Asp Ser Arg His Glu Leu Tyr Met Gly Val Ala Asp Trp Ala Ser Ala
                490                 495                 500

gat gtg ttg cag cgc cga gta gtc gag ttg ctt cgt gat gag atc gca   1651
Asp Val Leu Gln Arg Arg Val Val Glu Leu Leu Arg Asp Glu Ile Ala
            505                 510                 515

aaa ctg ggc gtt cct tac ggc gtc agc gtg atc gaa tct ctc agc gcc   1699
Lys Leu Gly Val Pro Tyr Gly Val Ser Val Ile Glu Ser Leu Ser Ala
        520                 525                 530

aca atc caa aac caa ctc atc gga cag ctt tct gat ctg gca aac aac   1747
Thr Ile Gln Asn Gln Leu Ile Gly Gln Leu Ser Asp Leu Ala Asn Asn
    535                 540                 545

cgt gca cct gag gct gtt caa cta gac gat gtc agc cgc agt gaa ctg   1795
Arg Ala Pro Glu Ala Val Gln Leu Asp Asp Val Ser Arg Ser Glu Leu
550                 555                 560                 565

gac aac agc aag ggc agg atc gac gat tct gac agc tac atc cag gaa   1843
Asp Asn Ser Lys Gly Arg Ile Asp Asp Ser Asp Ser Tyr Ile Gln Glu
                570                 575                 580

atc gtg tca cga tcc act ggt caa cta cac acc cgc gca gtg caa tac   1891
Ile Val Ser Arg Ser Thr Gly Gln Leu His Thr Arg Ala Val Gln Tyr
            585                 590                 595

att gcg gac cac atg gct tcg gtt ctg gac gat ttc ctc aaa aat ttc   1939
Ile Ala Asp His Met Ala Ser Val Leu Asp Asp Phe Leu Lys Asn Phe
        600                 605                 610

atc tac cca ctt cag cgc acc atc caa cgt gag cac cac tcc cta gaa   1987
Ile Tyr Pro Leu Gln Arg Thr Ile Gln Arg Glu His His Ser Leu Glu
    615                 620                 625

aag gac tac cag ctc acc aac gat gtg aac ctg gga atc tcc cag ctg   2035
Lys Asp Tyr Gln Leu Thr Asn Asp Val Asn Leu Gly Ile Ser Gln Leu
630                 635                 640                 645

aaa acc aac gtt cca gca ctg tgg cca gat gaa tct caa act acc gtc   2083
Lys Thr Asn Val Pro Ala Leu Trp Pro Asp Glu Ser Gln Thr Thr Val
                650                 655                 660

ccg tca cgt ttc agt cag gca gcc aac gaa gtc ttc ctg acc gat gtc   2131
Pro Ser Arg Phe Ser Gln Ala Ala Asn Glu Val Phe Leu Thr Asp Val
            665                 670                 675

gcc tcc ttc ccg gag cag ttc caa gca cac gtc cgc tcg tcc acc gat   2179
Ala Ser Phe Pro Glu Gln Phe Gln Ala His Val Arg Ser Ser Thr Asp
        680                 685                 690

gac atc aac gaa caa aac gat tac tcg agc gcc ctg caa gag gcc tca   2227
Asp Ile Asn Glu Gln Asn Asp Tyr Ser Ser Ala Leu Gln Glu Ala Ser
    695                 700                 705

act cga gta gtc agc ggt gtg tgg gaa tcc aag tcc ggc tct gaa aaa   2275
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Thr Arg Val Val Ser Gly Val Trp Glu Ser Lys Ser Gly Ser Glu Lys
710                 715                 720                 725

gca cca cgc gat ctc atc cgc ctc atc gac gta tgg gtt gcc cgt gac   2323
Ala Pro Arg Asp Leu Ile Arg Leu Ile Asp Val Trp Val Ala Arg Asp
                730                 735                 740

ctg acc agg gat ccg tcc ggt tcg gga agc ctc cgc gac cct aag caa   2371
Leu Thr Arg Asp Pro Ser Gly Ser Gly Ser Leu Arg Asp Pro Lys Gln
            745                 750                 755

gca cgc ttt gag ctg aag att gat acc ggc gaa gta ctc gag cgc tcc   2419
Ala Arg Phe Glu Leu Lys Ile Asp Thr Gly Glu Val Leu Glu Arg Ser
        760                 765                 770

cgc cag tac atc cgc cgc cct ggt ttc tcc ttc cag cag ttc atc gcc   2467
Arg Gln Tyr Ile Arg Arg Pro Gly Phe Ser Phe Gln Gln Phe Ile Ala
    775                 780                 785

agc tca ctg cgt gaa ttc atc acc gcg ccg ggc ttg gca gac cac gag   2515
Ser Ser Leu Arg Glu Phe Ile Thr Ala Pro Gly Leu Ala Asp His Glu
790                 795                 800                 805

cgt cgc gcg cgc cgt cag cag gtg ctg agc aag ttc agt gag gca atg   2563
Arg Arg Ala Arg Arg Gln Gln Val Leu Ser Lys Phe Ser Glu Ala Met
                810                 815                 820

acc tac gcg ctt cca ttg gct cag atc aac cct caa ctg gtt cgt gcg   2611
Thr Tyr Ala Leu Pro Leu Ala Gln Ile Asn Pro Gln Leu Val Arg Ala
            825                 830                 835

ctt tac ggc gat gaa gtc cgc tac aac ttc aac ttc tct cgc atc cca   2659
Leu Tyr Gly Asp Glu Val Arg Tyr Asn Phe Asn Phe Ser Arg Ile Pro
        840                 845                 850

ttt gcc ggc gat gag ctt gga tcc agc ctg gaa cag gca gtt cgt gat   2707
Phe Ala Gly Asp Glu Leu Gly Ser Ser Leu Glu Gln Ala Val Arg Asp
    855                 860                 865

tac ccg aac cac cga cca gca gat att tcc aag cca ctg ggc aag gct   2755
Tyr Pro Asn His Arg Pro Ala Asp Ile Ser Lys Pro Leu Gly Lys Ala
870                 875                 880                 885

ttg gtc tcc caa ggt gaa gag cgt tcc att gat atc ttc ggc tct tac   2803
Leu Val Ser Gln Gly Glu Glu Arg Ser Ile Asp Ile Phe Gly Ser Tyr
                890                 895                 900

ccc aac tac gcg ccg atc gtg ttt gac tcc ctg ctg cct cca atc gag   2851
Pro Asn Tyr Ala Pro Ile Val Phe Asp Ser Leu Leu Pro Pro Ile Glu
            905                 910                 915

aag cag tgg cgt cag atc acc ggc gat cgc acg gaa ttc tgg cat ggc   2899
Lys Gln Trp Arg Gln Ile Thr Gly Asp Arg Thr Glu Phe Trp His Gly
        920                 925                 930

cgc cgt act cgt cct ttg act gct gca ctt cca atg aca gac cta gag   2947
Arg Arg Thr Arg Pro Leu Thr Ala Ala Leu Pro Met Thr Asp Leu Glu
    935                 940                 945

cgc aac gcc atg gtc aag ggt tgg tac atc ggt cgt ctg gtc gga cga   2995
Arg Asn Ala Met Val Lys Gly Trp Tyr Ile Gly Arg Leu Val Gly Arg
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950                 955                 960                 965

gta ttc ttc ccc gca act cta gac act gcg gat acc act cca gtg cag   3043
Val Phe Phe Pro Ala Thr Leu Asp Thr Ala Asp Thr Thr Pro Val Gln
                970                 975                 980

atc tac gat gag aag tct gat tcg tgg atc aac ttc tcc acc cca atg   3091
Ile Tyr Asp Glu Lys Ser Asp Ser Trp Ile Asn Phe Ser Thr Pro Met
            985                 990                 995

ctc acc cca gtg tcc cgt ttc cgt gga agc ctc gat tgg ctg cca aac   3139
Leu Thr Pro Val Ser Arg Phe Arg Gly Ser Leu Asp Trp Leu Pro Asn
        1000                1005                1010

ctt ctg gaa tca gca tca ttg gca tgg gca cgg gca ggc gag cgt cct   3187
Leu Leu Glu Ser Ala Ser Leu Ala Trp Ala Arg Ala Gly Glu Arg Pro
    1015                1020                1025

gtc ttt gaa tcc gtc gag cct tac atc cag ctc cgc caa ctg tgg gat   3235
Val Phe Glu Ser Val Glu Pro Tyr Ile Gln Leu Arg Gln Leu Trp Asp
1030                1035                1040                1045

gat gct gcg agc cca tcc ttg cca gga cgc acc acc cgc ggt gag aag   3283
Asp Ala Ala Ser Pro Ser Leu Pro Gly Arg Thr Thr Arg Gly Glu Lys
                1050                1055                1060

ctg ctg cac gat tgg ctt ttc gac ggc aac cgc atg gct gga aac gtc   3331
Leu Leu His Asp Trp Leu Phe Asp Gly Asn Arg Met Ala Gly Asn Val
            1065                1070                1075

ctc cag atc cca gga acc gaa gct ggt gtc acc cca gct gca cgt ttt   3379
Leu Gln Ile Pro Gly Thr Glu Ala Gly Val Thr Pro Ala Ala Arg Phe
        1080                1085                1090

gag gct gcg aag aac ttc ctg cag cgc cag aac gag atc tcg caa aat   3427
Glu Ala Ala Lys Asn Phe Leu Gln Arg Gln Asn Glu Ile Ser Gln Asn
    1095                1100                1105

tac gtc cca agc gac aag ctt cgc caa ggc cgt ctg ttc acc acc gct   3475
Tyr Val Pro Ser Asp Lys Leu Arg Gln Gly Arg Leu Phe Thr Thr Ala
1110                1115                1120                1125

gat cgt cca ttt ggc gac gtc aag gat cgt gaa cta gca gca cag att   3523
Asp Arg Pro Phe Gly Asp Val Lys Asp Arg Glu Leu Ala Ala Gln Ile
                1130                1135                1140

cca gtg ttt gct gac ctt gca gcc gat gtt ttt gat ggc acc caa gaa   3571
Pro Val Phe Ala Asp Leu Ala Ala Asp Val Phe Asp Gly Thr Gln Glu
            1145                1150                1155

atc atc gac atc ctg gaa aag tgc ttg gct gca ggt cca cca tca gca   3619
Ile Ile Asp Ile Leu Glu Lys Cys Leu Ala Ala Gly Pro Pro Ser Ala
        1160                1165                1170

cag gtc ttt gac atg aac gta gct cgc cgc gac gtt tct tca gga cct   3667
Gln Val Phe Asp Met Asn Val Ala Arg Arg Asp Val Ser Ser Gly Pro
    1175                1180                1185

tct cta cct ggt gag ggt gag ttc taaatgtccg ccgcctattc gca         3714
Ser Leu Pro Gly Glu Gly Glu Phe
1190                1195
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<210> 1980
<211> 1197
<212> PRT
<213> Corynebacterium glutamicum

<400> 1980
Met Lys Lys Val Leu Val Val Gly Cys Gly Gly Ser Gly Ala Lys Thr
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Leu Ala Tyr Met Met Asp Gln Leu Lys Thr Thr Leu Ala Asp Ser Leu
20 25 30

Pro Glu Arg Tyr Pro Asn Pro Lys Glu Ala Lys Leu Pro Gly Ala Trp
35 40 45

Gln Phe Val Ser Val Asp Val Pro Thr Ser Pro Glu Ser Pro Gly Pro
50 55 60

Asn Leu Pro Asn Val Pro Glu Ala Gly Gly Arg Tyr Ile Ser Cys Gly
65 70 75 80

Ser Ser Asp Arg Tyr Ala Thr Val Asp Thr Ala Val Ser Asn Gln Leu
85 90 95

Ser Ser Arg Gly Ala Leu Gly Gly Val Ser Ser Trp Ala Leu Arg Asn
100 105 110

Pro Asp Ser Glu Thr Thr Pro Ile Ser Lys Gly Ala Gly Gln Tyr Arg
115 120 125

Ser Ile Gly Arg Met Leu Ile Leu Ser Arg Leu Gln Glu Ile Gln Ala
130 135 140

Glu Leu Arg Lys Ser Trp Asp Val Leu Phe Ser Gly Glu Thr Glu Arg
145 150 155 160

Glu Leu Ala Asp Leu Arg Ser Ala Leu Tyr Gly Thr Ser Val Ser Ser
165 170 175

Gly Glu Thr Ser Lys Glu Gln Pro Ile Ile Phe Gly Val Ser Ser Met
180 185 190

Ala Gly Gly Ala Gly Ala Ser Met Ala Leu Asp Ile Cys Arg Leu Leu
195 200 205

Thr Gly Leu Glu Gly Asn Ala Val Gly Leu Ser Ser Leu Phe Met Val
210 215 220

Thr Pro Asp Ile Phe Ser Gln Leu Ser Pro Asp Gln Val Ala Gly Thr
225 230 235 240

Asn Pro Asn Ala Leu Ala Met Phe Ala Glu Leu Ala Ala Ala Gln Met
245 250 255

Gly Ala Ala Ser Glu Glu Asp Ala Arg Leu Phe Asn Ala Leu Gly Val
260 265 270

Ser Val Gly Asp Asp Ser Ile Pro Val Gly Arg Ile Phe Pro Val Gly
275 280 285

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Ile Arg Ser Gly Glu Asn Gly Ala Leu Leu Gly Asp Gly Lys Pro Asp
    290                 295                 300

Thr Val Tyr Arg Ala Leu Gly Arg Gly Leu Ala Ala Leu Met Ala Asp
305                 310                 315                 320

Glu Val Ser Met Asp Asn Phe Glu Gln Phe Thr Leu Gly Asn Arg Gly
                325                 330                 335

Gly Gly Ser Ala Asp Gln Ser Lys Tyr Ala Trp Gly Ala Gln Glu Ala
            340                 345                 350

Lys Asn Ile Pro Trp Gly Ser Tyr Gly Tyr Ser Gln Leu Ser Met Gly
        355                 360                 365

Arg Asp Arg Tyr Ala Glu Tyr Ala Ala Gln Arg Leu Ala Arg Ser Ala
    370                 375                 380

Val Asp Arg Leu Leu Lys Gly His Phe Asp Pro Ser Asn Asp Ala Ala
385                 390                 395                 400

Ser Asp Gln Gln Leu Gln Lys Arg Leu Glu Asn Asn Arg Pro Ser Leu
                405                 410                 415

Met Gly Asn Leu Ser Asp Val Leu Pro Val Asn Ala Pro Ala Gly Asp
            420                 425                 430

Trp Ile Phe His Ser Phe Asn Gln Met Ile Glu Asn Trp Thr Gln Arg
        435                 440                 445

Met Lys Ala Ile Ile Lys Ser Gln Ile Pro Ala Ala Asn Gly Gln Arg
    450                 455                 460

Gly Ser Glu Trp Leu Gly Asp Val Gln Arg Ala Phe Gln Ser Ser Ser
465                 470                 475                 480

Gln Met Ile Asp Asn Asp Ser Arg His Glu Leu Tyr Met Gly Val Ala
                485                 490                 495

Asp Trp Ala Ser Ala Asp Val Leu Gln Arg Arg Val Val Glu Leu Leu
            500                 505                 510

Arg Asp Glu Ile Ala Lys Leu Gly Val Pro Tyr Gly Val Ser Val Ile
        515                 520                 525

Glu Ser Leu Ser Ala Thr Ile Gln Asn Gln Leu Ile Gly Gln Leu Ser
    530                 535                 540

Asp Leu Ala Asn Asn Arg Ala Pro Glu Ala Val Gln Leu Asp Asp Val
545                 550                 555                 560

Ser Arg Ser Glu Leu Asp Asn Ser Lys Gly Arg Ile Asp Asp Ser Asp
                565                 570                 575

Ser Tyr Ile Gln Glu Ile Val Ser Arg Ser Thr Gly Gln Leu His Thr
            580                 585                 590

Arg Ala Val Gln Tyr Ile Ala Asp His Met Ala Ser Val Leu Asp Asp
        595                 600                 605
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Phe Leu Lys Asn Phe Ile Tyr Pro Leu Gln Arg Thr Ile Gln Arg Glu
    610                 615                 620

His His Ser Leu Glu Lys Asp Tyr Gln Leu Thr Asn Asp Val Asn Leu
625                 630                 635                 640

Gly Ile Ser Gln Leu Lys Thr Asn Val Pro Ala Leu Trp Pro Asp Glu
                645                 650                 655

Ser Gln Thr Thr Val Pro Ser Arg Phe Ser Gln Ala Ala Asn Glu Val
            660                 665                 670

Phe Leu Thr Asp Val Ala Ser Phe Pro Glu Gln Phe Gln Ala His Val
        675                 680                 685

Arg Ser Ser Thr Asp Asp Ile Asn Glu Gln Asn Asp Tyr Ser Ser Ala
    690                 695                 700

Leu Gln Glu Ala Ser Thr Arg Val Val Ser Gly Val Trp Glu Ser Lys
705                 710                 715                 720

Ser Gly Ser Glu Lys Ala Pro Arg Asp Leu Ile Arg Leu Ile Asp Val
                725                 730                 735

Trp Val Ala Arg Asp Leu Thr Arg Asp Pro Ser Gly Ser Gly Ser Leu
            740                 745                 750

Arg Asp Pro Lys Gln Ala Arg Phe Glu Leu Lys Ile Asp Thr Gly Glu
        755                 760                 765

Val Leu Glu Arg Ser Arg Gln Tyr Ile Arg Arg Pro Gly Phe Ser Phe
    770                 775                 780

Gln Gln Phe Ile Ala Ser Ser Leu Arg Glu Phe Ile Thr Ala Pro Gly
785                 790                 795                 800

Leu Ala Asp His Glu Arg Arg Ala Arg Arg Gln Gln Val Leu Ser Lys
                805                 810                 815

Phe Ser Glu Ala Met Thr Tyr Ala Leu Pro Leu Ala Gln Ile Asn Pro
            820                 825                 830

Gln Leu Val Arg Ala Leu Tyr Gly Asp Glu Val Arg Tyr Asn Phe Asn
        835                 840                 845

Phe Ser Arg Ile Pro Phe Ala Gly Asp Glu Leu Gly Ser Ser Leu Glu
    850                 855                 860

Gln Ala Val Arg Asp Tyr Pro Asn His Arg Pro Ala Asp Ile Ser Lys
865                 870                 875                 880

Pro Leu Gly Lys Ala Leu Val Ser Gln Gly Glu Glu Arg Ser Ile Asp
                885                 890                 895

Ile Phe Gly Ser Tyr Pro Asn Tyr Ala Pro Ile Val Phe Asp Ser Leu
            900                 905                 910

Leu Pro Pro Ile Glu Lys Gln Trp Arg Gln Ile Thr Gly Asp Arg Thr
        915                 920                 925

Glu Phe Trp His Gly Arg Arg Thr Arg Pro Leu Thr Ala Ala Leu Pro
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    930                 935                 940

Met Thr Asp Leu Glu Arg Asn Ala Met Val Lys Gly Trp Tyr Ile Gly
945                 950                 955                 960

Arg Leu Val Gly Arg Val Phe Phe Pro Ala Thr Leu Asp Thr Ala Asp
                965                 970                 975

Thr Thr Pro Val Gln Ile Tyr Asp Glu Lys Ser Asp Ser Trp Ile Asn
            980                 985                 990

Phe Ser Thr Pro Met Leu Thr Pro Val Ser Arg Phe Arg Gly Ser Leu
        995                1000                1005

Asp Trp Leu Pro Asn Leu Leu Glu Ser Ala Ser Leu Ala Trp Ala Arg
    1010                1015                1020

Ala Gly Glu Arg Pro Val Phe Glu Ser Val Glu Pro Tyr Ile Gln Leu
1025                1030                1035                1040

Arg Gln Leu Trp Asp Asp Ala Ala Ser Pro Ser Leu Pro Gly Arg Thr
                1045                1050                1055

Thr Arg Gly Glu Lys Leu Leu His Asp Trp Leu Phe Asp Gly Asn Arg
            1060                1065                1070

Met Ala Gly Asn Val Leu Gln Ile Pro Gly Thr Glu Ala Gly Val Thr
        1075                1080                1085

Pro Ala Ala Arg Phe Glu Ala Ala Lys Asn Phe Leu Gln Arg Gln Asn
    1090                1095                1100

Glu Ile Ser Gln Asn Tyr Val Pro Ser Asp Lys Leu Arg Gln Gly Arg
1105                1110                1115                1120

Leu Phe Thr Thr Ala Asp Arg Pro Phe Gly Asp Val Lys Asp Arg Glu
                1125                1130                1135

Leu Ala Ala Gln Ile Pro Val Phe Ala Asp Leu Ala Ala Asp Val Phe
            1140                1145                1150

Asp Gly Thr Gln Glu Ile Ile Asp Ile Leu Glu Lys Cys Leu Ala Ala
        1155                1160                1165

Gly Pro Pro Ser Ala Gln Val Phe Asp Met Asn Val Ala Arg Arg Asp
    1170                1175                1180

Val Ser Ser Gly Pro Ser Leu Pro Gly Glu Gly Glu Phe
1185                1190                1195


<210> 1981
<211> 486
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(463)
<223> RXA00926
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<400> 1981
atggagacac ctggggctgg aaccaccaga aggcaccatc ggcgattatt agccacctta 60

ggtggccagg atgttccatg gtctggcaaa ctaactaacc atg gac atc gtt ttc 115
Met Asp Ile Val Phe
1 5

ctc ata att ctt cta gcc att ttt atc gtt ccc act ttc ctc atg agc 163
Leu Ile Ile Leu Leu Ala Ile Phe Ile Val Pro Thr Phe Leu Met Ser
10 15 20

cgc cgc cag cgc gca cgg atg act gaa atc caa aag ctg cag gac tct 211
Arg Arg Gln Arg Ala Arg Met Thr Glu Ile Gln Lys Leu Gln Asp Ser
25 30 35

gtc gtc cca ggc gac cgc atc gtc acc acc gcg gga cag cac gca acg 259
Val Val Pro Gly Asp Arg Ile Val Thr Thr Ala Gly Gln His Ala Thr
40 45 50

gtc att tcc acc act gca gaa acc gtt gat cta gag atc gcg ccg ggt 307
Val Ile Ser Thr Thr Ala Glu Thr Val Asp Leu Glu Ile Ala Pro Gly
55 60 65

atg atc agc act ttt gaa aag ctt gct atc gtg cgt gtg ctg tcc aag 355
Met Ile Ser Thr Phe Glu Lys Leu Ala Ile Val Arg Val Leu Ser Lys
70 75 80 85

gcc aat gaa cct cag atg ttg gat gag ccg acg ctg ttt gat cag cca 403
Ala Asn Glu Pro Gln Met Leu Asp Glu Pro Thr Leu Phe Asp Gln Pro
90 95 100

gaa gac gat cag ccg aac gat ggt ttc gat gga cgc act gac gga cat 451
Glu Asp Asp Gln Pro Asn Asp Gly Phe Asp Gly Arg Thr Asp Gly His
105 110 115

cct gag aat cgt tagaaattaa taataattca gca 486
Pro Glu Asn Arg
120

<210> 1982
<211> 121
<212> PRT
<213> Corynebacterium glutamicum

<400> 1982
Met Asp Ile Val Phe Leu Ile Ile Leu Leu Ala Ile Phe Ile Val Pro
1 5 10 15

Thr Phe Leu Met Ser Arg Arg Gln Arg Ala Arg Met Thr Glu Ile Gln
20 25 30

Lys Leu Gln Asp Ser Val Val Pro Gly Asp Arg Ile Val Thr Thr Ala
35 40 45

Gly Gln His Ala Thr Val Ile Ser Thr Thr Ala Glu Thr Val Asp Leu
50 55 60

Glu Ile Ala Pro Gly Met Ile Ser Thr Phe Glu Lys Leu Ala Ile Val
65 70 75 80

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Arg Val Leu Ser Lys Ala Asn Glu Pro Gln Met Leu Asp Glu Pro Thr
                85                  90                  95

Leu Phe Asp Gln Pro Glu Asp Asp Gln Pro Asn Asp Gly Phe Asp Gly
            100                 105                 110

Arg Thr Asp Gly His Pro Glu Asn Arg
        115                 120


<210> 1983
<211> 876
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(853)
<223> RXA00930

<400> 1983
acggcgcacc acacatttgg tggtgtattg agctatctct gggctgcgtg agaaaccatt 60

ttccggtgga tgatggaagc tagacgacga aagggagcat atg tct ggc cac tca   115
                                              Met Ser Gly His Ser
                                                1               5

aaa tgg gcg act acc aag cac aag aag gct gct aac gac gcc aag cga   163
Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala Asn Asp Ala Lys Arg
                10                  15                  20

ggc aag gaa ttt gcc aag ctg atc aag aac atc gaa gtt gcg gca cgt   211
Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile Glu Val Ala Ala Arg
            25                  30                  35

aca ggc ggt gga gat ccg tct gcg aac cca acg ctt gat gac atg atc   259
Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr Leu Asp Asp Met Ile
        40                  45                  50

aag aaa gcc aag aag gct tct gtg ccg aac gat aac atc gaa cgt gca   307
Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp Asn Ile Glu Arg Ala
    55                  60                  65

cgc aag cgt ggc tcc ggc gaa gaa gct ggt ggc gct gac tgg atg aac   355
Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly Ala Asp Trp Met Asn
70                  75                  80                  85

atc atg tac gag gga tac ggc ccc aac ggc gtt gcc atg ctt atc gag   403
Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val Ala Met Leu Ile Glu
                90                  95                 100

tgt ctg acc gac aac cgt aac cgc gca gct acc gaa gtt cgc acc gca   451
Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr Glu Val Arg Thr Ala
            105                 110                 115

atg acc aaa aac ggt ggc aac ttg ggc gag tcc ggt tcc gtg tcc tac   499
Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser Gly Ser Val Ser Tyr
        120                 125                 130

atg ttc acc cgc acc ggt gtc gtc acc gta caa aag ggc gat ctt agt   547
Met Phe Thr Arg Thr Gly Val Val Thr Val Gln Lys Gly Asp Leu Ser
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    135                 140                 145

gaa gat gac gtg ctc atg gct gtt ctt gaa gct ggt gct gaa gaa gtc   595
Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala Gly Ala Glu Glu Val
150                 155                 160                 165

aac gac aac ggc gat ctg ttc gag gtt acc tgc gca cca act gac att   643
Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys Ala Pro Thr Asp Ile
                170                 175                 180

cag gct gtt cgc gac gca ctc gtg gaa gct ggc att gaa gta gaa gat   691
Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly Ile Glu Val Glu Asp
            185                 190                 195

tct gaa tca gac ttc cgg gca tct gtt cag gtc ccc ctg gac gct gac   739
Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val Pro Leu Asp Ala Asp
        200                 205                 210

ggt gca cgc aag atc ttc aag ctt gtg gac gcg ttg gaa gat tcc gac   787
Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala Leu Glu Asp Ser Asp
    215                 220                 225

gat gtg caa aac gtc tac acc aac atc gac ttg agc gat gag gtt ttg   835
Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu Ser Asp Glu Val Leu
230                 235                 240                 245

aca gag ctg gaa aac gac tagttcgtat tttccgcact ccg                 876
Thr Glu Leu Glu Asn Asp
                250
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<210> 1984
<211> 251
<212> PRT
<213> Corynebacterium glutamicum

<400> 1984

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Met Ser Gly His Ser Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala
  1               5                  10                  15

Asn Asp Ala Lys Arg Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile
             20                  25                  30

Glu Val Ala Ala Arg Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr
         35                  40                  45

Leu Asp Asp Met Ile Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp
     50                  55                  60

Asn Ile Glu Arg Ala Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly
 65                  70                  75                  80

Ala Asp Trp Met Asn Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val
                 85                  90                  95

Ala Met Leu Ile Glu Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr
            100                 105                 110

Glu Val Arg Thr Ala Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser
        115                 120                 125
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Gly Ser Val Ser Tyr Met Phe Thr Arg Thr Gly Val Val Thr Val Gln
    130                 135                 140

Lys Gly Asp Leu Ser Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala
145                 150                 155                 160

Gly Ala Glu Glu Val Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys
                165                 170                 175

Ala Pro Thr Asp Ile Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly
            180                 185                 190

Ile Glu Val Glu Asp Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val
        195                 200                 205

Pro Leu Asp Ala Asp Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala
    210                 215                 220

Leu Glu Asp Ser Asp Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu
225                 230                 235                 240

Ser Asp Glu Val Leu Thr Glu Leu Glu Asn Asp
                245                 250


<210> 1985
<211> 597
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(574)
<223> RXA00932

<400> 1985
cccaattaat ttatgcactt cggtgaggtt actcacaaag agtagcgtgc aaagcccagc 60

aataaggtga tgtttcaacg attaggttac ggtaggggcc atg acg cca cag aaa   115
                                            Met Thr Pro Gln Lys
                                              1               5

ctt cac cgt ttt gca gcc ctt tta gaa atg ggt acc tgg acc ctg ctg   163
Leu His Arg Phe Ala Ala Leu Leu Glu Met Gly Thr Trp Thr Leu Leu
                 10                  15                  20

atc atc ggc atg atc tta aaa tac agt gga gtg aca gac gcc gta acc   211
Ile Ile Gly Met Ile Leu Lys Tyr Ser Gly Val Thr Asp Ala Val Thr
             25                  30                  35

cct att gcc ggc ggt atc cac ggc ttt ggc ttc ctc tgt ttt gca gcc   259
Pro Ile Ala Gly Gly Ile His Gly Phe Gly Phe Leu Cys Phe Ala Ala
         40                  45                  50

atc acc atc acc gtg tgg atc aat aat aag tgg aca ttc ccg cag ggt   307
Ile Thr Ile Thr Val Trp Ile Asn Asn Lys Trp Thr Phe Pro Gln Gly
     55                  60                  65

atc gca ggt ttg atc gtc tct gtt atc ccg tgg gct gca ttg cca ttt   355
Ile Ala Gly Leu Ile Val Ser Val Ile Pro Trp Ala Ala Leu Pro Phe
 70                  75                  80                  85
```

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gca ttg tgg gca gac aag aag ggc ctc gtt gcc ggc gga tgg cgc ttt   403
Ala Leu Trp Ala Asp Lys Lys Gly Leu Val Ala Gly Gly Trp Arg Phe
                 90                  95                 100

tca gat ccg tcc gaa aag cca cac act ttc ttt gac aag atc ttg gct   451
Ser Asp Pro Ser Glu Lys Pro His Thr Phe Phe Asp Lys Ile Leu Ala
            105                 110                 115

caa ttg gtc agg cac cca atc cga tcc att tta att ctg ctg gtg att   499
Gln Leu Val Arg His Pro Ile Arg Ser Ile Leu Ile Leu Leu Val Ile
        120                 125                 130

atc gcc gtc gtc ttc tct atc ttg ctg gcg atg gga cca cct tat gat   547
Ile Ala Val Val Phe Ser Ile Leu Leu Ala Met Gly Pro Pro Tyr Asp
    135                 140                 145

cca gat gcc atc gca aac act gtg gat taaacaacag cctccttcac         594
Pro Asp Ala Ile Ala Asn Thr Val Asp
150                 155

atg                                                               597


<210> 1986
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 1986
Met Thr Pro Gln Lys Leu His Arg Phe Ala Ala Leu Leu Glu Met Gly
  1               5                  10                  15

Thr Trp Thr Leu Leu Ile Ile Gly Met Ile Leu Lys Tyr Ser Gly Val
             20                  25                  30

Thr Asp Ala Val Thr Pro Ile Ala Gly Gly Ile His Gly Phe Gly Phe
         35                  40                  45

Leu Cys Phe Ala Ala Ile Thr Ile Thr Val Trp Ile Asn Asn Lys Trp
     50                  55                  60

Thr Phe Pro Gln Gly Ile Ala Gly Leu Ile Val Ser Val Ile Pro Trp
 65                  70                  75                  80

Ala Ala Leu Pro Phe Ala Leu Trp Ala Asp Lys Lys Gly Leu Val Ala
                 85                  90                  95

Gly Gly Trp Arg Phe Ser Asp Pro Ser Glu Lys Pro His Thr Phe Phe
            100                 105                 110

Asp Lys Ile Leu Ala Gln Leu Val Arg His Pro Ile Arg Ser Ile Leu
        115                 120                 125

Ile Leu Leu Val Ile Ile Ala Val Val Phe Ser Ile Leu Leu Ala Met
    130                 135                 140

Gly Pro Pro Tyr Asp Pro Asp Ala Ile Ala Asn Thr Val Asp
145                 150                 155
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<210> 1987
<211> 585
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(562)
<223> RXA00933

<400> 1987
ccgcggggct aaagcgcgca aacgcctacg actggtcgac agtatccacc caggtcatgg 60

cagtctatga aaccattgcg atcgacaaag tgaggcttgg atg acc ctt gtt tac 115
Met Thr Leu Val Tyr
1 5

ctc ctc atc gct gtc gtt gtc acc gca act gtt ctg tgg gcg tat ttc 163
Leu Leu Ile Ala Val Val Val Thr Ala Thr Val Leu Trp Ala Tyr Phe
10 15 20

aca gca caa cgc ctc aac cgg ctc cac atc cgc acc gac tca gca aga 211
Thr Ala Gln Arg Leu Asn Arg Leu His Ile Arg Thr Asp Ser Ala Arg
25 30 35

caa gcc ctg caa gca gca ctg gat cgc cga gca gca cta gta ggt gcg 259
Gln Ala Leu Gln Ala Ala Leu Asp Arg Arg Ala Ala Leu Val Gly Ala
40 45 50

ttg ttg ccc gat gca gca gaa gcc tca aaa cgc gct gag gca att ccc 307
Leu Leu Pro Asp Ala Ala Glu Ala Ser Lys Arg Ala Glu Ala Ile Pro
55 60 65

ctg gaa tac tcc cgc ttc tcc caa cgc gcc cgc gcc gaa cga gaa atc 355
Leu Glu Tyr Ser Arg Phe Ser Gln Arg Ala Arg Ala Glu Arg Glu Ile
70 75 80 85

tct gaa ctc atc ttg aaa cag ggg aag acc ctt cca gat tcc atc gtg 403
Ser Glu Leu Ile Leu Lys Gln Gly Lys Thr Leu Pro Asp Ser Ile Val
90 95 100

gac gct gcc acc cgc gtg gaa tta gcc cac cgc ttc tac aac gaa gcc 451
Asp Ala Ala Thr Arg Val Glu Leu Ala His Arg Phe Tyr Asn Glu Ala
105 110 115

gtc agt gac acc cgc gat ctt cga acc cga ttg atg gtc aga tcc ttc 499
Val Ser Asp Thr Arg Asp Leu Arg Thr Arg Leu Met Val Arg Ser Phe
120 125 130

cga ctc ggc ggc acc gca ccc ttg ccg gag tac ttc gaa cta ctc gat 547
Arg Leu Gly Gly Thr Ala Pro Leu Pro Glu Tyr Phe Glu Leu Leu Asp
135 140 145

aca gat ctg ctg act taaatgtaaa aaagcctcct tca 585
Thr Asp Leu Leu Thr
150

<210> 1988
<211> 154
<212> PRT

<213> Corynebacterium glutamicum

<400> 1988

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Met Thr Leu Val Tyr Leu Leu Ile Ala Val Val Val Thr Ala Thr Val
  1               5                  10                  15

Leu Trp Ala Tyr Phe Thr Ala Gln Arg Leu Asn Arg Leu His Ile Arg
             20                  25                  30

Thr Asp Ser Ala Arg Gln Ala Leu Gln Ala Ala Leu Asp Arg Arg Ala
         35                  40                  45

Ala Leu Val Gly Ala Leu Leu Pro Asp Ala Ala Glu Ala Ser Lys Arg
     50                  55                  60

Ala Glu Ala Ile Pro Leu Glu Tyr Ser Arg Phe Ser Gln Arg Ala Arg
 65                  70                  75                  80

Ala Glu Arg Glu Ile Ser Glu Leu Ile Leu Lys Gln Gly Lys Thr Leu
                 85                  90                  95

Pro Asp Ser Ile Val Asp Ala Ala Thr Arg Val Glu Leu Ala His Arg
            100                 105                 110

Phe Tyr Asn Glu Ala Val Ser Asp Thr Arg Asp Leu Arg Thr Arg Leu
        115                 120                 125

Met Val Arg Ser Phe Arg Leu Gly Gly Thr Ala Pro Leu Pro Glu Tyr
    130                 135                 140

Phe Glu Leu Leu Asp Thr Asp Leu Leu Thr
145                 150
```

<210> 1989
<211> 519
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(496)
<223> RXA00940

<400> 1989

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tgctcaacgg cacgctgaag ggcacggaca tggacatcat cacggcaggc gacccggacg 60

tggtcgcggt ggacgtgctg gcagaggcga tctgcgcaat gtg att ttg gtg ctg   115
                                        Val Ile Leu Val Leu
                                          1               5

ctg gaa gct gag tca atg cgc ggc tac cag atc atc acc acc atc agt   163
Leu Glu Ala Glu Ser Met Arg Gly Tyr Gln Ile Ile Thr Thr Ile Ser
                 10                  15                  20

gag caa aca gaa ggt aac tgg act cca agc cca gga acc atc tat cca   211
Glu Gln Thr Glu Gly Asn Trp Thr Pro Ser Pro Gly Thr Ile Tyr Pro
             25                  30                  35

acc ttg tcc atg ctt gaa gat gaa ggc ctg att tcc atc tcc cat gaa   259
Thr Leu Ser Met Leu Glu Asp Glu Gly Leu Ile Ser Ile Ser His Glu
```

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         40                  45                  50

atg ggc aga aaa atg gcg cgc ctt aca gaa gaa ggc gcg cag gaa gtg   307
Met Gly Arg Lys Met Ala Arg Leu Thr Glu Glu Gly Ala Gln Glu Val
     55                  60                  65

gca aag aac aag gat gcg tgg gga tca att ctg gag gct tat cgc aat   355
Ala Lys Asn Lys Asp Ala Trp Gly Ser Ile Leu Glu Ala Tyr Arg Asn
 70                  75                  80                  85

cca gaa tcc cga gag gtg cgg gtg ttt aac att cgc tct gag ttt cac   403
Pro Glu Ser Arg Glu Val Arg Val Phe Asn Ile Arg Ser Glu Phe His
                 90                  95                 100

aag gtc agg gaa gca gcg aaa gct gct ccc gac gat aaa gca gag caa   451
Lys Val Arg Glu Ala Ala Lys Ala Ala Pro Asp Asp Lys Ala Glu Gln
            105                 110                 115

ata atc gag att tta agg aga gca gca gat gac atc aag aga cta       496
Ile Ile Glu Ile Leu Arg Arg Ala Ala Asp Asp Ile Lys Arg Leu
        120                 125                 130

taaccccagt accatgcagc tgc                                        519


<210> 1990
<211> 132
<212> PRT
<213> Corynebacterium glutamicum

<400> 1990
Val Ile Leu Val Leu Leu Glu Ala Glu Ser Met Arg Gly Tyr Gln Ile
  1               5                  10                  15

Ile Thr Thr Ile Ser Glu Gln Thr Glu Gly Asn Trp Thr Pro Ser Pro
             20                  25                  30

Gly Thr Ile Tyr Pro Thr Leu Ser Met Leu Glu Asp Glu Gly Leu Ile
         35                  40                  45

Ser Ile Ser His Glu Met Gly Arg Lys Met Ala Arg Leu Thr Glu Glu
     50                  55                  60

Gly Ala Gln Glu Val Ala Lys Asn Lys Asp Ala Trp Gly Ser Ile Leu
 65                  70                  75                  80

Glu Ala Tyr Arg Asn Pro Glu Ser Arg Glu Val Arg Val Phe Asn Ile
                 85                  90                  95

Arg Ser Glu Phe His Lys Val Arg Glu Ala Ala Lys Ala Ala Pro Asp
            100                 105                 110

Asp Lys Ala Glu Gln Ile Ile Glu Ile Leu Arg Arg Ala Ala Asp Asp
        115                 120                 125

Ile Lys Arg Leu
    130


<210> 1991
<211> 771
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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(748)
<223> RXA00949

<400> 1991
gctcaaggat ccttcctggg caaaccaagc agccctcgca ctaggtgcgg aacccaggta 60

tgttcaccaa tacgactacg tactttaaag gagagttgac atg aag gtt ttc atc 115
Met Lys Val Phe Ile
1 5

atc ggc gct gcg ggt ggc atc ggc aat cga ctt tcc agc ctg ctt cac 163
Ile Gly Ala Ala Gly Gly Ile Gly Asn Arg Leu Ser Ser Leu Leu His
10 15 20

gcc agg gga gat gca gtt agc ggc atg cac cgc aat ctt gag cag gcc 211
Ala Arg Gly Asp Ala Val Ser Gly Met His Arg Asn Leu Glu Gln Ala
25 30 35

tca aaa atc aca gac act ggg gca act gcc gta ctc ggg gat ctc atc 259
Ser Lys Ile Thr Asp Thr Gly Ala Thr Ala Val Leu Gly Asp Leu Ile
40 45 50

cac aac agc acg gag gag ctt gcg gag ctt ttc cgc ggt cac gat gcc 307
His Asn Ser Thr Glu Glu Leu Ala Glu Leu Phe Arg Gly His Asp Ala
55 60 65

atc gta ttt tct gca ggc gcc cac gga aca ggg caa gaa aat acc acg 355
Ile Val Phe Ser Ala Gly Ala His Gly Thr Gly Gln Glu Asn Thr Thr
70 75 80 85

ctt atc gac ggc gcc ggc ctc cgt aaa gcc gcc gac gct gcc agc gcg 403
Leu Ile Asp Gly Ala Gly Leu Arg Lys Ala Ala Asp Ala Ala Ser Ala
90 95 100

gcc aac gtt tca cgc ttc atc ttg gtc tct gcg ttt ccg gaa tcc tcc 451
Ala Asn Val Ser Arg Phe Ile Leu Val Ser Ala Phe Pro Glu Ser Ser
105 110 115

cgc ggg gag aac acc acc gag aac ttt gag cac tat atg aag gtg aag 499
Arg Gly Glu Asn Thr Thr Glu Asn Phe Glu His Tyr Met Lys Val Lys
120 125 130

aag tcc gcc gat gtc tac ctc agt cac act gac cta gac tgg gtt att 547
Lys Ser Ala Asp Val Tyr Leu Ser His Thr Asp Leu Asp Trp Val Ile
135 140 145

gtc cga cca ggc gtg ctt caa gat gag gca ggg gat ggt tta gtc act 595
Val Arg Pro Gly Val Leu Gln Asp Glu Ala Gly Asp Gly Leu Val Thr
150 155 160 165

gct ggc tta gcg att aat tac ggc aat gtt gct cgc gat aat gtc gca 643
Ala Gly Leu Ala Ile Asn Tyr Gly Asn Val Ala Arg Asp Asn Val Ala
170 175 180

gcg ttc att gat gaa gct ctg cat caa ccg cag ttg tca aag atc att 691
Ala Phe Ile Asp Glu Ala Leu His Gln Pro Gln Leu Ser Lys Ile Ile

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            185                 190                 195

gtt gaa ctc acc gac ggt tca act ccg gtg gcg gaa gcc gta gaa cgc   739
Val Glu Leu Thr Asp Gly Ser Thr Pro Val Ala Glu Ala Val Glu Arg
        200                 205                 210

ctc atc aag taaagacgaa aagagggaga atg                             771
Leu Ile Lys
    215


<210> 1992
<211> 216
<212> PRT
<213> Corynebacterium glutamicum

<400> 1992
Met Lys Val Phe Ile Ile Gly Ala Ala Gly Gly Ile Gly Asn Arg Leu
  1               5                  10                  15

Ser Ser Leu Leu His Ala Arg Gly Asp Ala Val Ser Gly Met His Arg
             20                  25                  30

Asn Leu Glu Gln Ala Ser Lys Ile Thr Asp Thr Gly Ala Thr Ala Val
         35                  40                  45

Leu Gly Asp Leu Ile His Asn Ser Thr Glu Glu Leu Ala Glu Leu Phe
     50                  55                  60

Arg Gly His Asp Ala Ile Val Phe Ser Ala Gly Ala His Gly Thr Gly
 65                  70                  75                  80

Gln Glu Asn Thr Thr Leu Ile Asp Gly Ala Gly Leu Arg Lys Ala Ala
                 85                  90                  95

Asp Ala Ala Ser Ala Ala Asn Val Ser Arg Phe Ile Leu Val Ser Ala
            100                 105                 110

Phe Pro Glu Ser Ser Arg Gly Glu Asn Thr Thr Glu Asn Phe Glu His
        115                 120                 125

Tyr Met Lys Val Lys Lys Ser Ala Asp Val Tyr Leu Ser His Thr Asp
    130                 135                 140

Leu Asp Trp Val Ile Val Arg Pro Gly Val Leu Gln Asp Glu Ala Gly
145                 150                 155                 160

Asp Gly Leu Val Thr Ala Gly Leu Ala Ile Asn Tyr Gly Asn Val Ala
                165                 170                 175

Arg Asp Asn Val Ala Ala Phe Ile Asp Glu Ala Leu His Gln Pro Gln
            180                 185                 190

Leu Ser Lys Ile Ile Val Glu Leu Thr Asp Gly Ser Thr Pro Val Ala
        195                 200                 205

Glu Ala Val Glu Arg Leu Ile Lys
    210                 215


<210> 1993
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<211> 170
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(147)
<223> RXA00969

<400> 1993
atc cga cag gaa gag cgc gat gat gat gca cgt ctg atc gtg gtc acc 48
Ile Arg Gln Glu Glu Arg Asp Asp Asp Ala Arg Leu Ile Val Val Thr
1 5 10 15

cac tct gcg ctg gaa tct gat ctt tcc cgc acc gtt gaa ctg ctg aag 96
His Ser Ala Leu Glu Ser Asp Leu Ser Arg Thr Val Glu Leu Leu Lys
20 25 30

gct aag cct gtt gtt aag gca atc aac agt gtg atc cgc ctc gaa agg 144
Ala Lys Pro Val Val Lys Ala Ile Asn Ser Val Ile Arg Leu Glu Arg
35 40 45

gac taattttact gacatggcaa ttg 170
Asp

<210> 1994
<211> 49
<212> PRT
<213> Corynebacterium glutamicum

<400> 1994
Ile Arg Gln Glu Glu Arg Asp Asp Asp Ala Arg Leu Ile Val Val Thr
1 5 10 15

His Ser Ala Leu Glu Ser Asp Leu Ser Arg Thr Val Glu Leu Leu Lys
20 25 30

Ala Lys Pro Val Val Lys Ala Ile Asn Ser Val Ile Arg Leu Glu Arg
35 40 45

Asp

<210> 1995
<211> 726
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(703)
<223> RXA00973

<400> 1995
ttgttggtgc aggccttaca gccattgcac tgagttccat gctgtcgcag ccagtacagg 60

ccttcaccat gaccattgag atggtgagtg tatttttcac atg aac cac tct gac 115
Met Asn His Ser Asp

```
                                                    1               5

gac gat cgc atg caa aag tgg ttc cag atc cgc cgc gaa ctg ggc aaa   163
Asp Asp Arg Met Gln Lys Trp Phe Gln Ile Arg Arg Glu Leu Gly Lys
                10                  15                  20

gaa att gtg aaa cag ctt caa aag gat ctg ccc gca gtc gcc tct gac   211
Glu Ile Val Lys Gln Leu Gln Lys Asp Leu Pro Ala Val Ala Ser Asp
            25                  30                  35

atc ggc tcc atg gtg tat tcc tct gat caa gtt ccc ctc gga aac gcc   259
Ile Gly Ser Met Val Tyr Ser Ser Asp Gln Val Pro Leu Gly Asn Ala
        40                  45                  50

acg ctc act gca tac gga gac atc ggc aac cga gtc gct tcc gct gca   307
Thr Leu Thr Ala Tyr Gly Asp Ile Gly Asn Arg Val Ala Ser Ala Ala
    55                  60                  65

aca agt gcg aga tac aac gta gag gaa ctc ctg gac gca atc gaa aac   355
Thr Ser Ala Arg Tyr Asn Val Glu Glu Leu Leu Asp Ala Ile Glu Asn
70                  75                  80                  85

gca cga ttt gcc atc tgg gtt cca aat tac gac aac tcc tac tac ctc   403
Ala Arg Phe Ala Ile Trp Val Pro Asn Tyr Asp Asn Ser Tyr Tyr Leu
                90                  95                  100

tcc ggc gag gaa ggt gcc gac gaa ttc caa aca tac ctc atc aaa gat   451
Ser Gly Glu Glu Gly Ala Asp Glu Phe Gln Thr Tyr Leu Ile Lys Asp
            105                 110                 115

gcg tca aga ttt ctt gaa tcc tcc ggg aat act cca ccc gag aac ccg   499
Ala Ser Arg Phe Leu Glu Ser Ser Gly Asn Thr Pro Pro Glu Asn Pro
        120                 125                 130

cag tac agc gac tcc aaa tta acc ttt gct agc gaa cta ctc ccc ttc   547
Gln Tyr Ser Asp Ser Lys Leu Thr Phe Ala Ser Glu Leu Leu Pro Phe
    135                 140                 145

tac acc gca ttt aac aac tcg acc tac cca cta ctt cat gct tgt gtg   595
Tyr Thr Ala Phe Asn Asn Ser Thr Tyr Pro Leu Leu His Ala Cys Val
150                 155                 160                 165

caa ggt gaa cca act gaa gta gac ctc tac ttc tac gag ctc gag cag   643
Gln Gly Glu Pro Thr Glu Val Asp Leu Tyr Phe Tyr Glu Leu Glu Gln
                170                 175                 180

gca gaa ttg aag gaa aaa gag act gca cag ctc tcg agt gga tca agt   691
Ala Glu Leu Lys Glu Lys Glu Thr Ala Gln Leu Ser Ser Gly Ser Ser
            185                 190                 195

ttt ggc tcc agt tagtcagaat tctcctaaag ggc                        726
Phe Gly Ser Ser
        200
```

<210> 1996
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 1996

```
Met Asn His Ser Asp Asp Asp Arg Met Gln Lys Trp Phe Gln Ile Arg
  1               5                  10                  15

Arg Glu Leu Gly Lys Glu Ile Val Lys Gln Leu Gln Lys Asp Leu Pro
             20                  25                  30

Ala Val Ala Ser Asp Ile Gly Ser Met Val Tyr Ser Ser Asp Gln Val
         35                  40                  45

Pro Leu Gly Asn Ala Thr Leu Thr Ala Tyr Gly Asp Ile Gly Asn Arg
     50                  55                  60

Val Ala Ser Ala Ala Thr Ser Ala Arg Tyr Asn Val Glu Glu Leu Leu
 65                  70                  75                  80

Asp Ala Ile Glu Asn Ala Arg Phe Ala Ile Trp Val Pro Asn Tyr Asp
                 85                  90                  95

Asn Ser Tyr Tyr Leu Ser Gly Glu Glu Gly Ala Asp Glu Phe Gln Thr
            100                 105                 110

Tyr Leu Ile Lys Asp Ala Ser Arg Phe Leu Glu Ser Ser Gly Asn Thr
        115                 120                 125

Pro Pro Glu Asn Pro Gln Tyr Ser Asp Ser Lys Leu Thr Phe Ala Ser
    130                 135                 140

Glu Leu Leu Pro Phe Tyr Thr Ala Phe Asn Asn Ser Thr Tyr Pro Leu
145                 150                 155                 160

Leu His Ala Cys Val Gln Gly Glu Pro Thr Glu Val Asp Leu Tyr Phe
                165                 170                 175

Tyr Glu Leu Glu Gln Ala Glu Leu Lys Glu Lys Glu Thr Ala Gln Leu
            180                 185                 190

Ser Ser Gly Ser Ser Phe Gly Ser Ser
        195                 200
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<210> 1997
<211> 738
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(715)
<223> RXA00978

<400> 1997
tcctgggtag catgggctta tgagcactga tagccaaaac cctgtaagaa aatcctgcgc 60

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acagccacat tcttgttccc aagaggtgcg attgaaagcg atg tcc agg tca ccg   115
                                               Met Ser Arg Ser Pro
                                                 1               5

ctt act aaa ggt cta aat caa ctt gaa cac ctc gag tta gat aag tca   163
Leu Thr Lys Gly Leu Asn Gln Leu Glu His Leu Glu Leu Asp Lys Ser
                10                  15                  20
```

```
cta act gcg tgg tcg tgg gca gaa gat gat cct ttg tac ctc gca ggt   211
Leu Thr Ala Trp Ser Trp Ala Glu Asp Asp Pro Leu Tyr Leu Ala Gly
            25                  30                  35

gag aac tta aac ggc agt tac ctc att gtc gca gga cga gtg cgg gtc   259
Glu Asn Leu Asn Gly Ser Tyr Leu Ile Val Ala Gly Arg Val Arg Val
        40                  45                  50

tct cgc gac acc atc gac ggg aaa gaa ctc acc gtt gat att gca acg   307
Ser Arg Asp Thr Ile Asp Gly Lys Glu Leu Thr Val Asp Ile Ala Thr
    55                  60                  65

ccc ggc gat gtt att ggt gcg ata gat aca gaa cct cag ccg gca gta   355
Pro Gly Asp Val Ile Gly Ala Ile Asp Thr Glu Pro Gln Pro Ala Val
70                  75                  80                  85

gat tcc gct tgg gca ata gaa acc acc tgt gcg ctg ttt ctt cca gca   403
Asp Ser Ala Trp Ala Ile Glu Thr Thr Cys Ala Leu Phe Leu Pro Ala
                90                  95                  100

acc gcg ttg gca act gtg att gaa cag cat cca agt ttt gct ttg gcg   451
Thr Ala Leu Ala Thr Val Ile Glu Gln His Pro Ser Phe Ala Leu Ala
            105                 110                 115

atg att cgg atg cag cag caa cgt ttg gct aca gcc aga gat cat gaa   499
Met Ile Arg Met Gln Gln Gln Arg Leu Ala Thr Ala Arg Asp His Glu
        120                 125                 130

att aac ctg act acg acc aca gtt gag caa cga gta gct att gca gtg   547
Ile Asn Leu Thr Thr Thr Thr Val Glu Gln Arg Val Ala Ile Ala Val
    135                 140                 145

aga act ctg gga cga aaa atc ggg caa cga cga ccc gat gga atc ttg   595
Arg Thr Leu Gly Arg Lys Ile Gly Gln Arg Arg Pro Asp Gly Ile Leu
150                 155                 160                 165

ctc att caa gtt cga atc cgg cgg gaa gat gtt gcg ggt tta gca ggc   643
Leu Ile Gln Val Arg Ile Arg Arg Glu Asp Val Ala Gly Leu Ala Gly
                170                 175                 180

acc acc gtg gaa tct act tct aga gtt ttg gcg cga tta cgt aaa gaa   691
Thr Thr Val Glu Ser Thr Ser Arg Val Leu Ala Arg Leu Arg Lys Glu
            185                 190                 195

ggg gtc att gat agc ggt agg gaa tgattgccgt ggtcgatgaa cgg        738
Gly Val Ile Asp Ser Gly Arg Glu
        200                 205
```

<210> 1998
<211> 205
<212> PRT
<213> Corynebacterium glutamicum

<400> 1998

```
Met Ser Arg Ser Pro Leu Thr Lys Gly Leu Asn Gln Leu Glu His Leu
  1               5                  10                  15

Glu Leu Asp Lys Ser Leu Thr Ala Trp Ser Trp Ala Glu Asp Asp Pro
            20                  25                  30
```

```
Leu Tyr Leu Ala Gly Glu Asn Leu Asn Gly Ser Tyr Leu Ile Val Ala
         35                  40                  45

Gly Arg Val Arg Val Ser Arg Asp Thr Ile Asp Gly Lys Glu Leu Thr
     50                  55                  60

Val Asp Ile Ala Thr Pro Gly Asp Val Ile Gly Ala Ile Asp Thr Glu
 65                  70                  75                  80

Pro Gln Pro Ala Val Asp Ser Ala Trp Ala Ile Glu Thr Thr Cys Ala
                 85                  90                  95

Leu Phe Leu Pro Ala Thr Ala Leu Ala Thr Val Ile Glu Gln His Pro
            100                 105                 110

Ser Phe Ala Leu Ala Met Ile Arg Met Gln Gln Gln Arg Leu Ala Thr
        115                 120                 125

Ala Arg Asp His Glu Ile Asn Leu Thr Thr Thr Thr Val Glu Gln Arg
    130                 135                 140

Val Ala Ile Ala Val Arg Thr Leu Gly Arg Lys Ile Gly Gln Arg Arg
145                 150                 155                 160

Pro Asp Gly Ile Leu Leu Ile Gln Val Arg Ile Arg Arg Glu Asp Val
                165                 170                 175

Ala Gly Leu Ala Gly Thr Thr Val Glu Ser Thr Ser Arg Val Leu Ala
            180                 185                 190

Arg Leu Arg Lys Glu Gly Val Ile Asp Ser Gly Arg Glu
        195                 200                 205


<210> 1999
<211> 424
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (60)..(401)
<223> RXA00986

<400> 1999
ctactttgat aacaccgcca cccaagccaa gccggagtga tctccgtatc ctttaaggcatg 62
                                                                  Met
                                                                   1

act tta aaa gat aag tac gac act gaa gta gct gtt tct aat aat cag   110
Thr Leu Lys Asp Lys Tyr Asp Thr Glu Val Ala Val Ser Asn Asn Gln
              5                  10                  15

gac aag cac caa ttt gag gtc agt tac cct gaa gat gcc gtg act gct   158
Asp Lys His Gln Phe Glu Val Ser Tyr Pro Glu Asp Ala Val Thr Ala
         20                  25                  30

ggc ttt gct gca tac ctt gat aaa ggt gat tcg cgg atc ttc tat cac   206
Gly Phe Ala Ala Tyr Leu Asp Lys Gly Asp Ser Arg Ile Phe Tyr His
     35                  40                  45
```

```
acc gtt gtt ggc gat gaa ttc ggt ggc aag gga ctt gcg tca att ctt   254
Thr Val Val Gly Asp Glu Phe Gly Gly Lys Gly Leu Ala Ser Ile Leu
 50                  55                  60                  65

gtt tca gag gcg tta aaa gcc aca aaa gaa gct ggt ctt acc gtg gtt   302
Val Ser Glu Ala Leu Lys Ala Thr Lys Glu Ala Gly Leu Thr Val Val
                70                  75                  80

ccg gta tgt ccc ttt gtt aaa gga ttc gtg gaa aag aac gca ttc gag   350
Pro Val Cys Pro Phe Val Lys Gly Phe Val Glu Lys Asn Ala Phe Glu
             85                  90                  95

ggt tac cgc aaa cca aac cat gag gat atg gag ctg gtg aag agc cag   398
Gly Tyr Arg Lys Pro Asn His Glu Asp Met Glu Leu Val Lys Ser Gln
        100                 105                 110

atg tagaaactac tcaacttcca gaa                                    424
Met
```

<210> 2000
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 2000

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Met Thr Leu Lys Asp Lys Tyr Asp Thr Glu Val Ala Val Ser Asn Asn
  1               5                  10                  15

Gln Asp Lys His Gln Phe Glu Val Ser Tyr Pro Glu Asp Ala Val Thr
             20                  25                  30

Ala Gly Phe Ala Ala Tyr Leu Asp Lys Gly Asp Ser Arg Ile Phe Tyr
         35                  40                  45

His Thr Val Val Gly Asp Glu Phe Gly Gly Lys Gly Leu Ala Ser Ile
     50                  55                  60

Leu Val Ser Glu Ala Leu Lys Ala Thr Lys Glu Ala Gly Leu Thr Val
 65                  70                  75                  80

Val Pro Val Cys Pro Phe Val Lys Gly Phe Val Glu Lys Asn Ala Phe
                 85                  90                  95

Glu Gly Tyr Arg Lys Pro Asn His Glu Asp Met Glu Leu Val Lys Ser
            100                 105                 110

Gln Met
```

<210> 2001
<211> 588
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(565)
<223> RXA00987

<400> 2001
cgcgggctgc ttaccacgca gcacagctaa gctttaaggc cctccggggc ctttttgct 60

tttcgacgcc tacctccttc ggaggcgtat tctgtcgttc atg cct aaa tct ctg 115
Met Pro Lys Ser Leu
1 5

acc ttt gaa gac agc att aac atc gca gcg ccc atc aat cag gtc tac 163
Thr Phe Glu Asp Ser Ile Asn Ile Ala Ala Pro Ile Asn Gln Val Tyr
10 15 20

gca cta gtt tct gac atc act cga act gga gaa tgg tcg ccc gtg tgt 211
Ala Leu Val Ser Asp Ile Thr Arg Thr Gly Glu Trp Ser Pro Val Cys
25 30 35

gag aaa tgc tgg tgg gat gaa gac gaa ggc ccc gtc gtg ggt gcg cac 259
Glu Lys Cys Trp Trp Asp Glu Asp Glu Gly Pro Val Val Gly Ala His
40 45 50

ttt act ggc cga aac gtc aca cct gag cgc acc tgg gag aca cgg agc 307
Phe Thr Gly Arg Asn Val Thr Pro Glu Arg Thr Trp Glu Thr Arg Ser
55 60 65

gag gtt atc gtc gca gag cca aat cgt tgc ttt ggt tgg agc gtg act 355
Glu Val Ile Val Ala Glu Pro Asn Arg Cys Phe Gly Trp Ser Val Thr
70 75 80 85

gat gga aac gtc aag tgg att tat tcc atg gaa ccg tta gaa gaa ggc 403
Asp Gly Asn Val Lys Trp Ile Tyr Ser Met Glu Pro Leu Glu Glu Gly
90 95 100

aca gta ttg act gaa tca tgg gaa ttt acc ccc aaa ggt caa cga ttc 451
Thr Val Leu Thr Glu Ser Trp Glu Phe Thr Pro Lys Gly Gln Arg Phe
105 110 115

ttc cac gac aaa ttc ggc gac aaa tca att gaa gaa att gaa aag cga 499
Phe His Asp Lys Phe Gly Asp Lys Ser Ile Glu Glu Ile Glu Lys Arg
120 125 130

cgc ttg gca gct ata acc gga att cca gaa aca ctg gtt gcc att cag 547
Arg Leu Ala Ala Ile Thr Gly Ile Pro Glu Thr Leu Val Ala Ile Gln
135 140 145

cgc att ctg gaa gtt gag tagtttctac atctggctct tca 588
Arg Ile Leu Glu Val Glu
150 155

<210> 2002
<211> 155
<212> PRT
<213> Corynebacterium glutamicum

<400> 2002
Met Pro Lys Ser Leu Thr Phe Glu Asp Ser Ile Asn Ile Ala Ala Pro
1 5 10 15

Ile Asn Gln Val Tyr Ala Leu Val Ser Asp Ile Thr Arg Thr Gly Glu
20 25 30

```
Trp Ser Pro Val Cys Glu Lys Cys Trp Trp Asp Glu Asp Glu Gly Pro
         35                  40                  45

Val Val Gly Ala His Phe Thr Gly Arg Asn Val Thr Pro Glu Arg Thr
     50                  55                  60

Trp Glu Thr Arg Ser Glu Val Ile Val Ala Glu Pro Asn Arg Cys Phe
 65                  70                  75                  80

Gly Trp Ser Val Thr Asp Gly Asn Val Lys Trp Ile Tyr Ser Met Glu
                 85                  90                  95

Pro Leu Glu Glu Gly Thr Val Leu Thr Glu Ser Trp Glu Phe Thr Pro
            100                 105                 110

Lys Gly Gln Arg Phe Phe His Asp Lys Phe Gly Asp Lys Ser Ile Glu
        115                 120                 125

Glu Ile Glu Lys Arg Arg Leu Ala Ala Ile Thr Gly Ile Pro Glu Thr
    130                 135                 140

Leu Val Ala Ile Gln Arg Ile Leu Glu Val Glu
145                 150                 155


<210> 2003
<211> 546
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(523)
<223> RXA00988

<400> 2003
tagcagaaga caccgatgta cagtccggat caggtgttgt gatcaccggt tcaatcgtga 60

ccgccggcga tgcgcgcacg ctgtttggaa aggaacctgc atg agc aag cgt gaa   115
                                              Met Ser Lys Arg Glu
                                                1               5

gaa tca att gag tac gga cca tta ggc aaa ggc cac gat cca tta aag   163
Glu Ser Ile Glu Tyr Gly Pro Leu Gly Lys Gly His Asp Pro Leu Lys
                10                  15                  20

gat ccc atg aag ggt atc cga ggt gtc atg gcc ggc acc tta gtg atg   211
Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala Gly Thr Leu Val Met
            25                  30                  35

gaa gca atc acc tta ggt ctt gtt ctc acc gtg att ctg cgc gtg gac   259
Glu Ala Ile Thr Leu Gly Leu Val Leu Thr Val Ile Leu Arg Val Asp
        40                  45                  50

gac ggc atc tac tgg acc acc ttc aac tgg gtc tat gta tca gca gtc   307
Asp Gly Ile Tyr Trp Thr Thr Phe Asn Trp Val Tyr Val Ser Ala Val
    55                  60                  65

gcg atc gca cac ttt gtt gct gca ttt ctg caa agg ttt agt tgg tcc   355
Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln Arg Phe Ser Trp Ser
70                  75                  80                  85
```

```
atc ccg atg aac atc gtg ctg cag gtt ctt gca ctt gcc ggt ttc ttt   403
Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala Leu Ala Gly Phe Phe
                 90                  95                 100

gtt cac ccc gcg atg ggc ttc gcc gcc atc atc ttc atc atc gcg tgg   451
Val His Pro Ala Met Gly Phe Ala Ala Ile Ile Phe Ile Ile Ala Trp
            105                 110                 115

gcg tac ctg ttc tac ctg cgc tct aat ctg att gat cgc atg aaa cgc   499
Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile Asp Arg Met Lys Arg
        120                 125                 130

ggg ctg ctt acc acg cag cac agc taagctttaa ggccctccgg ggc         546
Gly Leu Leu Thr Thr Gln His Ser
    135                 140
```

<210> 2004
<211> 141
<212> PRT
<213> Corynebacterium glutamicum

<400> 2004

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Met Ser Lys Arg Glu Glu Ser Ile Glu Tyr Gly Pro Leu Gly Lys Gly
  1               5                  10                  15

His Asp Pro Leu Lys Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala
             20                  25                  30

Gly Thr Leu Val Met Glu Ala Ile Thr Leu Gly Leu Val Leu Thr Val
         35                  40                  45

Ile Leu Arg Val Asp Asp Gly Ile Tyr Trp Thr Thr Phe Asn Trp Val
     50                  55                  60

Tyr Val Ser Ala Val Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln
 65                  70                  75                  80

Arg Phe Ser Trp Ser Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala
                 85                  90                  95

Leu Ala Gly Phe Phe Val His Pro Ala Met Gly Phe Ala Ala Ile Ile
            100                 105                 110

Phe Ile Ile Ala Trp Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile
        115                 120                 125

Asp Arg Met Lys Arg Gly Leu Leu Thr Thr Gln His Ser
    130                 135                 140
```

<210> 2005
<211> 969
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(946)
<223> RXA01005

<400> 2005
tgggcaccgt caacgattgg actcacgaaa gctccgacga ctagaaatag taactgtgtt 60

ggacactttt cacctccgcg tattgagcga ggatgagtgg atg gaa cta gcc cgc 115
Met Glu Leu Ala Arg
1 5

gcc cac cac gcg cgg gct gat tca ttc acc aaa gac cac ttg aag cgt 163
Ala His His Ala Arg Ala Asp Ser Phe Thr Lys Asp His Leu Lys Arg
10 15 20

cga caa gcg cat atc aag cac ccc gtc ttc gac ttc ctc ttc gag tac 211
Arg Gln Ala His Ile Lys His Pro Val Phe Asp Phe Leu Phe Glu Tyr
25 30 35

tac ccc gtg cgc gtc gcg cac cta aaa acc tgg cac ccc ggc atc ggc 259
Tyr Pro Val Arg Val Ala His Leu Lys Thr Trp His Pro Gly Ile Gly
40 45 50

gtg ttt cta gaa ggc aca ccg ccg cat gcc acc atg cgc gat ttt ttg 307
Val Phe Leu Glu Gly Thr Pro Pro His Ala Thr Met Arg Asp Phe Leu
55 60 65

ctt gtc gac gcc tcc ctc cat cac gca gcc ggc gtc cag ctt gac ctg 355
Leu Val Asp Ala Ser Leu His His Ala Ala Gly Val Gln Leu Asp Leu
70 75 80 85

gcc tcc tat atg caa cgc cgt ggg tcc tct gtg cgc tac atc cac gaa 403
Ala Ser Tyr Met Gln Arg Arg Gly Ser Ser Val Arg Tyr Ile His Glu
90 95 100

ctg ttg tcc gcc acc cgc gac aac cac gcc caa ttt gat tgt ttt ggt 451
Leu Leu Ser Ala Thr Arg Asp Asn His Ala Gln Phe Asp Cys Phe Gly
105 110 115

ctg cac gaa tgg gca atg gtg tac aaa tca aac gat ctc cgc cat gac 499
Leu His Glu Trp Ala Met Val Tyr Lys Ser Asn Asp Leu Arg His Asp
120 125 130

ctt ccc ctg cgc ctt acc cca tcg gaa acc gac cgt gtg gtg gaa agc 547
Leu Pro Leu Arg Leu Thr Pro Ser Glu Thr Asp Arg Val Val Glu Ser
135 140 145

cac aac atc aaa tgc acc cac ttt gat gcc tac cga ttc ttc acc aca 595
His Asn Ile Lys Cys Thr His Phe Asp Ala Tyr Arg Phe Phe Thr Thr
150 155 160 165

cca gcc atc ccg ttg aac ctc acg gtg tta acc cgc gaa gat cag cca 643
Pro Ala Ile Pro Leu Asn Leu Thr Val Leu Thr Arg Glu Asp Gln Pro
170 175 180

cgc aac gat caa tgt ggt tgt ctg cat gcc acg atg gat cta tac aaa 691
Arg Asn Asp Gln Cys Gly Cys Leu His Ala Thr Met Asp Leu Tyr Lys
185 190 195

tgg tcc gca aag ctt ggc cct ctt gtg cca ggt gat ctt ttc ttg gac 739
Trp Ser Ala Lys Leu Gly Pro Leu Val Pro Gly Asp Leu Phe Leu Asp
200 205 210

gcg ttt gaa cta gcc cgc gac acc cgc atc ttg gac atg gag gct tcg 787

```
Ala Phe Glu Leu Ala Arg Asp Thr Arg Ile Leu Asp Met Glu Ala Ser
    215                 220                 225

cct tac gac gtc cgc gga tac ggc ttt ggc tac gtc ccc att gag acc   835
Pro Tyr Asp Val Arg Gly Tyr Gly Phe Gly Tyr Val Pro Ile Glu Thr
230                 235                 240                 245

gcc gag ggc aaa gcc gaa tat gtc agt aga caa cgc gag ctg tct gaa   883
Ala Glu Gly Lys Ala Glu Tyr Val Ser Arg Gln Arg Glu Leu Ser Glu
                250                 255                 260

cga gca aaa ccc atc cgt gac cgg ctt gtc tcc att act aaa caa gct   931
Arg Ala Lys Pro Ile Arg Asp Arg Leu Val Ser Ile Thr Lys Gln Ala
            265                 270                 275

cta cag gct agt att tagaaaatta gacttgtcaa tgt                    969
Leu Gln Ala Ser Ile
        280
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<210> 2006
<211> 282
<212> PRT
<213> Corynebacterium glutamicum

<400> 2006

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Met Glu Leu Ala Arg Ala His His Ala Arg Ala Asp Ser Phe Thr Lys
  1               5                  10                  15

Asp His Leu Lys Arg Arg Gln Ala His Ile Lys His Pro Val Phe Asp
             20                  25                  30

Phe Leu Phe Glu Tyr Tyr Pro Val Arg Val Ala His Leu Lys Thr Trp
         35                  40                  45

His Pro Gly Ile Gly Val Phe Leu Glu Gly Thr Pro Pro His Ala Thr
     50                  55                  60

Met Arg Asp Phe Leu Leu Val Asp Ala Ser Leu His His Ala Ala Gly
 65                  70                  75                  80

Val Gln Leu Asp Leu Ala Ser Tyr Met Gln Arg Arg Gly Ser Ser Val
                 85                  90                  95

Arg Tyr Ile His Glu Leu Leu Ser Ala Thr Arg Asp Asn His Ala Gln
            100                 105                 110

Phe Asp Cys Phe Gly Leu His Glu Trp Ala Met Val Tyr Lys Ser Asn
        115                 120                 125

Asp Leu Arg His Asp Leu Pro Leu Arg Leu Thr Pro Ser Glu Thr Asp
    130                 135                 140

Arg Val Val Glu Ser His Asn Ile Lys Cys Thr His Phe Asp Ala Tyr
145                 150                 155                 160

Arg Phe Phe Thr Thr Pro Ala Ile Pro Leu Asn Leu Thr Val Leu Thr
                165                 170                 175

Arg Glu Asp Gln Pro Arg Asn Asp Gln Cys Gly Cys Leu His Ala Thr
            180                 185                 190
```

```
Met Asp Leu Tyr Lys Trp Ser Ala Lys Leu Gly Pro Leu Val Pro Gly
        195                 200                 205

Asp Leu Phe Leu Asp Ala Phe Glu Leu Ala Arg Asp Thr Arg Ile Leu
    210                 215                 220

Asp Met Glu Ala Ser Pro Tyr Asp Val Arg Gly Tyr Gly Phe Gly Tyr
225                 230                 235                 240

Val Pro Ile Glu Thr Ala Glu Gly Lys Ala Glu Tyr Val Ser Arg Gln
                245                 250                 255

Arg Glu Leu Ser Glu Arg Ala Lys Pro Ile Arg Asp Arg Leu Val Ser
            260                 265                 270

Ile Thr Lys Gln Ala Leu Gln Ala Ser Ile
        275                 280


<210> 2007
<211> 1830
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1807)
<223> RXA01007

<400> 2007
tctgaaccaa tataccgatc agtctaaaag tgtgttaagt tctggaacat aaattagctg 60

acacgtaaag taacttaaag attcactgga ggtaagccta gtg ttt aaa aag cac   115
                                            Val Phe Lys Lys His
                                              1               5

aga cac ggt ctc ggc tcc ccc gaa acc aaa cca cgc tca ata acc cgc   163
Arg His Gly Leu Gly Ser Pro Glu Thr Lys Pro Arg Ser Ile Thr Arg
                10                  15                  20

cgg ttt ttc acc gcg gcc gcc gct acg ctg gca gga ttg gca gtc ctg   211
Arg Phe Phe Thr Ala Ala Ala Ala Thr Leu Ala Gly Leu Ala Val Leu
            25                  30                  35

tcc ggc tgc aca gca caa ccc tca caa gca gaa gac aac acg ctc act   259
Ser Gly Cys Thr Ala Gln Pro Ser Gln Ala Glu Asp Asn Thr Leu Thr
        40                  45                  50

tac tta gag cca cag ttc ttc cgc acc ctg tac cca cca tca gcg ggc   307
Tyr Leu Glu Pro Gln Phe Phe Arg Thr Leu Tyr Pro Pro Ser Ala Gly
    55                  60                  65

ttt tac ccc aac ggc agt gtg gtg aac aac att gca gac cgc ttg ctc   355
Phe Tyr Pro Asn Gly Ser Val Val Asn Asn Ile Ala Asp Arg Leu Leu
70                  75                  80                  85

tac cag gat cct gaa acc ttg gaa ctc aag ccg tgg atc gcc acc gaa   403
Tyr Gln Asp Pro Glu Thr Leu Glu Leu Lys Pro Trp Ile Ala Thr Glu
                90                  95                  100
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ctc cca gaa gta aac gaa gac gcc acg gaa ttt acc ttc aac atc cgc   451
Leu Pro Glu Val Asn Glu Asp Ala Thr Glu Phe Thr Phe Asn Ile Arg
            105                 110                 115

acc gat gtc acc tac tcc gat ggc acc ccg ctg acg gct gaa aac gtg   499
Thr Asp Val Thr Tyr Ser Asp Gly Thr Pro Leu Thr Ala Glu Asn Val
        120                 125                 130

gtg aaa aac ttc gat ctc tat ggc ctc ggc gat caa gat cga cgc ctc   547
Val Lys Asn Phe Asp Leu Tyr Gly Leu Gly Asp Gln Asp Arg Arg Leu
    135                 140                 145

acc atc tct gag cag atc acc aac tac gac cac ggc gaa gta gta gat   595
Thr Ile Ser Glu Gln Ile Thr Asn Tyr Asp His Gly Glu Val Val Asp
150                 155                 160                 165

gag gac acc gtc cga ttc cac ttc tct gag cct gca cct ggt ttt gct   643
Glu Asp Thr Val Arg Phe His Phe Ser Glu Pro Ala Pro Gly Phe Ala
                170                 175                 180

cag gcc acc agc tcc ttc aac gct ggc ctt tat gcc gat tcc acc ttg   691
Gln Ala Thr Ser Ser Phe Asn Ala Gly Leu Tyr Ala Asp Ser Thr Leu
            185                 190                 195

gag ttc gcc aat gag gat ttc gcg cca ggc aac gcc caa aac gtc atc   739
Glu Phe Ala Asn Glu Asp Phe Ala Pro Gly Asn Ala Gln Asn Val Ile
        200                 205                 210

ggc tcc ggt cct ttc gtg atc acc gat gaa acc cta ggc acc aac ctc   787
Gly Ser Gly Pro Phe Val Ile Thr Asp Glu Thr Leu Gly Thr Asn Leu
    215                 220                 225

acc ttg act gcg cgt gag gat tac gat tgg gca cca cca tca cgc gaa   835
Thr Leu Thr Ala Arg Glu Asp Tyr Asp Trp Ala Pro Pro Ser Arg Glu
230                 235                 240                 245

cat caa ggt cgc gcg aag ctt gac gcc gtc aat tat gtc ctc gcg ggt   883
His Gln Gly Arg Ala Lys Leu Asp Ala Val Asn Tyr Val Leu Ala Gly
                250                 255                 260

gaa gaa tcc gtc cgc atc gga gcc atc gtt gct ggc caa ggt gat atc   931
Glu Glu Ser Val Arg Ile Gly Ala Ile Val Ala Gly Gln Gly Asp Ile
            265                 270                 275

gcc cgc cag atc gaa gcg cca gtg gag gca cac ctg aag gat gca ggc   979
Ala Arg Gln Ile Glu Ala Pro Val Glu Ala His Leu Lys Asp Ala Gly
        280                 285                 290

atc ccg atc atc tcc gca gcc acc aac ggt gtg aac aac agc ttc aac   1027
Ile Pro Ile Ile Ser Ala Ala Thr Asn Gly Val Asn Asn Ser Phe Asn
    295                 300                 305

ttc cgc ttc aaa aac gag ctg ctc tca gac atc cgt gtt cgc caa gct   1075
Phe Arg Phe Lys Asn Glu Leu Leu Ser Asp Ile Arg Val Arg Gln Ala
310                 315                 320                 325

ctg atc cac gcg atc gac cgc gaa aag atc atg cgt gtg ctg ttt agt   1123
Leu Ile His Ala Ile Asp Arg Glu Lys Ile Met Arg Val Leu Phe Ser
                330                 335                 340

gat tcc tat ccg ctg gca act tct gtg ctt gcg caa aat gca ctg ggc   1171
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Asp Ser Tyr Pro Leu Ala Thr Ser Val Leu Ala Gln Asn Ala Leu Gly
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Tyr Lys Glu Gln Val Asp Ala Tyr Val Tyr Asp Leu Asp Lys Ala Thr
        360                 365                 370

gct ctg ctt gac gaa gcc ggc tgg acc ctt gat agc gac ggc atg cgt   1267
Ala Leu Leu Asp Glu Ala Gly Trp Thr Leu Asp Ser Asp Gly Met Arg
    375                 380                 385

cgc aag gac ggt gaa ctt cta gag ctc acc ttc aac gaa gcc ctc cca   1315
Arg Lys Asp Gly Glu Leu Leu Glu Leu Thr Phe Asn Glu Ala Leu Pro
390                 395                 400                 405

cag cct cgt tca cgc gaa gtt gtc acc atg gtc caa gaa cag ctc ggt   1363
Gln Pro Arg Ser Arg Glu Val Val Thr Met Val Gln Glu Gln Leu Gly
                410                 415                 420

gat ctg ggc atc aag gtc aac ctc aac cca ggt gac caa gca gcc cag   1411
Asp Leu Gly Ile Lys Val Asn Leu Asn Pro Gly Asp Gln Ala Ala Gln
            425                 430                 435

gac gct gac tcc aag gat ctc aac aag atc cag gtt cgc cac acc atg   1459
Asp Ala Asp Ser Lys Asp Leu Asn Lys Ile Gln Val Arg His Thr Met
        440                 445                 450

gtg ggt cgc gca gac tat gac gtg ctg aaa tcc cag ctg tac tcc acc   1507
Val Gly Arg Ala Asp Tyr Asp Val Leu Lys Ser Gln Leu Tyr Ser Thr
    455                 460                 465

aac cgc aac gag ctg ttg aac atg acc gtg gaa ggg gag acc gcc gat   1555
Asn Arg Asn Glu Leu Leu Asn Met Thr Val Glu Gly Glu Thr Ala Asp
470                 475                 480                 485

att ggc gat cct cat ttg gag gaa ctc ctc atg gct att gca tcc agc   1603
Ile Gly Asp Pro His Leu Glu Glu Leu Leu Met Ala Ile Ala Ser Ser
                490                 495                 500

cca cgc gaa gag gac cgt gca gca gca tct gcc gca gca cag gat tac   1651
Pro Arg Glu Glu Asp Arg Ala Ala Ala Ser Ala Ala Ala Gln Asp Tyr
            505                 510                 515

atc acc gag cag gca tat gtt ctt cca ctg ttt gaa gag cca gtt gtc   1699
Ile Thr Glu Gln Ala Tyr Val Leu Pro Leu Phe Glu Glu Pro Val Val
        520                 525                 530

tac ggc gtg cag cct tac gtg aag ggc ttt agc ccc gaa gtg atc ggc   1747
Tyr Gly Val Gln Pro Tyr Val Lys Gly Phe Ser Pro Glu Val Ile Gly
    535                 540                 545

cgc ccc agc ttc tat gag acc tac att gac cat tcc agc gac cat tcc   1795
Arg Pro Ser Phe Tyr Glu Thr Tyr Ile Asp His Ser Ser Asp His Ser
550                 555                 560                 565

agt gag gag gac taaatgacta cctcgcagat tct                        1830
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Do not enter new matter into this application

<210> 2008

<211> 569
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<213> Corynebacterium glutamicum

<400> 2008

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Gly Leu Ala Val Leu Ser Gly Cys Thr Ala Gln Pro Ser Gln Ala Glu
         35                  40                  45

Asp Asn Thr Leu Thr Tyr Leu Glu Pro Gln Phe Phe Arg Thr Leu Tyr
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Pro Pro Ser Ala Gly Phe Tyr Pro Asn Gly Ser Val Val Asn Asn Ile
 65                  70                  75                  80

Ala Asp Arg Leu Leu Tyr Gln Asp Pro Glu Thr Leu Glu Leu Lys Pro
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Trp Ile Ala Thr Glu Leu Pro Glu Val Asn Glu Asp Ala Thr Glu Phe
            100                 105                 110

Thr Phe Asn Ile Arg Thr Asp Val Thr Tyr Ser Asp Gly Thr Pro Leu
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Thr Ala Glu Asn Val Val Lys Asn Phe Asp Leu Tyr Gly Leu Gly Asp
    130                 135                 140

Gln Asp Arg Arg Leu Thr Ile Ser Glu Gln Ile Thr Asn Tyr Asp His
145                 150                 155                 160

Gly Glu Val Val Asp Glu Asp Thr Val Arg Phe His Phe Ser Glu Pro
                165                 170                 175

Ala Pro Gly Phe Ala Gln Ala Thr Ser Ser Phe Asn Ala Gly Leu Tyr
            180                 185                 190

Ala Asp Ser Thr Leu Glu Phe Ala Asn Glu Asp Phe Ala Pro Gly Asn
        195                 200                 205

Ala Gln Asn Val Ile Gly Ser Gly Pro Phe Val Ile Thr Asp Glu Thr
    210                 215                 220

Leu Gly Thr Asn Leu Thr Leu Thr Ala Arg Glu Asp Tyr Asp Trp Ala
225                 230                 235                 240

Pro Pro Ser Arg Glu His Gln Gly Arg Ala Lys Leu Asp Ala Val Asn
                245                 250                 255

Tyr Val Leu Ala Gly Glu Glu Ser Val Arg Ile Gly Ala Ile Val Ala
            260                 265                 270

Gly Gln Gly Asp Ile Ala Arg Gln Ile Glu Ala Pro Val Glu Ala His
        275                 280                 285

Leu Lys Asp Ala Gly Ile Pro Ile Ile Ser Ala Ala Thr Asn Gly Val
    290                 295                 300
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Asn Asn Ser Phe Asn Phe Arg Phe Lys Asn Glu Leu Leu Ser Asp Ile
305 310 315 320

Arg Val Arg Gln Ala Leu Ile His Ala Ile Asp Arg Glu Lys Ile Met
325 330 335

Arg Val Leu Phe Ser Asp Ser Tyr Pro Leu Ala Thr Ser Val Leu Ala
340 345 350

Gln Asn Ala Leu Gly Tyr Lys Glu Gln Val Asp Ala Tyr Val Tyr Asp
355 360 365

Leu Asp Lys Ala Thr Ala Leu Leu Asp Glu Ala Gly Trp Thr Leu Asp
370 375 380

Ser Asp Gly Met Arg Arg Lys Asp Gly Glu Leu Leu Glu Leu Thr Phe
385 390 395 400

Asn Glu Ala Leu Pro Gln Pro Arg Ser Arg Glu Val Val Thr Met Val
405 410 415

Gln Glu Gln Leu Gly Asp Leu Gly Ile Lys Val Asn Leu Asn Pro Gly
420 425 430

Asp Gln Ala Ala Gln Asp Ala Asp Ser Lys Asp Leu Asn Lys Ile Gln
435 440 445

Val Arg His Thr Met Val Gly Arg Ala Asp Tyr Asp Val Leu Lys Ser
450 455 460

Gln Leu Tyr Ser Thr Asn Arg Asn Glu Leu Leu Asn Met Thr Val Glu
465 470 475 480

Gly Glu Thr Ala Asp Ile Gly Asp Pro His Leu Glu Glu Leu Leu Met
485 490 495

Ala Ile Ala Ser Ser Pro Arg Glu Glu Asp Arg Ala Ala Ala Ser Ala
500 505 510

Ala Ala Gln Asp Tyr Ile Thr Glu Gln Ala Tyr Val Leu Pro Leu Phe
515 520 525

Glu Glu Pro Val Val Tyr Gly Val Gln Pro Tyr Val Lys Gly Phe Ser
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Pro Glu Val Ile Gly Arg Pro Ser Phe Tyr Glu Thr Tyr Ile Asp His
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Ser Ser Asp His Ser Ser Glu Glu Asp
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<223> RXA01008

<400> 2009

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                                            Val Ser Thr Thr Asp
                                              1               5

aag cag gta gcc atc gtt gga gtt ggc ccc aga ggt att tcc ata ctc   163
Lys Gln Val Ala Ile Val Gly Val Gly Pro Arg Gly Ile Ser Ile Leu
                 10                  15                  20

gaa agg atc gca gca gct ctc aac aca gtt tcc cgc ccc aaa caa ggc   211
Glu Arg Ile Ala Ala Ala Leu Asn Thr Val Ser Arg Pro Lys Gln Gly
             25                  30                  35

ttg acc atc cac ctg att gag gat gcc cag atg ggt gca ggc aac gtg   259
Leu Thr Ile His Leu Ile Glu Asp Ala Gln Met Gly Ala Gly Asn Val
         40                  45                  50

tgg cgc act gat caa acc cgc acg ctg tgc atg aat act ctg gcc ggt   307
Trp Arg Thr Asp Gln Thr Arg Thr Leu Cys Met Asn Thr Leu Ala Gly
     55                  60                  65

gcg gtg aca tta ttc aca gag cca ggc tct acg gtg agc gct cca gtg   355
Ala Val Thr Leu Phe Thr Glu Pro Gly Ser Thr Val Ser Ala Pro Val
 70                  75                  80                  85

gtg gaa gga cca ctg caa ttt gat tgg att cgc ctg ctg cgc ggc gat   403
Val Glu Gly Pro Leu Gln Phe Asp Trp Ile Arg Leu Leu Arg Gly Asp
                 90                  95                 100

gag gat ttg agc ggc att cct aca aaa gcc atc gag ctg ttc cgc acc   451
Glu Asp Leu Ser Gly Ile Pro Thr Lys Ala Ile Glu Leu Phe Arg Thr
             105                 110                 115

tac ccc cca gct gca tcc gtg gcg gag gat ttc aag gaa gag cta gca   499
Tyr Pro Pro Ala Ala Ser Val Ala Glu Asp Phe Lys Glu Glu Leu Ala
         120                 125                 130

gcc act gtt atc cag tcc aat cct tcc cgt gct ctt tat ggc gca tat   547
Ala Thr Val Ile Gln Ser Asn Pro Ser Arg Ala Leu Tyr Gly Ala Tyr
     135                 140                 145

ctg cgg tgg gct ttc gat gtc gct ttg cag ctg ttg cca cag tgg gtc   595
Leu Arg Trp Ala Phe Asp Val Ala Leu Gln Leu Leu Pro Gln Trp Val
150                 155                 160                 165

aag gtc gag cag cac cat gcg cgc gcg att ggc atc cgc gaa gat ggt   643
Lys Val Glu Gln His His Ala Arg Ala Ile Gly Ile Arg Glu Asp Gly
                170                 175                 180

gac cgc gat gtg atc acc tta gat aat tct gag atg att tcc gcc gat   691
Asp Arg Asp Val Ile Thr Leu Asp Asn Ser Glu Met Ile Ser Ala Asp
            185                 190                 195

tcc act gtg ttg gct gtc ggc tgg caa acc ccc gcc ccc aat gcg gag   739
Ser Thr Val Leu Ala Val Gly Trp Gln Thr Pro Ala Pro Asn Ala Glu
        200                 205                 210
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gag ctg tcc atc gcg gct gct ttg gag gag aac cct gat ctg gtg tgg   787
Glu Leu Ser Ile Ala Ala Ala Leu Glu Glu Asn Pro Asp Leu Val Trp
    215                 220                 225

gtc aag ccc ggc aac cct gtc gag cag gat gcc agc ctc att ccc gct   835
Val Lys Pro Gly Asn Pro Val Glu Gln Asp Ala Ser Leu Ile Pro Ala
230                 235                 240                 245

ggc gaa cag gtg ctt gtc cgc ggg ctg ggc atg gga ttt ttc gat atc   883
Gly Glu Gln Val Leu Val Arg Gly Leu Gly Met Gly Phe Phe Asp Ile
                250                 255                 260

atg gcg ctg acc acc atc gat cgt ggc ggc atc ttc cac gag gat ccc   931
Met Ala Leu Thr Thr Ile Asp Arg Gly Gly Ile Phe His Glu Asp Pro
            265                 270                 275

agc acc cgt tcc ggt ttg cgc tac gag gca tct ggt gag gaa cca cac   979
Ser Thr Arg Ser Gly Leu Arg Tyr Glu Ala Ser Gly Glu Glu Pro His
        280                 285                 290

ttt gtt att tcc tcc ggg cgc ggc tac ccc tac ctg cct aaa tcc gat  1027
Phe Val Ile Ser Ser Gly Arg Gly Tyr Pro Tyr Leu Pro Lys Ser Asp
    295                 300                 305

tac aaa tcg ctg cca cca ggg gca aag cta gcg cga ctc aag gct gtt  1075
Tyr Lys Ser Leu Pro Pro Gly Ala Lys Leu Ala Arg Leu Lys Ala Val
310                 315                 320                 325

atc gcg gcg atc aac gcg caa aat cgt ggt gtc gca tcc atc aac tat  1123
Ile Ala Ala Ile Asn Ala Gln Asn Arg Gly Val Ala Ser Ile Asn Tyr
                330                 335                 340

gat gcg gaa gtg tgg cca gct gtt gct cgc gac gcc tac gaa gcc tat  1171
Asp Ala Glu Val Trp Pro Ala Val Ala Arg Asp Ala Tyr Glu Ala Tyr
            345                 350                 355

tac gaa acc ctt gat cgc gta agc cca gaa tct atc cgg acc ggt ctg  1219
Tyr Glu Thr Leu Asp Arg Val Ser Pro Glu Ser Ile Arg Thr Gly Leu
        360                 365                 370

gat aaa att gtg gaa att att gat gag gtg gac gtc gat aag ctt cct  1267
Asp Lys Ile Val Glu Ile Ile Asp Glu Val Asp Val Asp Lys Leu Pro
    375                 380                 385

aaa gca ctc gcc gcg cac acc gat gac gtc ttt gac ctg cat gct tgg  1315
Lys Ala Leu Ala Ala His Thr Asp Asp Val Phe Asp Leu His Ala Trp
390                 395                 400                 405

gaa ttt ccg ctc gcg gga att aat gaa agc gtc gag gcg ctg acc gca  1363
Glu Phe Pro Leu Ala Gly Ile Asn Glu Ser Val Glu Ala Leu Thr Ala
                410                 415                 420

cgc atc gcg gac ggc atg gcc cgc gat att cgc cat gca gta acg gcc  1411
Arg Ile Ala Asp Gly Met Ala Arg Asp Ile Arg His Ala Val Thr Ala
            425                 430                 435

tgg gac agc ccg ctg aaa tcc gcg ctg tgg tcc att tcc gcc gcg cgc  1459
Trp Asp Ser Pro Leu Lys Ser Ala Leu Trp Ser Ile Ser Ala Ala Arg
        440                 445                 450

aaa ccc agc tcc atc ctg ggc gcg gaa ggc cgc ctg acc ttc gaa tcg  1507
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Lys Pro Ser Ser Ile Leu Gly Ala Glu Gly Arg Leu Thr Phe Glu Ser
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cgc cgc aac cgc ttc gcc gcc gtc atg gcg atc ggc cag atg gtc ggc   1555
Arg Arg Asn Arg Phe Ala Ala Val Met Ala Ile Gly Gln Met Val Gly
470                 475                 480                 485

tcc ggc cca ccg ctt ttc cgc acc cgc gaa ctt ctt gcg ctt gtc gac   1603
Ser Gly Pro Pro Leu Phe Arg Thr Arg Glu Leu Leu Ala Leu Val Asp
                490                 495                 500

gcc ggc ctc gct cac ttc gcc ggc gcc cgc ccc cgc ctc agc gtg agc   1651
Ala Gly Leu Ala His Phe Ala Gly Ala Arg Pro Arg Leu Ser Val Ser
            505                 510                 515

gac ggt caa tgg cag atc tcc tcg ccc acc acc ggc gat acg ccg ctg   1699
Asp Gly Gln Trp Gln Ile Ser Ser Pro Thr Thr Gly Asp Thr Pro Leu
        520                 525                 530

aga tcg aaa gtg ctt gtc gac gcg tgg atg cac aac cca gat gtg cgt   1747
Arg Ser Lys Val Leu Val Asp Ala Trp Met His Asn Pro Asp Val Arg
    535                 540                 545

cgc aac gcc gac ccg cta gca ctg tct ttg gaa gat gcc gac cgg gta   1795
Arg Asn Ala Asp Pro Leu Ala Leu Ser Leu Glu Asp Ala Asp Arg Val
550                 555                 560                 565

cgc ccc ttc aac gac tat tcc gtc gac gga acc gct gcc ccc aca ggc   1843
Arg Pro Phe Asn Asp Tyr Ser Val Asp Gly Thr Ala Ala Pro Thr Gly
                570                 575                 580

tcc ccc gaa gtt gat ccg gca acc cga ctt ttg gtt cac ccc aac ggc   1891
Ser Pro Glu Val Asp Pro Ala Thr Arg Leu Leu Val His Pro Asn Gly
            585                 590                 595

aac ctc gat ccg cgc gtg cac ctg att ggc atc cca acc tat ggg cag   1939
Asn Leu Asp Pro Arg Val His Leu Ile Gly Ile Pro Thr Tyr Gly Gln
        600                 605                 610

ctg gcc gac acc acc atc tcg ccg atg cct gga acc aac ccg ctc atg   1987
Leu Ala Asp Thr Thr Ile Ser Pro Met Pro Gly Thr Asn Pro Leu Met
    615                 620                 625

ctg caa gaa acc gac aaa aca gcc gtt cac gtg cta aag cag ctc ggc   2035
Leu Gln Glu Thr Asp Lys Thr Ala Val His Val Leu Lys Gln Leu Gly
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ttg atc tagggtgagg tgagttattt aaa                                2064
Leu Ile
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<210> 2010
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Gly Ala Gly Asn Val Trp Arg Thr Asp Gln Thr Arg Thr Leu Cys Met
    50                  55                  60

Asn Thr Leu Ala Gly Ala Val Thr Leu Phe Thr Glu Pro Gly Ser Thr
65                  70                  75                  80

Val Ser Ala Pro Val Val Glu Gly Pro Leu Gln Phe Asp Trp Ile Arg
                85                  90                  95

Leu Leu Arg Gly Asp Glu Asp Leu Ser Gly Ile Pro Thr Lys Ala Ile
            100                 105                 110

Glu Leu Phe Arg Thr Tyr Pro Pro Ala Ala Ser Val Ala Glu Asp Phe
        115                 120                 125

Lys Glu Glu Leu Ala Ala Thr Val Ile Gln Ser Asn Pro Ser Arg Ala
    130                 135                 140

Leu Tyr Gly Ala Tyr Leu Arg Trp Ala Phe Asp Val Ala Leu Gln Leu
145                 150                 155                 160

Leu Pro Gln Trp Val Lys Val Glu Gln His His Ala Arg Ala Ile Gly
                165                 170                 175

Ile Arg Glu Asp Gly Asp Arg Asp Val Ile Thr Leu Asp Asn Ser Glu
            180                 185                 190

Met Ile Ser Ala Asp Ser Thr Val Leu Ala Val Gly Trp Gln Thr Pro
        195                 200                 205

Ala Pro Asn Ala Glu Glu Leu Ser Ile Ala Ala Ala Leu Glu Glu Asn
    210                 215                 220

Pro Asp Leu Val Trp Val Lys Pro Gly Asn Pro Val Glu Gln Asp Ala
225                 230                 235                 240

Ser Leu Ile Pro Ala Gly Glu Gln Val Leu Val Arg Gly Leu Gly Met
                245                 250                 255

Gly Phe Phe Asp Ile Met Ala Leu Thr Thr Ile Asp Arg Gly Gly Ile
            260                 265                 270

Phe His Glu Asp Pro Ser Thr Arg Ser Gly Leu Arg Tyr Glu Ala Ser
        275                 280                 285

Gly Glu Glu Pro His Phe Val Ile Ser Ser Gly Arg Gly Tyr Pro Tyr
    290                 295                 300

Leu Pro Lys Ser Asp Tyr Lys Ser Leu Pro Pro Gly Ala Lys Leu Ala
305                 310                 315                 320

Arg Leu Lys Ala Val Ile Ala Ala Ile Asn Ala Gln Asn Arg Gly Val
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Ala Ser Ile Asn Tyr Asp Ala Glu Val Trp Pro Ala Val Ala Arg Asp
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            340                 345                 350

Ala Tyr Glu Ala Tyr Tyr Glu Thr Leu Asp Arg Val Ser Pro Glu Ser
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Val Asp Lys Leu Pro Lys Ala Leu Ala Ala His Thr Asp Asp Val Phe
385                 390                 395                 400

Asp Leu His Ala Trp Glu Phe Pro Leu Ala Gly Ile Asn Glu Ser Val
                405                 410                 415

Glu Ala Leu Thr Ala Arg Ile Ala Asp Gly Met Ala Arg Asp Ile Arg
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His Ala Val Thr Ala Trp Asp Ser Pro Leu Lys Ser Ala Leu Trp Ser
        435                 440                 445

Ile Ser Ala Ala Arg Lys Pro Ser Ser Ile Leu Gly Ala Glu Gly Arg
    450                 455                 460

Leu Thr Phe Glu Ser Arg Arg Asn Arg Phe Ala Ala Val Met Ala Ile
465                 470                 475                 480

Gly Gln Met Val Gly Ser Gly Pro Pro Leu Phe Arg Thr Arg Glu Leu
                485                 490                 495

Leu Ala Leu Val Asp Ala Gly Leu Ala His Phe Ala Gly Ala Arg Pro
            500                 505                 510

Arg Leu Ser Val Ser Asp Gly Gln Trp Gln Ile Ser Ser Pro Thr Thr
        515                 520                 525

Gly Asp Thr Pro Leu Arg Ser Lys Val Leu Val Asp Ala Trp Met His
    530                 535                 540

Asn Pro Asp Val Arg Arg Asn Ala Asp Pro Leu Ala Leu Ser Leu Glu
545                 550                 555                 560

Asp Ala Asp Arg Val Arg Pro Phe Asn Asp Tyr Ser Val Asp Gly Thr
                565                 570                 575

Ala Ala Pro Thr Gly Ser Pro Glu Val Asp Pro Ala Thr Arg Leu Leu
            580                 585                 590

Val His Pro Asn Gly Asn Leu Asp Pro Arg Val His Leu Ile Gly Ile
        595                 600                 605

Pro Thr Tyr Gly Gln Leu Ala Asp Thr Thr Ile Ser Pro Met Pro Gly
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Leu Lys Gln Leu Gly Leu Ile
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<223> RXA01011

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Met Ser Asp Leu Ile
1 5

gac atg ctg gtt gga gaa gac ctc cca cag ctg cgt gac aac cgt ccc 163
Asp Met Leu Val Gly Glu Asp Leu Pro Gln Leu Arg Asp Asn Arg Pro
10 15 20

caa gct cgc gac aat gca caa aag agc ttc gaa gct ctg ctc gaa ccg 211
Gln Ala Arg Asp Asn Ala Gln Lys Ser Phe Glu Ala Leu Leu Glu Pro
25 30 35

gtc aac cca gga acc ttc agc ttc ggc gag cgt tac gcc gtg gcc acc 259
Val Asn Pro Gly Thr Phe Ser Phe Gly Glu Arg Tyr Ala Val Ala Thr
40 45 50

tat gtt gca ggt ttg cac caa ttc gcg cca gct gta gat ctc tac caa 307
Tyr Val Ala Gly Leu His Gln Phe Ala Pro Ala Val Asp Leu Tyr Gln
55 60 65

gat ttg ctt ctc gac gac gcc cca acc acc ctg gca aac gcc gtc tcc 355
Asp Leu Leu Leu Asp Asp Ala Pro Thr Thr Leu Ala Asn Ala Val Ser
70 75 80 85

gat gcc atc gac gag ggc cta tcc gca ggc cca tac ggc acc tac cgt 403
Asp Ala Ile Asp Glu Gly Leu Ser Ala Gly Pro Tyr Gly Thr Tyr Arg
90 95 100

gaa cct gga ctt gag tcc gaa tca gag cca ggc gga tct gtg cgc aac 451
Glu Pro Gly Leu Glu Ser Glu Ser Glu Pro Gly Gly Ser Val Arg Asn
105 110 115

gat gcc gcc aag ctt ggc gag cga ctt gca gca gca ttt gat tac gca 499
Asp Ala Ala Lys Leu Gly Glu Arg Leu Ala Ala Ala Phe Asp Tyr Ala
120 125 130

cac cta cta gtt ttc cac ccc cgt gat tcc cgc ccc gag gtc ctt ggt 547
His Leu Leu Val Phe His Pro Arg Asp Ser Arg Pro Glu Val Leu Gly
135 140 145

cga ctc tcc ggc gct ggc tgg agc gcg gat gac acc gtg aca ttg gct 595
Arg Leu Ser Gly Ala Gly Trp Ser Ala Asp Asp Thr Val Thr Leu Ala
150 155 160 165

cag ctg gtg tcg ttc ctg gca ttc cag ctg cgt gtt gcc tac ggc ctg 643
Gln Leu Val Ser Phe Leu Ala Phe Gln Leu Arg Val Ala Tyr Gly Leu
170 175 180

cgc acc ctc aaa ggt gaa gac att cag gtg aaa gct cct cgc ctg agt 691

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Arg Thr Leu Lys Gly Glu Asp Ile Gln Val Lys Ala Pro Arg Leu Ser
            185                 190                 195

att cct gaa gcg aag tgg gaa ctg tcc aac aac ggc ttt gag atc tcc   739
Ile Pro Glu Ala Lys Trp Glu Leu Ser Asn Asn Gly Phe Glu Ile Ser
        200                 205                 210

acc tat gaa gaa ctc aac cgc cct gaa gcg ttt gtg aac cac tct ttg   787
Thr Tyr Glu Glu Leu Asn Arg Pro Glu Ala Phe Val Asn His Ser Leu
    215                 220                 225

ggc tgg aag cca tgg gta cca cca gta gca aag gca gat ctc acc gaa   835
Gly Trp Lys Pro Trp Val Pro Pro Val Ala Lys Ala Asp Leu Thr Glu
230                 235                 240                 245

gaa cag ctg gat tct ttg atc cag cct gag cgc gct gat atg cca tac   883
Glu Gln Leu Asp Ser Leu Ile Gln Pro Glu Arg Ala Asp Met Pro Tyr
                250                 255                 260

ttc cgt ctc ttg gca cgc gat cct gca gca ttg aag gcg cgt acc ctg   931
Phe Arg Leu Leu Ala Arg Asp Pro Ala Ala Leu Lys Ala Arg Thr Leu
            265                 270                 275

acc gat ctg gat atc ttc ttc aac act gac ggc gaa ggc cta gga cgt   979
Thr Asp Leu Asp Ile Phe Phe Asn Thr Asp Gly Glu Gly Leu Gly Arg
        280                 285                 290

gca gag cgt gaa ctc ggc gcc acc gtt act tcc cgc tac aac ggc tgc  1027
Ala Glu Arg Glu Leu Gly Ala Thr Val Thr Ser Arg Tyr Asn Gly Cys
    295                 300                 305

gtg tac tgc gca tcc gtg cac gca gga cgt gct cag gaa gaa tcc ggt  1075
Val Tyr Cys Ala Ser Val His Ala Gly Arg Ala Gln Glu Glu Ser Gly
310                 315                 320                 325

cga gct gat gat gtc aac gca ctg ttg gca agc atc gac tcc gat ctg  1123
Arg Ala Asp Asp Val Asn Ala Leu Leu Ala Ser Ile Asp Ser Asp Leu
                330                 335                 340

ggt tct gac cag tgg aat gtc atc cgt gac gct gct cgc gca ctg agc  1171
Gly Ser Asp Gln Trp Asn Val Ile Arg Asp Ala Ala Arg Ala Leu Ser
            345                 350                 355

tcc acc cct gct gct ttc aac cag gga tgc atc acc aag ctg cgt ggc  1219
Ser Thr Pro Ala Ala Phe Asn Gln Gly Cys Ile Thr Lys Leu Arg Gly
        360                 365                 370

gtt gga ttc agc gac ctg cag atc gtg gac ttg atc aac tct gtg gcg  1267
Val Gly Phe Ser Asp Leu Gln Ile Val Asp Leu Ile Asn Ser Val Ala
    375                 380                 385

ttc ttc aac tgg gcg aac cgc ctg atg ttg tca ctg ggt gaa ccc gaa  1315
Phe Phe Asn Trp Ala Asn Arg Leu Met Leu Ser Leu Gly Glu Pro Glu
390                 395                 400                 405

gtg cca aag cgt ttc ctg taaaacgcat aaccccgaat acc                1356
Val Pro Lys Arg Phe Leu
                410
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<210> 2012

<211> 411
<212> PRT
<213> Corynebacterium glutamicum

<400> 2012

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Met Ser Asp Leu Ile Asp Met Leu Val Gly Glu Asp Leu Pro Gln Leu
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Arg Asp Asn Arg Pro Gln Ala Arg Asp Asn Ala Gln Lys Ser Phe Glu
             20                  25                  30

Ala Leu Leu Glu Pro Val Asn Pro Gly Thr Phe Ser Phe Gly Glu Arg
         35                  40                  45

Tyr Ala Val Ala Thr Tyr Val Ala Gly Leu His Gln Phe Ala Pro Ala
     50                  55                  60

Val Asp Leu Tyr Gln Asp Leu Leu Leu Asp Asp Ala Pro Thr Thr Leu
 65                  70                  75                  80

Ala Asn Ala Val Ser Asp Ala Ile Asp Glu Gly Leu Ser Ala Gly Pro
                 85                  90                  95

Tyr Gly Thr Tyr Arg Glu Pro Gly Leu Glu Ser Glu Ser Glu Pro Gly
            100                 105                 110

Gly Ser Val Arg Asn Asp Ala Ala Lys Leu Gly Glu Arg Leu Ala Ala
        115                 120                 125

Ala Phe Asp Tyr Ala His Leu Leu Val Phe His Pro Arg Asp Ser Arg
    130                 135                 140

Pro Glu Val Leu Gly Arg Leu Ser Gly Ala Gly Trp Ser Ala Asp Asp
145                 150                 155                 160

Thr Val Thr Leu Ala Gln Leu Val Ser Phe Leu Ala Phe Gln Leu Arg
                165                 170                 175

Val Ala Tyr Gly Leu Arg Thr Leu Lys Gly Glu Asp Ile Gln Val Lys
            180                 185                 190

Ala Pro Arg Leu Ser Ile Pro Glu Ala Lys Trp Glu Leu Ser Asn Asn
        195                 200                 205

Gly Phe Glu Ile Ser Thr Tyr Glu Glu Leu Asn Arg Pro Glu Ala Phe
    210                 215                 220

Val Asn His Ser Leu Gly Trp Lys Pro Trp Val Pro Pro Val Ala Lys
225                 230                 235                 240

Ala Asp Leu Thr Glu Glu Gln Leu Asp Ser Leu Ile Gln Pro Glu Arg
                245                 250                 255

Ala Asp Met Pro Tyr Phe Arg Leu Leu Ala Arg Asp Pro Ala Ala Leu
            260                 265                 270

Lys Ala Arg Thr Leu Thr Asp Leu Asp Ile Phe Phe Asn Thr Asp Gly
        275                 280                 285

Glu Gly Leu Gly Arg Ala Glu Arg Glu Leu Gly Ala Thr Val Thr Ser
    290                 295                 300
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Arg Tyr Asn Gly Cys Val Tyr Cys Ala Ser Val His Ala Gly Arg Ala
305                 310                 315                 320

Gln Glu Glu Ser Gly Arg Ala Asp Asp Val Asn Ala Leu Leu Ala Ser
                325                 330                 335

Ile Asp Ser Asp Leu Gly Ser Asp Gln Trp Asn Val Ile Arg Asp Ala
            340                 345                 350

Ala Arg Ala Leu Ser Ser Thr Pro Ala Ala Phe Asn Gln Gly Cys Ile
        355                 360                 365

Thr Lys Leu Arg Gly Val Gly Phe Ser Asp Leu Gln Ile Val Asp Leu
    370                 375                 380

Ile Asn Ser Val Ala Phe Phe Asn Trp Ala Asn Arg Leu Met Leu Ser
385                 390                 395                 400

Leu Gly Glu Pro Glu Val Pro Lys Arg Phe Leu
                405                 410
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<210> 2013
<211> 732
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(709)
<223> RXA01017

<400> 2013

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agtgtggatt gctagaaaac tttaagaaag aggaaataat atg gct caa aaa gta   115
                                            Met Ala Gln Lys Val
                                              1               5

acc ttc tgg ttc gat acc acc tgc cca ttc tgc tgg gtc acc tcc cgc   163
Thr Phe Trp Phe Asp Thr Thr Cys Pro Phe Cys Trp Val Thr Ser Arg
                 10                  15                  20

tgg att aag gaa gtc gaa caa gtc cgc gat att gaa atc cag tgg gtt   211
Trp Ile Lys Glu Val Glu Gln Val Arg Asp Ile Glu Ile Gln Trp Val
             25                  30                  35

cca atg agc ctc gct gtc cta aac gaa ggc cgt gat ctc cca gag gat   259
Pro Met Ser Leu Ala Val Leu Asn Glu Gly Arg Asp Leu Pro Glu Asp
         40                  45                  50

tac aag gag cgc atg aag gct gca tgg gga cca gca cgc gtt ttc gca   307
Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro Ala Arg Val Phe Ala
     55                  60                  65

gct gtc gcc acc gac cat gct gac aag ctc ggc gac ctg tac acc gca   355
Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly Asp Leu Tyr Thr Ala
 70                  75                  80                  85

atg ggt acc cgc atc cac aac gac ggt cgc gga cca atc gaa ggt tcc   403
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Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly Pro Ile Glu Gly Ser
                 90                  95                  100

ttc aat gat gtc atc gca gag gca ctt gaa gag gtc ggc cta gac gct   451
Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu Val Gly Leu Asp Ala
            105                 110                 115

gca ctt ggt gaa gtt gca gac acc acc gaa tgg gac gac gca ctt cgc   499
Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp Asp Asp Ala Leu Arg
        120                 125                 130

gca ttc cac cag acc gca atg gac gag gtc ggc aac gat gtc gga acc   547
Ala Phe His Gln Thr Ala Met Asp Glu Val Gly Asn Asp Val Gly Thr
    135                 140                 145

cca gtg gtc aag ctc ggc gac acc gct ttc ttc ggc cca gtg ctc acc   595
Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe Gly Pro Val Leu Thr
150                 155                 160                 165

cgc atc cca cgc ggc gag gaa gca gga gag atc ttc gac gct tcc ttc   643
Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile Phe Asp Ala Ser Phe
                170                 175                 180

aag ctc gca agc tat ccc cac ttc ttt gaa atc aag cgc agc cgc act   691
Lys Leu Ala Ser Tyr Pro His Phe Phe Glu Ile Lys Arg Ser Arg Thr
            185                 190                 195

gag aac cca cag ttc gac taattaacgc tgtctctgct tat                732
Glu Asn Pro Gln Phe Asp
        200


<210> 2014
<211> 203
<212> PRT
<213> Corynebacterium glutamicum

<400> 2014
Met Ala Gln Lys Val Thr Phe Trp Phe Asp Thr Thr Cys Pro Phe Cys
  1               5                  10                  15

Trp Val Thr Ser Arg Trp Ile Lys Glu Val Glu Gln Val Arg Asp Ile
             20                  25                  30

Glu Ile Gln Trp Val Pro Met Ser Leu Ala Val Leu Asn Glu Gly Arg
         35                  40                  45

Asp Leu Pro Glu Asp Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro
     50                  55                  60

Ala Arg Val Phe Ala Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly
 65                  70                  75                  80

Asp Leu Tyr Thr Ala Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly
                 85                  90                  95

Pro Ile Glu Gly Ser Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu
            100                 105                 110

Val Gly Leu Asp Ala Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp
        115                 120                 125
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Asp Asp Ala Leu Arg Ala Phe His Gln Thr Ala Met Asp Glu Val Gly
    130                 135                 140

Asn Asp Val Gly Thr Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe
145                 150                 155                 160

Gly Pro Val Leu Thr Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile
                165                 170                 175

Phe Asp Ala Ser Phe Lys Leu Ala Ser Tyr Pro His Phe Phe Glu Ile
            180                 185                 190

Lys Arg Ser Arg Thr Glu Asn Pro Gln Phe Asp
        195                 200


<210> 2015
<211> 622
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(622)
<223> RXA01021

<400> 2015
cgagaggctt ttttggctct aagcctttta gtcgtgcgaa cgaaatctta agcagcctcg 60

gtgccaccga gatcgattgg tcgctgtaag gtatctgatt atg tcc agt tcc gaa   115
                                              Met Ser Ser Ser Glu
                                                1               5

agc tcg cgt tcc gaa ggc tcg cag cca gca ccg tct gta cag cct gaa   163
Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro Ser Val Gln Pro Glu
                10                  15                  20

cgc cgt gct gat tca acg ggg gct cct gcg gca gct tcc aag gaa gct   211
Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala Ala Ser Lys Glu Ala
            25                  30                  35

tcc caa caa atg gac gct gcc gga gtt ctt gag tgg gcc agg acc gct   259
Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu Trp Ala Arg Thr Ala
        40                  45                  50

gtc gag cag ctt tct gaa cgt cgt gca gag atc aat gca ctg aat gtc   307
Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile Asn Ala Leu Asn Val
    55                  60                  65

ttt cct gtt cca gat gca gac act gga tca aac atg acc tac acc atg   355
Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn Met Thr Tyr Thr Met
70                  75                  80                  85

aca gct gcg ttg gat gaa gcg ctg aaa ctg ggg gag ttg ggt gat gtc   403
Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly Glu Leu Gly Asp Val
                90                  95                  100

gca agg att act gag gct ttg gct gtt ggt tct gtg cgt gga gcc cga   451
Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser Val Arg Gly Ala Arg
            105                 110                 115
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gga aat tct gga gta gtc ctt agt cag gtc ctt cgc gct att gct cag   499
Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu Arg Ala Ile Ala Gln
        120                 125                 130

gca gct gct gac ggg gtt att gat ggc cac aca atc caa gaa gcg cta   547
Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr Ile Gln Glu Ala Leu
    135                 140                 145

tcc att gct cgc tcc cta gtt gat cgc gca att aca gat cct gtg gag   595
Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile Thr Asp Pro Val Glu
150                 155                 160                 165

ggc act gtt gtc act gtg ttg cgt tct                              622
Gly Thr Val Val Thr Val Leu Arg Ser
                170
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<210> 2016
<211> 174
<212> PRT
<213> Corynebacterium glutamicum

<400> 2016

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Met Ser Ser Ser Glu Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro
  1               5                  10                  15

Ser Val Gln Pro Glu Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala
             20                  25                  30

Ala Ser Lys Glu Ala Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu
         35                  40                  45

Trp Ala Arg Thr Ala Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile
     50                  55                  60

Asn Ala Leu Asn Val Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn
 65                  70                  75                  80

Met Thr Tyr Thr Met Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly
                 85                  90                  95

Glu Leu Gly Asp Val Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser
            100                 105                 110

Val Arg Gly Ala Arg Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu
        115                 120                 125

Arg Ala Ile Ala Gln Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr
    130                 135                 140

Ile Gln Glu Ala Leu Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile
145                 150                 155                 160

Thr Asp Pro Val Glu Gly Thr Val Val Thr Val Leu Arg Ser
                165                 170
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<210> 2017
<211> 612
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(589)
<223> RXA01029

<400> 2017
atgggtggtt gtcttaatta agggtgttgc gtgaaacacg caaccggaga ggagggtgaa 60

gtgtggggtt ccttgcgggc gtatgtccgg ggtgcttgct atg ctt caa acg att 115
Met Leu Gln Thr Ile
1 5

tca ttc aag aaa ctt aat tta tta aca act ctt aaa aga aaa gga gag 163
Ser Phe Lys Lys Leu Asn Leu Leu Thr Thr Leu Lys Arg Lys Gly Glu
10 15 20

ctg gtc atc atg atc act cgt cac gat gtt ccc tac atc atc gct ccg 211
Leu Val Ile Met Ile Thr Arg His Asp Val Pro Tyr Ile Ile Ala Pro
25 30 35

cct gtc tac gcg atc ttt gcg agc ctg atg acc acg cca cca tgg ttt 259
Pro Val Tyr Ala Ile Phe Ala Ser Leu Met Thr Thr Pro Pro Trp Phe
40 45 50

tat cga acc acc tac acc att gac ggt ttc gat ttt aag atc agc tgg 307
Tyr Arg Thr Thr Tyr Thr Ile Asp Gly Phe Asp Phe Lys Ile Ser Trp
55 60 65

gtc tac acc atc acc atc tac atc agc ctc atg atc ctc att atc ggg 355
Val Tyr Thr Ile Thr Ile Tyr Ile Ser Leu Met Ile Leu Ile Ile Gly
70 75 80 85

ttc tac caa gcc aat atg cgc aaa gcg tgc cct tat gag gaa gat cct 403
Phe Tyr Gln Ala Asn Met Arg Lys Ala Cys Pro Tyr Glu Glu Asp Pro
90 95 100

ttg gtc gat att tgg cac aag gtg tgg agc act gca ctc ttt atc cta 451
Leu Val Asp Ile Trp His Lys Val Trp Ser Thr Ala Leu Phe Ile Leu
105 110 115

cct atc gtt tta tcc atc gcg gtg tac tca ctg atc aca cag cgc ggg 499
Pro Ile Val Leu Ser Ile Ala Val Tyr Ser Leu Ile Thr Gln Arg Gly
120 125 130

ttt gac tgg tat gtc atg gtg ttt att ctc cct gta ggc ttg atg atc 547
Phe Asp Trp Tyr Val Met Val Phe Ile Leu Pro Val Gly Leu Met Ile
135 140 145

gct tat gga ttc ttc aag ccc tgt gat tgc gac aaa cac cgt 589
Ala Tyr Gly Phe Phe Lys Pro Cys Asp Cys Asp Lys His Arg
150 155 160

taaggtatac ttgtccaaga ctt 612

<210> 2018
<211> 163
<212> PRT
<213> Corynebacterium glutamicum

<400> 2018
Met Leu Gln Thr Ile Ser Phe Lys Lys Leu Asn Leu Leu Thr Thr Leu
1 5 10 15

Lys Arg Lys Gly Glu Leu Val Ile Met Ile Thr Arg His Asp Val Pro
20 25 30

Tyr Ile Ile Ala Pro Pro Val Tyr Ala Ile Phe Ala Ser Leu Met Thr
35 40 45

Thr Pro Pro Trp Phe Tyr Arg Thr Thr Tyr Thr Ile Asp Gly Phe Asp
50 55 60

Phe Lys Ile Ser Trp Val Tyr Thr Ile Thr Ile Tyr Ile Ser Leu Met
65 70 75 80

Ile Leu Ile Ile Gly Phe Tyr Gln Ala Asn Met Arg Lys Ala Cys Pro
85 90 95

Tyr Glu Glu Asp Pro Leu Val Asp Ile Trp His Lys Val Trp Ser Thr
100 105 110

Ala Leu Phe Ile Leu Pro Ile Val Leu Ser Ile Ala Val Tyr Ser Leu
115 120 125

Ile Thr Gln Arg Gly Phe Asp Trp Tyr Val Met Val Phe Ile Leu Pro
130 135 140

Val Gly Leu Met Ile Ala Tyr Gly Phe Phe Lys Pro Cys Asp Cys Asp
145 150 155 160

Lys His Arg

<210> 2019
<211> 789
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(766)
<223> RXA01031

<400> 2019
cagctgaact tgatcatttt gatgatctgc cagtacagcg ccaagaagat cttggcacct 60

tagttgttat ctctgctgtt cacgcaagcg actctgcggc atg aaa ctg ctg caa 115
Met Lys Leu Leu Gln
1 5

tac gca ggt ggt gct gtc tat gtc gat cca gaa gat tct gcg cag tcc 163
Tyr Ala Gly Gly Ala Val Tyr Val Asp Pro Glu Asp Ser Ala Gln Ser
10 15 20

caa gac ctg gat gcc agc act gca cgt gat gtt atc gac gct acc aac 211
Gln Asp Leu Asp Ala Ser Thr Ala Arg Asp Val Ile Asp Ala Thr Asn
25 30 35

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acc gcc atg acc act att acc tct cgc ccc acc atg att gtg cac ctg   259
Thr Ala Met Thr Thr Ile Thr Ser Arg Pro Thr Met Ile Val His Leu
         40                  45                  50

cac aag gtg cga aaa gtc att gag att tta tgc aac cct gca ctc ggc   307
His Lys Val Arg Lys Val Ile Glu Ile Leu Cys Asn Pro Ala Leu Gly
     55                  60                  65

ggt gaa cct gtc aat atc gac cag gac gag acc gga aaa cag gtg tac   355
Gly Glu Pro Val Asn Ile Asp Gln Asp Glu Thr Gly Lys Gln Val Tyr
 70                  75                  80                  85

aca ccc acc cca acg ctt gtc gcc tat cgc ttt atc tct gac aaa gaa   403
Thr Pro Thr Pro Thr Leu Val Ala Tyr Arg Phe Ile Ser Asp Lys Glu
                 90                  95                 100

atc ctg ctt cat tac ctg gcg cag gcg ggt gtg cag ggt gtg gag gtt   451
Ile Leu Leu His Tyr Leu Ala Gln Ala Gly Val Gln Gly Val Glu Val
            105                 110                 115

ttt gac ggg tcg cct gac atg ctg agc cgt tgg aat gcg gga cgc att   499
Phe Asp Gly Ser Pro Asp Met Leu Ser Arg Trp Asn Ala Gly Arg Ile
        120                 125                 130

ccg gtc tta ctt ttg cag cct gcg tct gct ggt cac ggc ttg aat ttc   547
Pro Val Leu Leu Leu Gln Pro Ala Ser Ala Gly His Gly Leu Asn Phe
    135                 140                 145

cag cac ggc ggg cat cgc ttg gtg tgg tac aac ctg ccc gat aat aac   595
Gln His Gly Gly His Arg Leu Val Trp Tyr Asn Leu Pro Asp Asn Asn
150                 155                 160                 165

gag cat tat atg caa gcg aat gct cgt cta cat cgc att ggt caa aag   643
Glu His Tyr Met Gln Ala Asn Ala Arg Leu His Arg Ile Gly Gln Lys
                170                 175                 180

aat ccc gtg acc att cac cgc att att acc gct gat act tat gat gcg   691
Asn Pro Val Thr Ile His Arg Ile Ile Thr Ala Asp Thr Tyr Asp Ala
            185                 190                 195

aat atg ccg gcg att ctg gcc ggt aaa gca aat aga cag caa cgt ctc   739
Asn Met Pro Ala Ile Leu Ala Gly Lys Ala Asn Arg Gln Gln Arg Leu
        200                 205                 210

atc gac gcc gtg cgc cgt gat cca gtc taagaccggc acgatcgcac         786
Ile Asp Ala Val Arg Arg Asp Pro Val
    215                 220

cgt                                                               789
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Translation Express Inc. 2005-2006

<210> 2020
<211> 222
<212> PRT
<213> Corynebacterium glutamicum

<400> 2020

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Met Lys Leu Leu Gln Tyr Ala Gly Gly Ala Val Tyr Val Asp Pro Glu
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Asp Ser Ala Gln Ser Gln Asp Leu Asp Ala Ser Thr Ala Arg Asp Val
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             20                  25                  30

Ile Asp Ala Thr Asn Thr Ala Met Thr Thr Ile Thr Ser Arg Pro Thr
         35                  40                  45

Met Ile Val His Leu His Lys Val Arg Lys Val Ile Glu Ile Leu Cys
     50                  55                  60

Asn Pro Ala Leu Gly Gly Glu Pro Val Asn Ile Asp Gln Asp Glu Thr
 65                  70                  75                  80

Gly Lys Gln Val Tyr Thr Pro Thr Pro Thr Leu Val Ala Tyr Arg Phe
                 85                  90                  95

Ile Ser Asp Lys Glu Ile Leu Leu His Tyr Leu Ala Gln Ala Gly Val
            100                 105                 110

Gln Gly Val Glu Val Phe Asp Gly Ser Pro Asp Met Leu Ser Arg Trp
        115                 120                 125

Asn Ala Gly Arg Ile Pro Val Leu Leu Leu Gln Pro Ala Ser Ala Gly
    130                 135                 140

His Gly Leu Asn Phe Gln His Gly Gly His Arg Leu Val Trp Tyr Asn
145                 150                 155                 160

Leu Pro Asp Asn Asn Glu His Tyr Met Gln Ala Asn Ala Arg Leu His
                165                 170                 175

Arg Ile Gly Gln Lys Asn Pro Val Thr Ile His Arg Ile Ile Thr Ala
            180                 185                 190

Asp Thr Tyr Asp Ala Asn Met Pro Ala Ile Leu Ala Gly Lys Ala Asn
        195                 200                 205

Arg Gln Gln Arg Leu Ile Asp Ala Val Arg Arg Asp Pro Val
    210                 215                 220
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<210> 2021
<211> 498
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(475)
<223> RXA01032

<400> 2021
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tggggtgtgt cttatcccct aagaaagtga cacctttacc atg tca gac cac gac 115
                                            Met Ser Asp His Asp
                                              1   5

gcc cca caa aca ccg atc ccc aag ggg ttt tgg cag cag atc gac cac 163
Ala Pro Gln Thr Pro Ile Pro Lys Gly Phe Trp Gln Gln Ile Asp His
                10   15   20

caa ctc gat cgc ctc ggc acg cag cgc cca gag acc ttc gca gca ctg 211

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Gln Leu Asp Arg Leu Gly Thr Gln Arg Pro Glu Thr Phe Ala Ala Leu
            25                  30                  35

cgt gac att ttg ctt gat cct gcc tac acc gcc att gtt cat gac cgt   259
Arg Asp Ile Leu Leu Asp Pro Ala Tyr Thr Ala Ile Val His Asp Arg
         40                  45                  50

aat cgc tac ggc gtt gtc acc ttt gac acc aac tca gcc ttc ttc tca   307
Asn Arg Tyr Gly Val Val Thr Phe Asp Thr Asn Ser Ala Phe Phe Ser
     55                  60                  65

ggc tct ggc gga gac aac ggc tta gcc gac gta ctc att aac tgt gat   355
Gly Ser Gly Gly Asp Asn Gly Leu Ala Asp Val Leu Ile Asn Cys Asp
 70                  75                  80                  85

tgg cgc atg act gac tac cgc gcc gag tac tac tac gtc atg aca cat   403
Trp Arg Met Thr Asp Tyr Arg Ala Glu Tyr Tyr Tyr Val Met Thr His
                90                  95                 100

aaa tac acc aag gaa tcg ttt acc tat atc gag ggc gac gtg aaa cgc   451
Lys Tyr Thr Lys Glu Ser Phe Thr Tyr Ile Glu Gly Asp Val Lys Arg
            105                 110                 115

ggc gac ctc atc ccg cct aat aat taaggacaac cgccatgact cag         498
Gly Asp Leu Ile Pro Pro Asn Asn
        120                 125


<210> 2022
<211> 125
<212> PRT
<213> Corynebacterium glutamicum

<400> 2022
Met Ser Asp His Asp Ala Pro Gln Thr Pro Ile Pro Lys Gly Phe Trp
  1               5                  10                  15

Gln Gln Ile Asp His Gln Leu Asp Arg Leu Gly Thr Gln Arg Pro Glu
            20                  25                  30

Thr Phe Ala Ala Leu Arg Asp Ile Leu Leu Asp Pro Ala Tyr Thr Ala
        35                  40                  45

Ile Val His Asp Arg Asn Arg Tyr Gly Val Val Thr Phe Asp Thr Asn
    50                  55                  60

Ser Ala Phe Phe Ser Gly Ser Gly Gly Asp Asn Gly Leu Ala Asp Val
65                  70                  75                  80

Leu Ile Asn Cys Asp Trp Arg Met Thr Asp Tyr Arg Ala Glu Tyr Tyr
                85                  90                  95

Tyr Val Met Thr His Lys Tyr Thr Lys Glu Ser Phe Thr Tyr Ile Glu
            100                 105                 110

Gly Asp Val Lys Arg Gly Asp Leu Ile Pro Pro Asn Asn
        115                 120                 125


<210> 2023
<211> 459
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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(436)
<223> RXA01033

<400> 2023
acgtcatgac acataaatac accaaggaat cgtttaccta tatcgagggc gacgtgaaac 60

gcggcgacct catcccgcct aataattaag gacaaccgcc atg act cag atc gcc 115
Met Thr Gln Ile Ala
1 5

atg tat ctc gca gga ccc atg aca ggt atc cct gaa tac aac tac ccc 163
Met Tyr Leu Ala Gly Pro Met Thr Gly Ile Pro Glu Tyr Asn Tyr Pro
10 15 20

acc ttc cat gca gcg gct aat aag ttc cgt gca gct ggc tac acc gta 211
Thr Phe His Ala Ala Ala Asn Lys Phe Arg Ala Ala Gly Tyr Thr Val
25 30 35

ctc tcc ccc gct gaa gac gaa tat gaa tcc cag ctc act gca cca ttg 259
Leu Ser Pro Ala Glu Asp Glu Tyr Glu Ser Gln Leu Thr Ala Pro Leu
40 45 50

cct gag aac gct gag cac aaa tac gac cac tac ttg cgt ctc ggt atc 307
Pro Glu Asn Ala Glu His Lys Tyr Asp His Tyr Leu Arg Leu Gly Ile
55 60 65

gaa aag ctg ctc aag gct gat gct gtc cac atg ctt cag gga tgg cag 355
Glu Lys Leu Leu Lys Ala Asp Ala Val His Met Leu Gln Gly Trp Gln
70 75 80 85

agt agc gcc ggt gcc act ctt gag cac gat att gca cag aaa ttg agg 403
Ser Ser Ala Gly Ala Thr Leu Glu His Asp Ile Ala Gln Lys Leu Arg
90 95 100

ctt gcc att acc tat gaa gaa cca cca gca tcc taaggcgcct ccggcatagc 456
Leu Ala Ile Thr Tyr Glu Glu Pro Pro Ala Ser
105 110

gta 459

<210> 2024
<211> 112
<212> PRT
<213> Corynebacterium glutamicum

<400> 2024
Met Thr Gln Ile Ala Met Tyr Leu Ala Gly Pro Met Thr Gly Ile Pro
1 5 10 15

Glu Tyr Asn Tyr Pro Thr Phe His Ala Ala Ala Asn Lys Phe Arg Ala
20 25 30

Ala Gly Tyr Thr Val Leu Ser Pro Ala Glu Asp Glu Tyr Glu Ser Gln
35 40 45

```
Leu Thr Ala Pro Leu Pro Glu Asn Ala Glu His Lys Tyr Asp His Tyr
     50                  55                  60

Leu Arg Leu Gly Ile Glu Lys Leu Leu Lys Ala Asp Ala Val His Met
 65                  70                  75                  80

Leu Gln Gly Trp Gln Ser Ser Ala Gly Ala Thr Leu Glu His Asp Ile
                 85                  90                  95

Ala Gln Lys Leu Arg Leu Ala Ile Thr Tyr Glu Glu Pro Pro Ala Ser
            100                 105                 110
```

<210> 2025
<211> 477
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(454)
<223> RXA01034

<400> 2025
agaaagtatg tcaataactt tgacataacc taaacacaat aaattatgta gtattatgtg 60

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acactaagtt attacattta ttacatgatt ggttaggact atg gac atg gcc att   115
                                            Met Asp Met Ala Ile
                                              1               5

att cag tcg gtc gaa tac aca tct gat gtc tca cat gag cgc atc acc   163
Ile Gln Ser Val Glu Tyr Thr Ser Asp Val Ser His Glu Arg Ile Thr
                 10                  15                  20

aat gtc gtc tct gta ggc gtg gtc tac gag ggt aaa cag tat gta gtg   211
Asn Val Val Ser Val Gly Val Val Tyr Glu Gly Lys Gln Tyr Val Val
             25                  30                  35

gac ctt aat ggt gac gac att gat act gag ctc gat atg atc acg ctc   259
Asp Leu Asn Gly Asp Asp Ile Asp Thr Glu Leu Asp Met Ile Thr Leu
         40                  45                  50

aaa gaa gtc atc aag att ggt cgt gag gaa tct gca cgc cag atc cgt   307
Lys Glu Val Ile Lys Ile Gly Arg Glu Glu Ser Ala Arg Gln Ile Arg
     55                  60                  65

cgt gga tct gta gat gca gag ctg cac cgt aag gcg cgt ttg tgg gct   355
Arg Gly Ser Val Asp Ala Glu Leu His Arg Lys Ala Arg Leu Trp Ala
 70                  75                  80                  85

att gac aat gac atg gcc gtt ggt caa cgt ggt atc gtg cca cag gaa   403
Ile Asp Asn Asp Met Ala Val Gly Gln Arg Gly Ile Val Pro Gln Glu
                 90                  95                 100

atc atc gac gcg tac aaa gag tac tgc gaa aaa gaa ggc att cct ttc   451
Ile Ile Asp Ala Tyr Lys Glu Tyr Cys Glu Lys Glu Gly Ile Pro Phe
            105                 110                 115
```

gaa taagagccct gtggagaatt gtt 477
Glu

<210> 2026
<211> 118
<212> PRT
<213> Corynebacterium glutamicum

<400> 2026
Met Asp Met Ala Ile Ile Gln Ser Val Glu Tyr Thr Ser Asp Val Ser
1 5 10 15

His Glu Arg Ile Thr Asn Val Val Ser Val Gly Val Val Tyr Glu Gly
20 25 30

Lys Gln Tyr Val Val Asp Leu Asn Gly Asp Asp Ile Asp Thr Glu Leu
35 40 45

Asp Met Ile Thr Leu Lys Glu Val Ile Lys Ile Gly Arg Glu Glu Ser
50 55 60

Ala Arg Gln Ile Arg Arg Gly Ser Val Asp Ala Glu Leu His Arg Lys
65 70 75 80

Ala Arg Leu Trp Ala Ile Asp Asn Asp Met Ala Val Gly Gln Arg Gly
85 90 95

Ile Val Pro Gln Glu Ile Ile Asp Ala Tyr Lys Glu Tyr Cys Glu Lys
100 105 110

Glu Gly Ile Pro Phe Glu
115

<210> 2027
<211> 729
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(706)
<223> RXA01035

<400> 2027
ggcagtgatg caccgcactt gagaaaaata aatcatctca agaaacaaac taatacgtta 60

ttattgtaat ttaattagag aaaagaaagt gacttttaaa gtg ctt att cgc atc 115
Val Leu Ile Arg Ile
1 5

gcc gag cat caa ggc cgg ctc cat gtc cat agc ccc tac tca aag gct 163
Ala Glu His Gln Gly Arg Leu His Val His Ser Pro Tyr Ser Lys Ala
10 15 20

ttt gcc gcc cgc gct cga aag ctc aac ggt ctc tgg tca ccc gaa acg 211
Phe Ala Ala Arg Ala Arg Lys Leu Asn Gly Leu Trp Ser Pro Glu Thr
25 30 35

```
aag acc tgg cat ttc agc ccc gat aaa gaa caa ccg gtg aga cgc gca   259
Lys Thr Trp His Phe Ser Pro Asp Lys Glu Gln Pro Val Arg Arg Ala
         40                  45                  50

ctc aag gat gtc tac ggc tgg gat gaa ttc acc aca ccc gag cta tgc   307
Leu Lys Asp Val Tyr Gly Trp Asp Glu Phe Thr Thr Pro Glu Leu Cys
     55                  60                  65

acg gtg cag ctc act gtg acc cca gag gca gtg ctc aac aaa cac aca   355
Thr Val Gln Leu Thr Val Thr Pro Glu Ala Val Leu Asn Lys His Thr
 70                  75                  80                  85

ctc acc atc gct ggt gtt aca ctt ctg agc cgt tta cgc aga aat tac   403
Leu Thr Ile Ala Gly Val Thr Leu Leu Ser Arg Leu Arg Arg Asn Tyr
                 90                  95                 100

tcg gtg tgg ttg ggt gat aat gtc cgc atc atc agt ggc aat ttc cca   451
Ser Val Trp Leu Gly Asp Asn Val Arg Ile Ile Ser Gly Asn Phe Pro
            105                 110                 115

gaa gca gca gga tca ccc cag tac ccc ctc atc atg ggt gtg aag gct   499
Glu Ala Ala Gly Ser Pro Gln Tyr Pro Leu Ile Met Gly Val Lys Ala
        120                 125                 130

caa ccc gtt gtt atc cat gtg cag gaa ttc cct gta gat gct gtt tcg   547
Gln Pro Val Val Ile His Val Gln Glu Phe Pro Val Asp Ala Val Ser
    135                 140                 145

act att ccc ccg cga ttt aat cct att gtt atc act gca ccg ccg agc   595
Thr Ile Pro Pro Arg Phe Asn Pro Ile Val Ile Thr Ala Pro Pro Ser
150                 155                 160                 165

att gat att gct gct ctt cga gct gaa cgc gaa cag ctc acc cga cgc   643
Ile Asp Ile Ala Ala Leu Arg Ala Glu Arg Glu Gln Leu Thr Arg Arg
                170                 175                 180

atc agc gaa att gac aag aaa atc gca cgt gct gtg cat cca acc att   691
Ile Ser Glu Ile Asp Lys Lys Ile Ala Arg Ala Val His Pro Thr Ile
            185                 190                 195

cag act gag gct gcc taataatgat gcagactctc aag                    729
Gln Thr Glu Ala Ala
        200
```

Sequence Listing.ST25.txt

<210> 2028
<211> 202
<212> PRT
<213> Corynebacterium glutamicum

<400> 2028

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Val Leu Ile Arg Ile Ala Glu His Gln Gly Arg Leu His Val His Ser
  1               5                  10                  15

Pro Tyr Ser Lys Ala Phe Ala Ala Arg Ala Arg Lys Leu Asn Gly Leu
             20                  25                  30

Trp Ser Pro Glu Thr Lys Thr Trp His Phe Ser Pro Asp Lys Glu Gln
         35                  40                  45

Pro Val Arg Arg Ala Leu Lys Asp Val Tyr Gly Trp Asp Glu Phe Thr
```

```
     50                  55                  60

Thr Pro Glu Leu Cys Thr Val Gln Leu Thr Val Thr Pro Glu Ala Val
 65                  70                  75                  80

Leu Asn Lys His Thr Leu Thr Ile Ala Gly Val Thr Leu Leu Ser Arg
                85                  90                  95

Leu Arg Arg Asn Tyr Ser Val Trp Leu Gly Asp Asn Val Arg Ile Ile
            100                 105                 110

Ser Gly Asn Phe Pro Glu Ala Ala Gly Ser Pro Gln Tyr Pro Leu Ile
        115                 120                 125

Met Gly Val Lys Ala Gln Pro Val Val Ile His Val Gln Glu Phe Pro
    130                 135                 140

Val Asp Ala Val Ser Thr Ile Pro Pro Arg Phe Asn Pro Ile Val Ile
145                 150                 155                 160

Thr Ala Pro Pro Ser Ile Asp Ile Ala Ala Leu Arg Ala Glu Arg Glu
                165                 170                 175

Gln Leu Thr Arg Arg Ile Ser Glu Ile Asp Lys Lys Ile Ala Arg Ala
            180                 185                 190

Val His Pro Thr Ile Gln Thr Glu Ala Ala
        195                 200
```

<210> 2029
<211> 576
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(553)
<223> RXA01036

<400> 2029

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ctgaggctgc ctaataatga tgcagactct caagcggaaa attccgctca tctcatgcaa 60

tgacctcaaa gaagtgcagt tacttttttct taaaggtcag atg cac aca gtc ggc   115
                                            Met His Thr Val Gly
                                              1               5

tac aag cta gat acc gat ctt cgc aag ctc act aat acc gat gtg ctt   163
Tyr Lys Leu Asp Thr Asp Leu Arg Lys Leu Thr Asn Thr Asp Val Leu
                10                  15                  20

gat ctt att aac gcg ctc ttc ggc acc act gtg acc agc gca gat gac   211
Asp Leu Ile Asn Ala Leu Phe Gly Thr Thr Val Thr Ser Ala Asp Asp
            25                  30                  35

gaa gca gca gat ttc att gac tct gat cct cag ttt gca gtg ctc gtt   259
Glu Ala Ala Asp Phe Ile Asp Ser Asp Pro Gln Phe Ala Val Leu Val
        40                  45                  50

gag ctg gcc tac cac gac tgt gca cgc cgc gct gcc atg ggt cta tcc   307
Glu Leu Ala Tyr His Asp Cys Ala Arg Arg Ala Ala Met Gly Leu Ser
```

```
     55                  60                  65

agg gta cag cag ctc atc tat gac aat gcg gct aaa tca acc tac tac   355
Arg Val Gln Gln Leu Ile Tyr Asp Asn Ala Ala Lys Ser Thr Tyr Tyr
 70                  75                  80                  85

cgc agc gtc gca gct aga cat cgc aaa cac atc cgt gaa ctc cac gag   403
Arg Ser Val Ala Ala Arg His Arg Lys His Ile Arg Glu Leu His Glu
                90                  95                 100

caa aca cag cga gat ggt att cac ttc gac aac ccg ttg tct cgt gca   451
Gln Thr Gln Arg Asp Gly Ile His Phe Asp Asn Pro Leu Ser Arg Ala
            105                 110                 115

gtc atc aac gat ctc agc atg tcc atg aac cgt gct cga cta aac cgc   499
Val Ile Asn Asp Leu Ser Met Ser Met Asn Arg Ala Arg Leu Asn Arg
        120                 125                 130

atc gct tca tgg aaa tca gcc ggc gta cag cgc tat ctc aac ccc act   547
Ile Ala Ser Trp Lys Ser Ala Gly Val Gln Arg Tyr Leu Asn Pro Thr
    135                 140                 145

atc tct tagaaccaca cacaaccaag aaa                                 576
Ile Ser
150
```

Sequence Listing - Page 2305 - 2030-1.ST25.txt

<210> 2030
<211> 151
<212> PRT
<213> Corynebacterium glutamicum

<400> 2030

```
Met His Thr Val Gly Tyr Lys Leu Asp Thr Asp Leu Arg Lys Leu Thr
  1               5                  10                  15

Asn Thr Asp Val Leu Asp Leu Ile Asn Ala Leu Phe Gly Thr Thr Val
             20                  25                  30

Thr Ser Ala Asp Asp Glu Ala Ala Asp Phe Ile Asp Ser Asp Pro Gln
         35                  40                  45

Phe Ala Val Leu Val Glu Leu Ala Tyr His Asp Cys Ala Arg Arg Ala
     50                  55                  60

Ala Met Gly Leu Ser Arg Val Gln Gln Leu Ile Tyr Asp Asn Ala Ala
 65                  70                  75                  80

Lys Ser Thr Tyr Tyr Arg Ser Val Ala Ala Arg His Arg Lys His Ile
                85                  90                  95

Arg Glu Leu His Glu Gln Thr Gln Arg Asp Gly Ile His Phe Asp Asn
            100                 105                 110

Pro Leu Ser Arg Ala Val Ile Asn Asp Leu Ser Met Ser Met Asn Arg
        115                 120                 125

Ala Arg Leu Asn Arg Ile Ala Ser Trp Lys Ser Ala Gly Val Gln Arg
    130                 135                 140

Tyr Leu Asn Pro Thr Ile Ser
```

145 150

<210> 2031
<211> 651
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(628)
<223> RXA01037

<400> 2031
cgactaaacc gcatcgcttc atggaaatca gccggcgtac agcgctatct caaccccact 60

atctcttaga accacacaca accaagaaag cagtcactac atg acc acc tca tca 115
Met Thr Thr Ser Ser
1 5

ccc ctt aag tcc aaa aat tcc ctt aac ggc gcg cag acc aca ttt gtc 163
Pro Leu Lys Ser Lys Asn Ser Leu Asn Gly Ala Gln Thr Thr Phe Val
10 15 20

cgc aat tgt gtt gca gac ggc cca acc gag gta aaa gcc acc att gat 211
Arg Asn Cys Val Ala Asp Gly Pro Thr Glu Val Lys Ala Thr Ile Asp
25 30 35

gca cgt ggc ggt atc gaa cag ctc cgt gac aat gag att tca cag ctc 259
Ala Arg Gly Gly Ile Glu Gln Leu Arg Asp Asn Glu Ile Ser Gln Leu
40 45 50

ccc gac aag ctg tgg ttc aat agc gca acc tcc gca tcc aat gac gag 307
Pro Asp Lys Leu Trp Phe Asn Ser Ala Thr Ser Ala Ser Asn Asp Glu
55 60 65

ttc acc acc gat aac atc cga ctt ggg ttg ctc tac aac atg gca ctg 355
Phe Thr Thr Asp Asn Ile Arg Leu Gly Leu Leu Tyr Asn Met Ala Leu
70 75 80 85

aat aag gca tcg gct cat cgc tat gag ctt gct gcc cgc tgg tac gcc 403
Asn Lys Ala Ser Ala His Arg Tyr Glu Leu Ala Ala Arg Trp Tyr Ala
90 95 100

att gtt agc cct cag cca tcg caa gaa gct agc cac aag cgc atc gcg 451
Ile Val Ser Pro Gln Pro Ser Gln Glu Ala Ser His Lys Arg Ile Ala
105 110 115

tcc tgg cac ctt acc cag ctg cac gca ctg gtg acc cta tct cgc acc 499
Ser Trp His Leu Thr Gln Leu His Ala Leu Val Thr Leu Ser Arg Thr
120 125 130

cta ggg gtc atc att cct ggt gat gag atc gac gct cta gcg cag tct 547
Leu Gly Val Ile Ile Pro Gly Asp Glu Ile Asp Ala Leu Ala Gln Ser
135 140 145

atg gag aat gct cgt caa gtt ggc acc gag aat tgg tcc act gtc acc 595
Met Glu Asn Ala Arg Gln Val Gly Thr Glu Asn Trp Ser Thr Val Thr
150 155 160 165

atg cgc acc tac gtg acc aac cgc aag gca tcc taatgactcg cgatattttc 648

Met Arg Thr Tyr Val Thr Asn Arg Lys Ala Ser
170 175

cac 651

<210> 2032
<211> 176
<212> PRT
<213> Corynebacterium glutamicum

<400> 2032
Met Thr Thr Ser Ser Pro Leu Lys Ser Lys Asn Ser Leu Asn Gly Ala
1 5 10 15

Gln Thr Thr Phe Val Arg Asn Cys Val Ala Asp Gly Pro Thr Glu Val
20 25 30

Lys Ala Thr Ile Asp Ala Arg Gly Gly Ile Glu Gln Leu Arg Asp Asn
35 40 45

Glu Ile Ser Gln Leu Pro Asp Lys Leu Trp Phe Asn Ser Ala Thr Ser
50 55 60

Ala Ser Asn Asp Glu Phe Thr Thr Asp Asn Ile Arg Leu Gly Leu Leu
65 70 75 80

Tyr Asn Met Ala Leu Asn Lys Ala Ser Ala His Arg Tyr Glu Leu Ala
85 90 95

Ala Arg Trp Tyr Ala Ile Val Ser Pro Gln Pro Ser Gln Glu Ala Ser
100 105 110

His Lys Arg Ile Ala Ser Trp His Leu Thr Gln Leu His Ala Leu Val
115 120 125

Thr Leu Ser Arg Thr Leu Gly Val Ile Ile Pro Gly Asp Glu Ile Asp
130 135 140

Ala Leu Ala Gln Ser Met Glu Asn Ala Arg Gln Val Gly Thr Glu Asn
145 150 155 160

Trp Ser Thr Val Thr Met Arg Thr Tyr Val Thr Asn Arg Lys Ala Ser
165 170 175

<210> 2033
<211> 870
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(847)
<223> RXA01038

<400> 2033
acgctctagc gcagtctatg gagaatgctc gtcaagttgg caccgagaat tggtccactg 60

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tcaccatgcg cacctacgtg accaaccgca aggcatccta atg act cgc gat att   115
                                              Met Thr Arg Asp Ile
                                                1               5

ttc cac gag gct gca aaa ctc atc gca cac ctg ggg tgg agg gac gct   163
Phe His Glu Ala Ala Lys Leu Ile Ala His Leu Gly Trp Arg Asp Ala
               10                  15                  20

ttt cca gca cta cag cgc act gac cca gcg cca aca cat gct gtg ccg   211
Phe Pro Ala Leu Gln Arg Thr Asp Pro Ala Pro Thr His Ala Val Pro
            25                  30                  35

atc agg gcc ttt gat ctc aag gcg ggc gcc gtc atc acc gat gaa aat   259
Ile Arg Ala Phe Asp Leu Lys Ala Gly Ala Val Ile Thr Asp Glu Asn
         40                  45                  50

cga agc aat gct tat atc tat gac acc ctt gtc atc acg cag cca tat   307
Arg Ser Asn Ala Tyr Ile Tyr Asp Thr Leu Val Ile Thr Gln Pro Tyr
     55                  60                  65

aag cac gag tta cct cat caa aac acc cac cct ttt gag tgg gcc ctg   355
Lys His Glu Leu Pro His Gln Asn Thr His Pro Phe Glu Trp Ala Leu
 70                  75                  80                  85

gaa caa att gcc acg ctt gat ccg gcg ttc tcg atc aag ctc gat cgc   403
Glu Gln Ile Ala Thr Leu Asp Pro Ala Phe Ser Ile Lys Leu Asp Arg
               90                  95                 100

tca gtg acc gtc cct gaa att gga ctc tac gcc cgc aca ctg cat gac   451
Ser Val Thr Val Pro Glu Ile Gly Leu Tyr Ala Arg Thr Leu His Asp
            105                 110                 115

ctt aat act cgg cat caa gac ttc ttg gca cag cgc aac gcc atg ttg   499
Leu Asn Thr Arg His Gln Asp Phe Leu Ala Gln Arg Asn Ala Met Leu
        120                 125                 130

ctt gtt gtt gcc cgt cgt ggt gtt gat cca aaa aat atc gca gac gta   547
Leu Val Val Ala Arg Arg Gly Val Asp Pro Lys Asn Ile Ala Asp Val
    135                 140                 145

ctt ggt tta acc acc aat cag ata cat cgg att ctc agt gct act ccg   595
Leu Gly Leu Thr Thr Asn Gln Ile His Arg Ile Leu Ser Ala Thr Pro
150                 155                 160                 165

gct gat tcc cct act gat tta ggc gtt aac ccc gcc aca aca atg ggt   643
Ala Asp Ser Pro Thr Asp Leu Gly Val Asn Pro Ala Thr Thr Met Gly
               170                 175                 180

gat gta gtg agg ttt atc aag aaa cgt cgc acc act atg caa cta cgc   691
Asp Val Val Arg Phe Ile Lys Lys Arg Arg Thr Thr Met Gln Leu Arg
            185                 190                 195

ggc acc gct gtc cgt gca ctg ctc tat cac ggc ctt acg ccg gca gtc   739
Gly Thr Ala Val Arg Ala Leu Leu Tyr His Gly Leu Thr Pro Ala Val
        200                 205                 210

atc tcc cga cta agc ggc atg tcg cgt gcg ggt gtc atc aac gca gcc   787
Ile Ser Arg Leu Ser Gly Met Ser Arg Ala Gly Val Ile Asn Ala Ala
    215                 220                 225
```

```
aag gca ttc ccc acc acc atc aac cac aag gtc aag aaa aga aag cag   835
Lys Ala Phe Pro Thr Thr Ile Asn His Lys Val Lys Lys Arg Lys Gln
230                 235                 240                 245

cac ttc cat gtc taatctcggc acatactatg cag                       870
His Phe His Val
```

<210> 2034
<211> 249
<212> PRT
<213> Corynebacterium glutamicum

<400> 2034

```
Met Thr Arg Asp Ile Phe His Glu Ala Ala Lys Leu Ile Ala His Leu
  1               5                  10                  15

Gly Trp Arg Asp Ala Phe Pro Ala Leu Gln Arg Thr Asp Pro Ala Pro
             20                  25                  30

Thr His Ala Val Pro Ile Arg Ala Phe Asp Leu Lys Ala Gly Ala Val
         35                  40                  45

Ile Thr Asp Glu Asn Arg Ser Asn Ala Tyr Ile Tyr Asp Thr Leu Val
     50                  55                  60

Ile Thr Gln Pro Tyr Lys His Glu Leu Pro His Gln Asn Thr His Pro
 65                  70                  75                  80

Phe Glu Trp Ala Leu Glu Gln Ile Ala Thr Leu Asp Pro Ala Phe Ser
                 85                  90                  95

Ile Lys Leu Asp Arg Ser Val Thr Val Pro Glu Ile Gly Leu Tyr Ala
            100                 105                 110

Arg Thr Leu His Asp Leu Asn Thr Arg His Gln Asp Phe Leu Ala Gln
        115                 120                 125

Arg Asn Ala Met Leu Leu Val Val Ala Arg Arg Gly Val Asp Pro Lys
    130                 135                 140

Asn Ile Ala Asp Val Leu Gly Leu Thr Thr Asn Gln Ile His Arg Ile
145                 150                 155                 160

Leu Ser Ala Thr Pro Ala Asp Ser Pro Thr Asp Leu Gly Val Asn Pro
                165                 170                 175

Ala Thr Thr Met Gly Asp Val Val Arg Phe Ile Lys Lys Arg Arg Thr
            180                 185                 190

Thr Met Gln Leu Arg Gly Thr Ala Val Arg Ala Leu Leu Tyr His Gly
        195                 200                 205

Leu Thr Pro Ala Val Ile Ser Arg Leu Ser Gly Met Ser Arg Ala Gly
    210                 215                 220

Val Ile Asn Ala Ala Lys Ala Phe Pro Thr Thr Ile Asn His Lys Val
225                 230                 235                 240

Lys Lys Arg Lys Gln His Phe His Val
```

245

<210> 2035
<211> 699
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(676)
<223> RXA01039

<400> 2035
aaacctatat gttaatagta acagaaatta ataagatact agagtttaat ttgtagtatc 60

cagggaacat taaacgggta aaggtaaagg acaaacgaac atg gcg att aaa ggc 115
Met Ala Ile Lys Gly
1 5

gca atg ccg aaa aat cga gta cca ggt gtg gca gca ggt gcg ttt att 163
Ala Met Pro Lys Asn Arg Val Pro Gly Val Ala Ala Gly Ala Phe Ile
10 15 20

gct gct gcc gtt att gca ggt gga tca ggc gtg acc ttt ctc gcc caa 211
Ala Ala Ala Val Ile Ala Gly Gly Ser Gly Val Thr Phe Leu Ala Gln
25 30 35

ggc ggt ggt gat gtc aat aca gtg gcc gtc gtc gag cca cag gac gag 259
Gly Gly Gly Asp Val Asn Thr Val Ala Val Val Glu Pro Gln Asp Glu
40 45 50

gta aaa aat cag gtc gtg aca gaa acc gaa att gtc acg aag gtt cac 307
Val Lys Asn Gln Val Val Thr Glu Thr Glu Ile Val Thr Lys Val His
55 60 65

gat cct tct tca tct gac gcc agt gat gct gac agc aac aca ggc acc 355
Asp Pro Ser Ser Ser Asp Ala Ser Asp Ala Asp Ser Asn Thr Gly Thr
70 75 80 85

gcc gaa ggc gca gac tca gat cac aaa gaa ccc cgt gag cac gac agt 403
Ala Glu Gly Ala Asp Ser Asp His Lys Glu Pro Arg Glu His Asp Ser
90 95 100

gct caa gag cca acg gct ccg acc gac ccc acc ttg acc att acc ggc 451
Ala Gln Glu Pro Thr Ala Pro Thr Asp Pro Thr Leu Thr Ile Thr Gly
105 110 115

aac ggt gac aca cca gta tca gca ctt gat gct gtc gca gga cct gcc 499
Asn Gly Asp Thr Pro Val Ser Ala Leu Asp Ala Val Ala Gly Pro Ala
120 125 130

cgt cca ggt acg gtg cac gtc att gag aat ggc gaa acc ttg tcc tct 547
Arg Pro Gly Thr Val His Val Ile Glu Asn Gly Glu Thr Leu Ser Ser
135 140 145

att tct cag gac agt ggt gtg ccg gtt ggg ttg atc att gat cgc aac 595
Ile Ser Gln Asp Ser Gly Val Pro Val Gly Leu Ile Ile Asp Arg Asn
150 155 160 165

aag ctt gtt gat cca gac ctg atc tat gca ggc acg cca ttg gcg att 643

```
Lys Leu Val Asp Pro Asp Leu Ile Tyr Ala Gly Thr Pro Leu Ala Ile
                170                 175                 180

ccg act gag cag gaa ctt gct gct gcg ata cag taatgtagtg gtagagggtt 696
Pro Thr Glu Gln Glu Leu Ala Ala Ala Ile Gln
            185                 190

aaa                                                               699
```

<210> 2036
<211> 192
<212> PRT
<213> Corynebacterium glutamicum

<400> 2036

```
Met Ala Ile Lys Gly Ala Met Pro Lys Asn Arg Val Pro Gly Val Ala
  1               5                  10                  15

Ala Gly Ala Phe Ile Ala Ala Ala Val Ile Ala Gly Gly Ser Gly Val
             20                  25                  30

Thr Phe Leu Ala Gln Gly Gly Gly Asp Val Asn Thr Val Ala Val Val
         35                  40                  45

Glu Pro Gln Asp Glu Val Lys Asn Gln Val Val Thr Glu Thr Glu Ile
     50                  55                  60

Val Thr Lys Val His Asp Pro Ser Ser Ser Asp Ala Ser Asp Ala Asp
 65                  70                  75                  80

Ser Asn Thr Gly Thr Ala Glu Gly Ala Asp Ser Asp His Lys Glu Pro
                 85                  90                  95

Arg Glu His Asp Ser Ala Gln Glu Pro Thr Ala Pro Thr Asp Pro Thr
            100                 105                 110

Leu Thr Ile Thr Gly Asn Gly Asp Thr Pro Val Ser Ala Leu Asp Ala
        115                 120                 125

Val Ala Gly Pro Ala Arg Pro Gly Thr Val His Val Ile Glu Asn Gly
    130                 135                 140

Glu Thr Leu Ser Ser Ile Ser Gln Asp Ser Gly Val Pro Val Gly Leu
145                 150                 155                 160

Ile Ile Asp Arg Asn Lys Leu Val Asp Pro Asp Leu Ile Tyr Ala Gly
                165                 170                 175

Thr Pro Leu Ala Ile Pro Thr Glu Gln Glu Leu Ala Ala Ala Ile Gln
            180                 185                 190
```

<210> 2037
<211> 1026
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1003)
<223> RXA01040

<400> 2037
taatttctgt tactattaac atataggttt tttaaagttt cgtctacata aacctgcaac 60

agaaatcact acacccagtt ctcgaaaggc tttttctctc atg acc tac cca gtt 115
Met Thr Tyr Pro Val
1 5

acc cct caa cct gtg cag cca gca cca gtc gcc gaa aag atc aag gca 163
Thr Pro Gln Pro Val Gln Pro Ala Pro Val Ala Glu Lys Ile Lys Ala
10 15 20

tca agc ctc aaa gaa ggc act cag gta ttt atc aaa ggt cgg gtt aat 211
Ser Ser Leu Lys Glu Gly Thr Gln Val Phe Ile Lys Gly Arg Val Asn
25 30 35

tac tcc cgc atc gca agc ttt att act ggt acc gag cgc gaa aac cgt 259
Tyr Ser Arg Ile Ala Ser Phe Ile Thr Gly Thr Glu Arg Glu Asn Arg
40 45 50

aat cgc gac agg ctt cac cca atc gaa ttc gac tac acc tcc ctg act 307
Asn Arg Asp Arg Leu His Pro Ile Glu Phe Asp Tyr Thr Ser Leu Thr
55 60 65

ttg agc cac cct gaa atc atc tac ggc aac ccg caa caa aag acc aat 355
Leu Ser His Pro Glu Ile Ile Tyr Gly Asn Pro Gln Gln Lys Thr Asn
70 75 80 85

gaa gaa ctc ttc ctt gag cag cga atc ttt gtc ggc aag aag cgt cct 403
Glu Glu Leu Phe Leu Glu Gln Arg Ile Phe Val Gly Lys Lys Arg Pro
90 95 100

gaa gag ggt cca aaa ttc tcc att gac aac aag agc aac cgt cta cca 451
Glu Glu Gly Pro Lys Phe Ser Ile Asp Asn Lys Ser Asn Arg Leu Pro
105 110 115

cag gtt tgg gtg cca tcc acc aat gct gat ggt act tat gag cag ctt 499
Gln Val Trp Val Pro Ser Thr Asn Ala Asp Gly Thr Tyr Glu Gln Leu
120 125 130

gaa ggt ctc gaa ggt gag ctc gac gca ggg ctc aac gtc att att ctc 547
Glu Gly Leu Glu Gly Glu Leu Asp Ala Gly Leu Asn Val Ile Ile Leu
135 140 145

atc gag ttc tat aag cca cgt aca cag gtt aat cgc ggc tcc cgc ctc 595
Ile Glu Phe Tyr Lys Pro Arg Thr Gln Val Asn Arg Gly Ser Arg Leu
150 155 160 165

aac gcc gtg ttc ctg cag gag ccc att cgt tac tac acc cct ggt tac 643
Asn Ala Val Phe Leu Gln Glu Pro Ile Arg Tyr Tyr Thr Pro Gly Tyr
170 175 180

aat gca gat aag ctc gct gcc ctc gga atc gta ctt aac gca ccg cca 691
Asn Ala Asp Lys Leu Ala Ala Leu Gly Ile Val Leu Asn Ala Pro Pro
185 190 195

aag gac act att cag ctc gtt cct aat gag gtc gct gca gga caa gac 739

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Lys Asp Thr Ile Gln Leu Val Pro Asn Glu Val Ala Ala Gly Gln Asp
        200                 205                 210

cag tcc acc acc gat gca tcc ggt ctc ccg ctt cca ggc cag gga tat   787
Gln Ser Thr Thr Asp Ala Ser Gly Leu Pro Leu Pro Gly Gln Gly Tyr
    215                 220                 225

agc gca cct gat cag cca tat cag gcg cag cct cag tat cag cag gca   835
Ser Ala Pro Asp Gln Pro Tyr Gln Ala Gln Pro Gln Tyr Gln Gln Ala
230                 235                 240                 245

acc cca gcg gct gca cct cag cag tac cag gcc cca cag ccc cag tac   883
Thr Pro Ala Ala Ala Pro Gln Gln Tyr Gln Ala Pro Gln Pro Gln Tyr
                250                 255                 260

cag cag tca gct cca cag gca caa cct gca ccg gca cca gtt gcg cag   931
Gln Gln Ser Ala Pro Gln Ala Gln Pro Ala Pro Ala Pro Val Ala Gln
            265                 270                 275

ttc cag cag gca agc gcc tca ggc acc tgc tca gcc agc aca gca gca   979
Phe Gln Gln Ala Ser Ala Ser Gly Thr Cys Ser Ala Ser Thr Ala Ala
        280                 285                 290

gta tca ggc acc act tcc tgc cgg taatcctctt gcagcaggtc agc        1026
Val Ser Gly Thr Thr Ser Cys Arg
    295                 300


<210> 2038
<211> 301
<212> PRT
<213> Corynebacterium glutamicum

<400> 2038
Met Thr Tyr Pro Val Thr Pro Gln Pro Val Gln Pro Ala Pro Val Ala
  1               5                  10                  15

Glu Lys Ile Lys Ala Ser Ser Leu Lys Glu Gly Thr Gln Val Phe Ile
             20                  25                  30

Lys Gly Arg Val Asn Tyr Ser Arg Ile Ala Ser Phe Ile Thr Gly Thr
         35                  40                  45

Glu Arg Glu Asn Arg Asn Arg Asp Arg Leu His Pro Ile Glu Phe Asp
     50                  55                  60

Tyr Thr Ser Leu Thr Leu Ser His Pro Glu Ile Ile Tyr Gly Asn Pro
 65                  70                  75                  80

Gln Gln Lys Thr Asn Glu Glu Leu Phe Leu Glu Gln Arg Ile Phe Val
                 85                  90                  95

Gly Lys Lys Arg Pro Glu Glu Gly Pro Lys Phe Ser Ile Asp Asn Lys
            100                 105                 110

Ser Asn Arg Leu Pro Gln Val Trp Val Pro Ser Thr Asn Ala Asp Gly
        115                 120                 125

Thr Tyr Glu Gln Leu Glu Gly Leu Glu Gly Glu Leu Asp Ala Gly Leu
    130                 135                 140
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Asn Val Ile Ile Leu Ile Glu Phe Tyr Lys Pro Arg Thr Gln Val Asn
145                 150                 155                 160

Arg Gly Ser Arg Leu Asn Ala Val Phe Leu Gln Glu Pro Ile Arg Tyr
                165                 170                 175

Tyr Thr Pro Gly Tyr Asn Ala Asp Lys Leu Ala Ala Leu Gly Ile Val
            180                 185                 190

Leu Asn Ala Pro Pro Lys Asp Thr Ile Gln Leu Val Pro Asn Glu Val
        195                 200                 205

Ala Ala Gly Gln Asp Gln Ser Thr Thr Asp Ala Ser Gly Leu Pro Leu
    210                 215                 220

Pro Gly Gln Gly Tyr Ser Ala Pro Asp Gln Pro Tyr Gln Ala Gln Pro
225                 230                 235                 240

Gln Tyr Gln Gln Ala Thr Pro Ala Ala Ala Pro Gln Gln Tyr Gln Ala
                245                 250                 255

Pro Gln Pro Gln Tyr Gln Gln Ser Ala Pro Gln Ala Gln Pro Ala Pro
            260                 265                 270

Ala Pro Val Ala Gln Phe Gln Gln Ala Ser Ala Ser Gly Thr Cys Ser
        275                 280                 285

Ala Ser Thr Ala Ala Val Ser Gly Thr Thr Ser Cys Arg
    290                 295                 300


<210> 2039
<211> 276
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(253)
<223> RXA01041

<400> 2039
acagcaggca atgcctaccc aagccccaca aacaccggca caaccagttc agccaccagc 60

accacaagcc ggttctgcat ttaccgatgc tccgggtgct gtg cca cag gca cca   115
                                        Val Pro Gln Ala Pro
                                          1               5

gca gtt cag gct gct ccc gct gta gct cag gcg cct gtc gcg cca gta   163
Ala Val Gln Ala Ala Pro Ala Val Ala Gln Ala Pro Val Ala Pro Val
                10                  15                  20

gtt gat atg acc gag cca gca tcc cca tgg gat ctt cca gct gca cct   211
Val Asp Met Thr Glu Pro Ala Ser Pro Trp Asp Leu Pro Ala Ala Pro
            25                  30                  35

agt cag cca gcg cag cca gct cag ggc atc acc tac ccg gca           253
Ser Gln Pro Ala Gln Pro Ala Gln Gly Ile Thr Tyr Pro Ala
        40                  45                  50

taacaaccag cacaaccctt aga                                         276
```

<210> 2040
<211> 51
<212> PRT
<213> Corynebacterium glutamicum

<400> 2040
Val Pro Gln Ala Pro Ala Val Gln Ala Ala Pro Ala Val Ala Gln Ala
1 5 10 15

Pro Val Ala Pro Val Val Asp Met Thr Glu Pro Ala Ser Pro Trp Asp
20 25 30

Leu Pro Ala Ala Pro Ser Gln Pro Ala Gln Pro Ala Gln Gly Ile Thr
35 40 45

Tyr Pro Ala
50

<210> 2041
<211> 1401
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1378)
<223> RXA01042

<400> 2041
tttttcacc agggtcgagg cgcggtctgt gtgcccacct cgacccactt ttcgcccacc 60

acttttcgtc aacctaccaa caacaaagcc caggtcactt atg gtc aac cct ttt 115
Met Val Asn Pro Phe
1 5

cac acg ctt gat aac tca ccg ttt gat ccg gtg gca cag ttt cct gcg 163
His Thr Leu Asp Asn Ser Pro Phe Asp Pro Val Ala Gln Phe Pro Ala
10 15 20

ttt tat cac aac ccg ctt atc aat cac ttg ggc cgc cgt cgc gcc tgg 211
Phe Tyr His Asn Pro Leu Ile Asn His Leu Gly Arg Arg Arg Ala Trp
25 30 35

aca atc tca gac atc aac aaa cgc ccc atc aat gtc caa cag atg ctg 259
Thr Ile Ser Asp Ile Asn Lys Arg Pro Ile Asn Val Gln Gln Met Leu
40 45 50

acc acg gcc acc tac ggt agc ccc gtt att cat ggt gcc cgc att gaa 307
Thr Thr Ala Thr Tyr Gly Ser Pro Val Ile His Gly Ala Arg Ile Glu
55 60 65

gac gca gca acc tcc cta ctt acc ctg gat gaa ctg cgt aca cag att 355
Asp Ala Ala Thr Ser Leu Leu Thr Leu Asp Glu Leu Arg Thr Gln Ile
70 75 80 85

ccc acc gct gcc aac aat gcg ttt tat ctc gat gct gtc caa gat ggc 403
Pro Thr Ala Ala Asn Asn Ala Phe Tyr Leu Asp Ala Val Gln Asp Gly
90 95 100

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tgt ctt att tta gat att gaa aaa acc tgt ccc ccc gag gtc gca gcc   451
Cys Leu Ile Leu Asp Ile Glu Lys Thr Cys Pro Pro Glu Val Ala Ala
            105                 110                 115

aca cta ctc acg ctc tcc ccc acc gcc ttt tac aca gag gtg tcc atg   499
Thr Leu Leu Thr Leu Ser Pro Thr Ala Phe Tyr Thr Glu Val Ser Met
        120                 125                 130

agt ggt cgt ggc tat cac ctc gtt atg ccg ata cca gag aat ttt gca   547
Ser Gly Arg Gly Tyr His Leu Val Met Pro Ile Pro Glu Asn Phe Ala
    135                 140                 145

gcg ttt cct gcc gta cac aac aaa ccc agt atc aaa cac ccc aag cgc   595
Ala Phe Pro Ala Val His Asn Lys Pro Ser Ile Lys His Pro Lys Arg
150                 155                 160                 165

tgg ttc gaa att ctt acc tca cag tgg atc acc ttc acc cga caa cca   643
Trp Phe Glu Ile Leu Thr Ser Gln Trp Ile Thr Phe Thr Arg Gln Pro
                170                 175                 180

atc cca gag cat gtt ctc cat cac agt gaa tct gct aac aca agt gct   691
Ile Pro Glu His Val Leu His His Ser Glu Ser Ala Asn Thr Ser Ala
            185                 190                 195

gtg cca tgg ttg aat gat caa cca ctt aca tgg gaa aac gtc ttt gca   739
Val Pro Trp Leu Asn Asp Gln Pro Leu Thr Trp Glu Asn Val Phe Ala
        200                 205                 210

gac tta gct aaa act gtt gca ccc aac tta aaa acc ggt gcc gga ctt   787
Asp Leu Ala Lys Thr Val Ala Pro Asn Leu Lys Thr Gly Ala Gly Leu
    215                 220                 225

acc atc aca ccc aat gca ctg atg cca cca gat ctc agc gat gct gag   835
Thr Ile Thr Pro Asn Ala Leu Met Pro Pro Asp Leu Ser Asp Ala Glu
230                 235                 240                 245

cgc att cgc gac gat gaa gtc atc gac tcg acc tgt cga tta ttt gcc   883
Arg Ile Arg Asp Asp Glu Val Ile Asp Ser Thr Cys Arg Leu Phe Ala
                250                 255                 260

gaa cat tac tcg aaa aca ctt gcg gac ttc tat gat gat gca tcc cgg   931
Glu His Tyr Ser Lys Thr Leu Ala Asp Phe Tyr Asp Asp Ala Ser Arg
            265                 270                 275

ttc gag ttc agc caa att ggt gtc att atc aat cta ctg ctc ccc act   979
Phe Glu Phe Ser Gln Ile Gly Val Ile Ile Asn Leu Leu Leu Pro Thr
        280                 285                 290

atg agg atg cat ccc acc acg atc agt ctc gac aaa ccc atc aac tcc   1027
Met Arg Met His Pro Thr Thr Ile Ser Leu Asp Lys Pro Ile Asn Ser
    295                 300                 305

gat cac atc atc aga ctt ctg ttc gct gtc gct act cgc gtg atc act   1075
Asp His Ile Ile Arg Leu Leu Phe Ala Val Ala Thr Arg Val Ile Thr
310                 315                 320                 325

cac cgc agc aaa cat gat gag gag cga tct ggc gtt ccg tat ctg atg   1123
His Arg Ser Lys His Asp Glu Glu Arg Ser Gly Val Pro Tyr Leu Met
                330                 335                 340
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tat cag gtt att tcc tgc ctt gac atg cga gaa cac ccc gac aat ggc   1171
Tyr Gln Val Ile Ser Cys Leu Asp Met Arg Glu His Pro Asp Asn Gly
            345                 350                 355

gac tac cgt gtc gta ccc tcc cgg cat aat aga gac caa cac agc aac   1219
Asp Tyr Arg Val Val Pro Ser Arg His Asn Arg Asp Gln His Ser Asn
        360                 365                 370

aac ccc tca gct cat gtg gtc cac caa caa cca caa ccc cag ccc agc   1267
Asn Pro Ser Ala His Val Val His Gln Gln Pro Gln Pro Gln Pro Ser
    375                 380                 385

gca gca gat tcg cca cat cac tac cgt gca cta ccc caa gaa aac acg   1315
Ala Ala Asp Ser Pro His His Tyr Arg Ala Leu Pro Gln Glu Asn Thr
390                 395                 400                 405

gtg tcc gaa cac agt ttt aaa atc tat aac cca cca gcc aca ccc cct   1363
Val Ser Glu His Ser Phe Lys Ile Tyr Asn Pro Pro Ala Thr Pro Pro
                410                 415                 420

cta gga ggt gaa aat tagatttatt attaaaacac ttg                    1401
Leu Gly Gly Glu Asn
            425
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Sequence Listing 20090330 20090330 20090330 20090330

<210> 2042
<211> 426
<212> PRT
<213> Corynebacterium glutamicum

<400> 2042

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Met Val Asn Pro Phe His Thr Leu Asp Asn Ser Pro Phe Asp Pro Val
  1               5                  10                  15

Ala Gln Phe Pro Ala Phe Tyr His Asn Pro Leu Ile Asn His Leu Gly
             20                  25                  30

Arg Arg Arg Ala Trp Thr Ile Ser Asp Ile Asn Lys Arg Pro Ile Asn
         35                  40                  45

Val Gln Gln Met Leu Thr Thr Ala Thr Tyr Gly Ser Pro Val Ile His
     50                  55                  60

Gly Ala Arg Ile Glu Asp Ala Ala Thr Ser Leu Leu Thr Leu Asp Glu
 65                  70                  75                  80

Leu Arg Thr Gln Ile Pro Thr Ala Ala Asn Asn Ala Phe Tyr Leu Asp
                85                  90                  95

Ala Val Gln Asp Gly Cys Leu Ile Leu Asp Ile Glu Lys Thr Cys Pro
            100                 105                 110

Pro Glu Val Ala Ala Thr Leu Leu Thr Leu Ser Pro Thr Ala Phe Tyr
        115                 120                 125

Thr Glu Val Ser Met Ser Gly Arg Gly Tyr His Leu Val Met Pro Ile
    130                 135                 140

Pro Glu Asn Phe Ala Ala Phe Pro Ala Val His Asn Lys Pro Ser Ile
145                 150                 155                 160
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Lys His Pro Lys Arg Trp Phe Glu Ile Leu Thr Ser Gln Trp Ile Thr
165 170 175

Phe Thr Arg Gln Pro Ile Pro Glu His Val Leu His His Ser Glu Ser
180 185 190

Ala Asn Thr Ser Ala Val Pro Trp Leu Asn Asp Gln Pro Leu Thr Trp
195 200 205

Glu Asn Val Phe Ala Asp Leu Ala Lys Thr Val Ala Pro Asn Leu Lys
210 215 220

Thr Gly Ala Gly Leu Thr Ile Thr Pro Asn Ala Leu Met Pro Pro Asp
225 230 235 240

Leu Ser Asp Ala Glu Arg Ile Arg Asp Asp Glu Val Ile Asp Ser Thr
245 250 255

Cys Arg Leu Phe Ala Glu His Tyr Ser Lys Thr Leu Ala Asp Phe Tyr
260 265 270

Asp Asp Ala Ser Arg Phe Glu Phe Ser Gln Ile Gly Val Ile Ile Asn
275 280 285

Leu Leu Leu Pro Thr Met Arg Met His Pro Thr Thr Ile Ser Leu Asp
290 295 300

Lys Pro Ile Asn Ser Asp His Ile Ile Arg Leu Leu Phe Ala Val Ala
305 310 315 320

Thr Arg Val Ile Thr His Arg Ser Lys His Asp Glu Glu Arg Ser Gly
325 330 335

Val Pro Tyr Leu Met Tyr Gln Val Ile Ser Cys Leu Asp Met Arg Glu
340 345 350

His Pro Asp Asn Gly Asp Tyr Arg Val Val Pro Ser Arg His Asn Arg
355 360 365

Asp Gln His Ser Asn Asn Pro Ser Ala His Val Val His Gln Gln Pro
370 375 380

Gln Pro Gln Pro Ser Ala Ala Asp Ser Pro His His Tyr Arg Ala Leu
385 390 395 400

Pro Gln Glu Asn Thr Val Ser Glu His Ser Phe Lys Ile Tyr Asn Pro
405 410 415

Pro Ala Thr Pro Pro Leu Gly Gly Glu Asn
420 425

<210> 2043
<211> 696
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(673)
<223> RXA01043

<400> 2043
tactaggtat agcaacggat taaataatca ctataattaa ttctttccgt actcatttta 60

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atcactacct attcaccact tgaacggagc gtttttcgcc atg ttg aaa ttc cgc   115
                                           Met Leu Lys Phe Arg
                                             1               5

atc atc tcc aca gtc act act gga tct cag cca act cca cga aaa agc   163
Ile Ile Ser Thr Val Thr Thr Gly Ser Gln Pro Thr Pro Arg Lys Ser
                 10                  15                  20

tgg agc cac ccc gac acc act ctc ctg gtc acc atg gtc act gca cca   211
Trp Ser His Pro Asp Thr Thr Leu Leu Val Thr Met Val Thr Ala Pro
             25                  30                  35

tcg ctg tgc tca gcc atc aac gtg tgg aac gca act gag cgt att ccc   259
Ser Leu Cys Ser Ala Ile Asn Val Trp Asn Ala Thr Glu Arg Ile Pro
         40                  45                  50

gct caa aaa atc ctt aat gtc gaa gaa gta cac gtt ctt ggt gag tgc   307
Ala Gln Lys Ile Leu Asn Val Glu Glu Val His Val Leu Gly Glu Cys
     55                  60                  65

agc gac gcc atc atc tct acg tca cta acc aaa aag gac aat ccg cac   355
Ser Asp Ala Ile Ile Ser Thr Ser Leu Thr Lys Lys Asp Asn Pro His
 70                  75                  80                  85

gca ctt gtg ccc gat gat ttc gac caa atc ggc gat gtg ttt ggc tat   403
Ala Leu Val Pro Asp Asp Phe Asp Gln Ile Gly Asp Val Phe Gly Tyr
                 90                  95                 100

gcg caa gac aat gta gct gtt ttt gat gtc att gtc gca gca ctg ggc   451
Ala Gln Asp Asn Val Ala Val Phe Asp Val Ile Val Ala Ala Leu Gly
            105                 110                 115

ggt gct ggt tat ggc ctg cta ccc gga ctg gtc atg cac cac att gat   499
Gly Ala Gly Tyr Gly Leu Leu Pro Gly Leu Val Met His His Ile Asp
        120                 125                 130

gag cac acc gtt gca ctt gtc ttt gat act gat tcc cct act ggg acg   547
Glu His Thr Val Ala Leu Val Phe Asp Thr Asp Ser Pro Thr Gly Thr
    135                 140                 145

cat atc ctc ggt gag cgc tgc gtg tac tcc gac atc att cac atg act   595
His Ile Leu Gly Glu Arg Cys Val Tyr Ser Asp Ile Ile His Met Thr
150                 155                 160                 165

gac gat aag tct gcc cgt ggc tgg ggt gca gtc att gcc ata gca cga   643
Asp Asp Lys Ser Ala Arg Gly Trp Gly Ala Val Ile Ala Ile Ala Arg
                170                 175                 180

gcc atc atc ctc aaa gtc gaa cag atc atg tagtacccca ccatgactca     693
Ala Ile Ile Leu Lys Val Glu Gln Ile Met
            185                 190

ctt                                                               696
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<210> 2044
<211> 191

<212> PRT
<213> Corynebacterium glutamicum

<400> 2044
Met Leu Lys Phe Arg Ile Ile Ser Thr Val Thr Thr Gly Ser Gln Pro
1 5 10 15

Thr Pro Arg Lys Ser Trp Ser His Pro Asp Thr Thr Leu Leu Val Thr
20 25 30

Met Val Thr Ala Pro Ser Leu Cys Ser Ala Ile Asn Val Trp Asn Ala
35 40 45

Thr Glu Arg Ile Pro Ala Gln Lys Ile Leu Asn Val Glu Glu Val His
50 55 60

Val Leu Gly Glu Cys Ser Asp Ala Ile Ile Ser Thr Ser Leu Thr Lys
65 70 75 80

Lys Asp Asn Pro His Ala Leu Val Pro Asp Asp Phe Asp Gln Ile Gly
85 90 95

Asp Val Phe Gly Tyr Ala Gln Asp Asn Val Ala Val Phe Asp Val Ile
100 105 110

Val Ala Ala Leu Gly Gly Ala Gly Tyr Gly Leu Leu Pro Gly Leu Val
115 120 125

Met His His Ile Asp Glu His Thr Val Ala Leu Val Phe Asp Thr Asp
130 135 140

Ser Pro Thr Gly Thr His Ile Leu Gly Glu Arg Cys Val Tyr Ser Asp
145 150 155 160

Ile Ile His Met Thr Asp Asp Lys Ser Ala Arg Gly Trp Gly Ala Val
165 170 175

Ile Ala Ile Ala Arg Ala Ile Ile Leu Lys Val Glu Gln Ile Met
180 185 190

<210> 2045
<211> 1380
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1357)
<223> RXA01044

<400> 2045
cagatagcca ctacctacac gcatctgttg tgctgaaaca acagcgcgac actcactctt 60

ctcattactc aacaacttac ttttaaggac tacataactt atg tct ctc tac ctt 115
Met Ser Leu Tyr Leu
1 5

gac gac act ttg tct cgc atc gtt gaa ctt gat ctc aaa gac acc cgc 163
Asp Asp Thr Leu Ser Arg Ile Val Glu Leu Asp Leu Lys Asp Thr Arg
10 15 20

```
att gtg ccg ttt ctt gct ggt gaa cca ggt atc ggt aaa acc tca ttc   211
Ile Val Pro Phe Leu Ala Gly Glu Pro Gly Ile Gly Lys Thr Ser Phe
            25                  30                  35

atc tac ggc atc ggc gaa cgt gca ggc tac aaa gtc ttc agt atc tcg   259
Ile Tyr Gly Ile Gly Glu Arg Ala Gly Tyr Lys Val Phe Ser Ile Ser
        40                  45                  50

gtt aac acc ctt gcc gat aag ggt gac ctc acg ggc gct cgc acc ctg   307
Val Asn Thr Leu Ala Asp Lys Gly Asp Leu Thr Gly Ala Arg Thr Leu
    55                  60                  65

cag gac cct gcc gat ggc aag tgg aag cag atg ttt ttc ccg cac gcg   355
Gln Asp Pro Ala Asp Gly Lys Trp Lys Gln Met Phe Phe Pro His Ala
70                  75                  80                  85

acc ttc gtc gaa gca aat gac tat gca cta gca aac cca aac gaa acg   403
Thr Phe Val Glu Ala Asn Asp Tyr Ala Leu Ala Asn Pro Asn Glu Thr
                90                  95                  100

gtc gtc att ctt ctc gat gag att aac cga act gat tcg gat gtc acc   451
Val Val Ile Leu Leu Asp Glu Ile Asn Arg Thr Asp Ser Asp Val Thr
            105                 110                 115

tct gcc tcg atg act atc tct act gag cgt cgc gtt ggt acc acc gat   499
Ser Ala Ser Met Thr Ile Ser Thr Glu Arg Arg Val Gly Thr Thr Asp
        120                 125                 130

cta gca ccc aat gtc cgc ctt gct gtc acc gga aac ctc acc ggt aat   547
Leu Ala Pro Asn Val Arg Leu Ala Val Thr Gly Asn Leu Thr Gly Asn
    135                 140                 145

gtc acc cac ctt gat tca gca tct ctg acc agg ttc tcc ctc tat gag   595
Val Thr His Leu Asp Ser Ala Ser Leu Thr Arg Phe Ser Leu Tyr Glu
150                 155                 160                 165

gtc aag cca tcc gca gag acc ttc atg aac atc atg ggc ggc cgc ctc   643
Val Lys Pro Ser Ala Glu Thr Phe Met Asn Ile Met Gly Gly Arg Leu
                170                 175                 180

aac aag tac atc cgt acc gtg ctg acc aaa tac ccg gaa tac atc ttc   691
Asn Lys Tyr Ile Arg Thr Val Leu Thr Lys Tyr Pro Glu Tyr Ile Phe
            185                 190                 195

atg aag cca act act gct act gct ctt att acc act ggc gat gat gat   739
Met Lys Pro Thr Thr Ala Thr Ala Leu Ile Thr Thr Gly Asp Asp Asp
        200                 205                 210

gac gac cat aca acc aat gcg aag caa atg atg gac ttc aac gct gtg   787
Asp Asp His Thr Thr Asn Ala Lys Gln Met Met Asp Phe Asn Ala Val
    215                 220                 225

ctc ggt tca gac caa gac atg gtt caa ttt acc gca cct aga act atc   835
Leu Gly Ser Asp Gln Asp Met Val Gln Phe Thr Ala Pro Arg Thr Ile
230                 235                 240                 245

gaa ggt ttg tcc gtc tgg ctc aac aac gcc gat gat gac ttt ctt cgt   883
Glu Gly Leu Ser Val Trp Leu Asn Asn Ala Asp Asp Asp Phe Leu Arg
                250                 255                 260
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```
cta ctt cta caa gaa aag gtg gat ggt ctt gct cga tcc atg agc ttg   931
Leu Leu Leu Gln Glu Lys Val Asp Gly Leu Ala Arg Ser Met Ser Leu
            265                 270                 275

ctg cag gct acg ctc gaa tct cac acc ggc gat acc gct ttt acc gca   979
Leu Gln Ala Thr Leu Glu Ser His Thr Gly Asp Thr Ala Phe Thr Ala
        280                 285                 290

gaa gtc ctc agc gaa atg acc aat gat ctg ctg agc tcc gca tcg caa   1027
Glu Val Leu Ser Glu Met Thr Asn Asp Leu Leu Ser Ser Ala Ser Gln
    295                 300                 305

gct cct agt ggt cca atc aaa cca ttt gtc tac gac cga ctc gct gct   1075
Ala Pro Ser Gly Pro Ile Lys Pro Phe Val Tyr Asp Arg Leu Ala Ala
310                 315                 320                 325

gca cca agc aat act gta ctg gaa caa gag gtt cac aca ctc agt ctc   1123
Ala Pro Ser Asn Thr Val Leu Glu Gln Glu Val His Thr Leu Ser Leu
                330                 335                 340

aat gac cgc gcc gat gtc ttg ttg ttt gcc ctc cat gac act gta aac   1171
Asn Asp Arg Ala Asp Val Leu Leu Phe Ala Leu His Asp Thr Val Asn
            345                 350                 355

aac gct gca cca agc atc atc gct cac ctt gca tct gaa ggc gta ctt   1219
Asn Ala Ala Pro Ser Ile Ile Ala His Leu Ala Ser Glu Gly Val Leu
        360                 365                 370

gat gaa ctg ccc aaa gac aga atc agc aaa att gtt tca ctc ggt cct   1267
Asp Glu Leu Pro Lys Asp Arg Ile Ser Lys Ile Val Ser Leu Gly Pro
    375                 380                 385

gta cca acg gca aac tat cac gcc ttg acc aga cag gat aca acg ttg   1315
Val Pro Thr Ala Asn Tyr His Ala Leu Thr Arg Gln Asp Thr Thr Leu
390                 395                 400                 405

act cga aat ctc ggt ccc gct gtc ttg ggc ttc ttg gaa agt           1357
Thr Arg Asn Leu Gly Pro Ala Val Leu Gly Phe Leu Glu Ser
                410                 415

taaagcaatt tcctaagtac ctt                                        1380
```

<210> 2046
<211> 419
<212> PRT
<213> Corynebacterium glutamicum

<400> 2046

```
Met Ser Leu Tyr Leu Asp Asp Thr Leu Ser Arg Ile Val Glu Leu Asp
  1               5                  10                  15

Leu Lys Asp Thr Arg Ile Val Pro Phe Leu Ala Gly Glu Pro Gly Ile
             20                  25                  30

Gly Lys Thr Ser Phe Ile Tyr Gly Ile Gly Glu Arg Ala Gly Tyr Lys
         35                  40                  45

Val Phe Ser Ile Ser Val Asn Thr Leu Ala Asp Lys Gly Asp Leu Thr
     50                  55                  60
```

Gly Ala Arg Thr Leu Gln Asp Pro Ala Asp Gly Lys Trp Lys Gln Met
65 70 75 80

Phe Phe Pro His Ala Thr Phe Val Glu Ala Asn Asp Tyr Ala Leu Ala
85 90 95

Asn Pro Asn Glu Thr Val Val Ile Leu Leu Asp Glu Ile Asn Arg Thr
100 105 110

Asp Ser Asp Val Thr Ser Ala Ser Met Thr Ile Ser Thr Glu Arg Arg
115 120 125

Val Gly Thr Thr Asp Leu Ala Pro Asn Val Arg Leu Ala Val Thr Gly
130 135 140

Asn Leu Thr Gly Asn Val Thr His Leu Asp Ser Ala Ser Leu Thr Arg
145 150 155 160

Phe Ser Leu Tyr Glu Val Lys Pro Ser Ala Glu Thr Phe Met Asn Ile
165 170 175

Met Gly Gly Arg Leu Asn Lys Tyr Ile Arg Thr Val Leu Thr Lys Tyr
180 185 190

Pro Glu Tyr Ile Phe Met Lys Pro Thr Thr Ala Thr Ala Leu Ile Thr
195 200 205

Thr Gly Asp Asp Asp Asp Asp His Thr Thr Asn Ala Lys Gln Met Met
210 215 220

Asp Phe Asn Ala Val Leu Gly Ser Asp Gln Asp Met Val Gln Phe Thr
225 230 235 240

Ala Pro Arg Thr Ile Glu Gly Leu Ser Val Trp Leu Asn Asn Ala Asp
245 250 255

Asp Asp Phe Leu Arg Leu Leu Leu Gln Glu Lys Val Asp Gly Leu Ala
260 265 270

Arg Ser Met Ser Leu Leu Gln Ala Thr Leu Glu Ser His Thr Gly Asp
275 280 285

Thr Ala Phe Thr Ala Glu Val Leu Ser Glu Met Thr Asn Asp Leu Leu
290 295 300

Ser Ser Ala Ser Gln Ala Pro Ser Gly Pro Ile Lys Pro Phe Val Tyr
305 310 315 320

Asp Arg Leu Ala Ala Ala Pro Ser Asn Thr Val Leu Glu Gln Glu Val
325 330 335

His Thr Leu Ser Leu Asn Asp Arg Ala Asp Val Leu Leu Phe Ala Leu
340 345 350

His Asp Thr Val Asn Asn Ala Ala Pro Ser Ile Ile Ala His Leu Ala
355 360 365

Ser Glu Gly Val Leu Asp Glu Leu Pro Lys Asp Arg Ile Ser Lys Ile
370 375 380

Val Ser Leu Gly Pro Val Pro Thr Ala Asn Tyr His Ala Leu Thr Arg

```
385                 390                 395                 400

Gln Asp Thr Thr Leu Thr Arg Asn Leu Gly Pro Ala Val Leu Gly Phe
                405                 410                 415

Leu Glu Ser
```

<210> 2047
<211> 1947
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1924)
<223> RXA01045

<400> 2047

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cagctgaggt agtcatctgt ctacctgcgt ggagtagaca ctaaatcctg tccacgcacc 60

cttacccttc ttgacactag taattgaaag cgatcccctc atg gtt acc ttc agc   115
                                            Met Val Thr Phe Ser
                                              1               5

gtc gca aat cac gcg cct cat act ttt agc cca ttc gat att gaa cca   163
Val Ala Asn His Ala Pro His Thr Phe Ser Pro Phe Asp Ile Glu Pro
                10                  15                  20

cca ctc acc ggt aac gcc acc acc gac gaa cat ggt tac gaa cac acc   211
Pro Leu Thr Gly Asn Ala Thr Thr Asp Glu His Gly Tyr Glu His Thr
            25                  30                  35

tca gtg cta gaa aaa cta gcc tcc aac cac ctg ttc aat cca atc aat   259
Ser Val Leu Glu Lys Leu Ala Ser Asn His Leu Phe Asn Pro Ile Asn
        40                  45                  50

ccg caa cac cca gtc act atc aca gcc acc gaa aac gga tca acc gtt   307
Pro Gln His Pro Val Thr Ile Thr Ala Thr Glu Asn Gly Ser Thr Val
    55                  60                  65

gat ctt gat gca gca gca cta gca caa cat ctt gct cta gcg att acc   355
Asp Leu Asp Ala Ala Ala Leu Ala Gln His Leu Ala Leu Ala Ile Thr
70                  75                  80                  85

cca gac tca atg ctg gca aat cat caa ggc tac aac cgt gac atg atg   403
Pro Asp Ser Met Leu Ala Asn His Gln Gly Tyr Asn Arg Asp Met Met
                90                  95                  100

ggt cta ctt tcg cag ctt act aac cat gtt ggc ttt gat cgc cga ttc   451
Gly Leu Leu Ser Gln Leu Thr Asn His Val Gly Phe Asp Arg Arg Phe
            105                 110                 115

att gtt gac caa ctc ttt atc tcc caa gtg ctc aaa gcg aat cgt cta   499
Ile Val Asp Gln Leu Phe Ile Ser Gln Val Leu Lys Ala Asn Arg Leu
        120                 125                 130

cca gca ccg gca aac aac gtt att tac acc gtg ccc aat gac gtt atc   547
Pro Ala Pro Ala Asn Asn Val Ile Tyr Thr Val Pro Asn Asp Val Ile
    135                 140                 145
```

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cca tct gct aaa gac atc ttg tcc acc act gca aaa atg aac aat cca   595
Pro Ser Ala Lys Asp Ile Leu Ser Thr Thr Ala Lys Met Asn Asn Pro
150                 155                 160                 165

ctg aca gtt act gca agt gcc cca att act gtt gac gac att cac aca   643
Leu Thr Val Thr Ala Ser Ala Pro Ile Thr Val Asp Asp Ile His Thr
                170                 175                 180

gcc tat gag gta ttt ttc gct tct ctt gcc tca gtg ttt ttc cct tat   691
Ala Tyr Glu Val Phe Phe Ala Ser Leu Ala Ser Val Phe Phe Pro Tyr
            185                 190                 195

acc tac ggt gcg gta ttc ctt aac aac gca gaa ttc gtt gag ttt gtt   739
Thr Tyr Gly Ala Val Phe Leu Asn Asn Ala Glu Phe Val Glu Phe Val
        200                 205                 210

gat tac ctt att aac gaa gca aca aca ctg cac tcg gca tca ctc atc   787
Asp Tyr Leu Ile Asn Glu Ala Thr Thr Leu His Ser Ala Ser Leu Ile
    215                 220                 225

tcc aac aac acc ttt aat agg ttc caa tca atg cgt aac atc tcc att   835
Ser Asn Asn Thr Phe Asn Arg Phe Gln Ser Met Arg Asn Ile Ser Ile
230                 235                 240                 245

gat aat ctc acc gcc gag ttt ctc tta cgc aaa aat gaa gca gag aca   883
Asp Asn Leu Thr Ala Glu Phe Leu Leu Arg Lys Asn Glu Ala Glu Thr
                250                 255                 260

act gat gat tat tca ttc ccc cgc gta ctt gtt tcc ctg ctg cat tct   931
Thr Asp Asp Tyr Ser Phe Pro Arg Val Leu Val Ser Leu Leu His Ser
            265                 270                 275

tgg gtg aaa ctc aat cac gat gat gct cgt gct aac aat gat gca ccc   979
Trp Val Lys Leu Asn His Asp Asp Ala Arg Ala Asn Asn Asp Ala Pro
        280                 285                 290

acc tgt gca cta gca ccg ttt agt gtg gct caa tgg atc atg ccg gag   1027
Thr Cys Ala Leu Ala Pro Phe Ser Val Ala Gln Trp Ile Met Pro Glu
    295                 300                 305

acc att gtg ttt att aat gct gaa gct cat gct cat gca tcc tcc cag   1075
Thr Ile Val Phe Ile Asn Ala Glu Ala His Ala His Ala Ser Ser Gln
310                 315                 320                 325

gac att gag aag aaa tgg aag gaa att aat gcg gcg tta aca ggg tct   1123
Asp Ile Glu Lys Lys Trp Lys Glu Ile Asn Ala Ala Leu Thr Gly Ser
                330                 335                 340

att cgt att atg tcg cca aat gca att tcc aag ctg caa tct gct cag   1171
Ile Arg Ile Met Ser Pro Asn Ala Ile Ser Lys Leu Gln Ser Ala Gln
            345                 350                 355

cat ctc ggg atg caa gca caa atg cag gcc atg cgt gct cga aaa gat   1219
His Leu Gly Met Gln Ala Gln Met Gln Ala Met Arg Ala Arg Lys Asp
        360                 365                 370

cac cac aac atg cag aag cgt tcc tca caa gaa aac gac ttt tcc aag   1267
His His Asn Met Gln Lys Arg Ser Ser Gln Glu Asn Asp Phe Ser Lys
    375                 380                 385
```

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gca ctc ccc tca cca cag act atc gtg ctt tct gtc gca gag gtt ctg   1315
Ala Leu Pro Ser Pro Gln Thr Ile Val Leu Ser Val Ala Glu Val Leu
390                 395                 400                 405

cgc aaa ctc act cac gta cgc caa tcg cac aac cct cag aaa tac cag   1363
Arg Lys Leu Thr His Val Arg Gln Ser His Asn Pro Gln Lys Tyr Gln
                410                 415                 420

aag aag tct ctg acc aga gct tct cgc cga cac ccg gat aac cct aat   1411
Lys Lys Ser Leu Thr Arg Ala Ser Arg Arg His Pro Asp Asn Pro Asn
            425                 430                 435

gtc cct ggc acc att aag agc aag ctc ttc tac cct gac ctg cat gtt   1459
Val Pro Gly Thr Ile Lys Ser Lys Leu Phe Tyr Pro Asp Leu His Val
        440                 445                 450

tat gta gat act tct ggt tcg att agt gaa gaa agc tac cgc aac tct   1507
Tyr Val Asp Thr Ser Gly Ser Ile Ser Glu Glu Ser Tyr Arg Asn Ser
    455                 460                 465

gtg gtt ctg ctc atg cag ctt gcc acc aaa ctg gac atc aac ctc tat   1555
Val Val Leu Leu Met Gln Leu Ala Thr Lys Leu Asp Ile Asn Leu Tyr
470                 475                 480                 485

ttc tcc acc ttc tct cac gtg ctc tcc gaa gaa gta cta ttg ccg acc   1603
Phe Ser Thr Phe Ser His Val Leu Ser Glu Glu Val Leu Leu Pro Thr
                490                 495                 500

aag ggt aaa aca cca cag caa ttg gca gct ctt att tcg gcc atc cca   1651
Lys Gly Lys Thr Pro Gln Gln Leu Ala Ala Leu Ile Ser Ala Ile Pro
            505                 510                 515

aag gtc tct ggc ggt act gac tat cac cag att tgg gat tac atc cag   1699
Lys Val Ser Gly Gly Thr Asp Tyr His Gln Ile Trp Asp Tyr Ile Gln
        520                 525                 530

atc aat ccg cag cgc caa gaa cgc atg aat ctt gtg tta act gac ttc   1747
Ile Asn Pro Gln Arg Gln Glu Arg Met Asn Leu Val Leu Thr Asp Phe
    535                 540                 545

gga ttc atg ccg aat cgc ggc tta aac atc gac cac cca agt tct att   1795
Gly Phe Met Pro Asn Arg Gly Leu Asn Ile Asp His Pro Ser Ser Ile
550                 555                 560                 565

ttc tac gtc cca atc ctg cct gac tac ggc agc tgg tca atg gtt cga   1843
Phe Tyr Val Pro Ile Leu Pro Asp Tyr Gly Ser Trp Ser Met Val Arg
                570                 575                 580

aga gat atg tct cat ttc gca aat gaa atg gtt gac ttc gac ccc tat   1891
Arg Asp Met Ser His Phe Ala Asn Glu Met Val Asp Phe Asp Pro Tyr
            585                 590                 595

atc cac agc cga cta ctc ggc gta cac gga aaa tagcagctga tccatctagg 1944
Ile His Ser Arg Leu Leu Gly Val His Gly Lys
        600                 605

gtc                                                               1947
```

<210> 2048
<211> 608

<212> PRT
<213> Corynebacterium glutamicum

<400> 2048

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Met Val Thr Phe Ser Val Ala Asn His Ala Pro His Thr Phe Ser Pro
  1               5                  10                  15

Phe Asp Ile Glu Pro Pro Leu Thr Gly Asn Ala Thr Thr Asp Glu His
            20                  25                  30

Gly Tyr Glu His Thr Ser Val Leu Glu Lys Leu Ala Ser Asn His Leu
        35                  40                  45

Phe Asn Pro Ile Asn Pro Gln His Pro Val Thr Ile Thr Ala Thr Glu
    50                  55                  60

Asn Gly Ser Thr Val Asp Leu Asp Ala Ala Ala Leu Ala Gln His Leu
65                  70                  75                  80

Ala Leu Ala Ile Thr Pro Asp Ser Met Leu Ala Asn His Gln Gly Tyr
                85                  90                  95

Asn Arg Asp Met Met Gly Leu Leu Ser Gln Leu Thr Asn His Val Gly
            100                 105                 110

Phe Asp Arg Arg Phe Ile Val Asp Gln Leu Phe Ile Ser Gln Val Leu
        115                 120                 125

Lys Ala Asn Arg Leu Pro Ala Pro Ala Asn Asn Val Ile Tyr Thr Val
    130                 135                 140

Pro Asn Asp Val Ile Pro Ser Ala Lys Asp Ile Leu Ser Thr Thr Ala
145                 150                 155                 160

Lys Met Asn Asn Pro Leu Thr Val Thr Ala Ser Ala Pro Ile Thr Val
                165                 170                 175

Asp Asp Ile His Thr Ala Tyr Glu Val Phe Phe Ala Ser Leu Ala Ser
            180                 185                 190

Val Phe Phe Pro Tyr Thr Tyr Gly Ala Val Phe Leu Asn Asn Ala Glu
        195                 200                 205

Phe Val Glu Phe Val Asp Tyr Leu Ile Asn Glu Ala Thr Thr Leu His
    210                 215                 220

Ser Ala Ser Leu Ile Ser Asn Asn Thr Phe Asn Arg Phe Gln Ser Met
225                 230                 235                 240

Arg Asn Ile Ser Ile Asp Asn Leu Thr Ala Glu Phe Leu Leu Arg Lys
                245                 250                 255

Asn Glu Ala Glu Thr Thr Asp Asp Tyr Ser Phe Pro Arg Val Leu Val
            260                 265                 270

Ser Leu Leu His Ser Trp Val Lys Leu Asn His Asp Asp Ala Arg Ala
        275                 280                 285

Asn Asn Asp Ala Pro Thr Cys Ala Leu Ala Pro Phe Ser Val Ala Gln
    290                 295                 300
```

```
Trp Ile Met Pro Glu Thr Ile Val Phe Ile Asn Ala Glu Ala His Ala
305                 310                 315                 320

His Ala Ser Ser Gln Asp Ile Glu Lys Lys Trp Lys Glu Ile Asn Ala
                325                 330                 335

Ala Leu Thr Gly Ser Ile Arg Ile Met Ser Pro Asn Ala Ile Ser Lys
            340                 345                 350

Leu Gln Ser Ala Gln His Leu Gly Met Gln Ala Gln Met Gln Ala Met
        355                 360                 365

Arg Ala Arg Lys Asp His His Asn Met Gln Lys Arg Ser Ser Gln Glu
    370                 375                 380

Asn Asp Phe Ser Lys Ala Leu Pro Ser Pro Gln Thr Ile Val Leu Ser
385                 390                 395                 400

Val Ala Glu Val Leu Arg Lys Leu Thr His Val Arg Gln Ser His Asn
                405                 410                 415

Pro Gln Lys Tyr Gln Lys Lys Ser Leu Thr Arg Ala Ser Arg Arg His
            420                 425                 430

Pro Asp Asn Pro Asn Val Pro Gly Thr Ile Lys Ser Lys Leu Phe Tyr
        435                 440                 445

Pro Asp Leu His Val Tyr Val Asp Thr Ser Gly Ser Ile Ser Glu Glu
    450                 455                 460

Ser Tyr Arg Asn Ser Val Val Leu Leu Met Gln Leu Ala Thr Lys Leu
465                 470                 475                 480

Asp Ile Asn Leu Tyr Phe Ser Thr Phe Ser His Val Leu Ser Glu Glu
                485                 490                 495

Val Leu Leu Pro Thr Lys Gly Lys Thr Pro Gln Gln Leu Ala Ala Leu
            500                 505                 510

Ile Ser Ala Ile Pro Lys Val Ser Gly Gly Thr Asp Tyr His Gln Ile
        515                 520                 525

Trp Asp Tyr Ile Gln Ile Asn Pro Gln Arg Gln Glu Arg Met Asn Leu
    530                 535                 540

Val Leu Thr Asp Phe Gly Phe Met Pro Asn Arg Gly Leu Asn Ile Asp
545                 550                 555                 560

His Pro Ser Ser Ile Phe Tyr Val Pro Ile Leu Pro Asp Tyr Gly Ser
                565                 570                 575

Trp Ser Met Val Arg Arg Asp Met Ser His Phe Ala Asn Glu Met Val
            580                 585                 590

Asp Phe Asp Pro Tyr Ile His Ser Arg Leu Leu Gly Val His Gly Lys
        595                 600                 605
```

<210> 2049
<211> 1902
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1879)
<223> RXA01046

<400> 2049
tagcgatcct aggcaaaatg caccagctaa ccccaccgct caaccgccat ctgcccccac 60

ctcacactca tcacagcagg gtctccctcc gggcgccatt atg atc cct ttt cca 115
Met Ile Pro Phe Pro
1 5

ggg caa ccg cag cag caa agc gca ccc aat gac gag acc cgt ttc atc 163
Gly Gln Pro Gln Gln Gln Ser Ala Pro Asn Asp Glu Thr Arg Phe Ile
10 15 20

gac ctt aac gaa cgt cat aaa gat gat gaa cca gcc ctg ttt cgc gat 211
Asp Leu Asn Glu Arg His Lys Asp Asp Glu Pro Ala Leu Phe Arg Asp
25 30 35

gat gtt att gat caa act ctc gct att ttg atc agt aaa aat aag ccc 259
Asp Val Ile Asp Gln Thr Leu Ala Ile Leu Ile Ser Lys Asn Lys Pro
40 45 50

aat gcg cta ctc gtt ggg cct gcc ggt aca ggt aaa tcc cgt atc gca 307
Asn Ala Leu Leu Val Gly Pro Ala Gly Thr Gly Lys Ser Arg Ile Ala
55 60 65

gaa gat att gcg cgc cgc ctt gcc aat gat gac gta tct att ccc gat 355
Glu Asp Ile Ala Arg Arg Leu Ala Asn Asp Asp Val Ser Ile Pro Asp
70 75 80 85

cag ctt gtc ggc cac cgt att ctt gat gtc tcc att gca gag ctt gtt 403
Gln Leu Val Gly His Arg Ile Leu Asp Val Ser Ile Ala Glu Leu Val
90 95 100

gct ggt gct ggc gtt gtt ggt cag ctc aag aaa cgc att ctg gat ctc 451
Ala Gly Ala Gly Val Val Gly Gln Leu Lys Lys Arg Ile Leu Asp Leu
105 110 115

atc aag tat gcg acc gac ccg agt aac aaa gtc att atc ttt att gac 499
Ile Lys Tyr Ala Thr Asp Pro Ser Asn Lys Val Ile Ile Phe Ile Asp
120 125 130

gag att cac caa att gct ggt gat cag tcc agt cac agt gga tcg caa 547
Glu Ile His Gln Ile Ala Gly Asp Gln Ser Ser His Ser Gly Ser Gln
135 140 145

gcc aaa gtt gct cag att ctc aaa ccc tat ctt gcc cgt ggt gac ctt 595
Ala Lys Val Ala Gln Ile Leu Lys Pro Tyr Leu Ala Arg Gly Asp Leu
150 155 160 165

cgt gtt att ggt gcc acc acc acc cag gaa gct cgt gac ttc gat cat 643
Arg Val Ile Gly Ala Thr Thr Thr Gln Glu Ala Arg Asp Phe Asp His
170 175 180

```
gat cca gcc ctc aaa cgc cgt ttt agc aga gta aat gtc gat gaa ttt   691
Asp Pro Ala Leu Lys Arg Arg Phe Ser Arg Val Asn Val Asp Glu Phe
            185                 190                 195

gat cga gat caa acg ctc act att ctt cat gct gca cgt gat ggt tac   739
Asp Arg Asp Gln Thr Leu Thr Ile Leu His Ala Ala Arg Asp Gly Tyr
        200                 205                 210

ctc aaa cat ttc aac aac gct gtc acg gta tct gac gac gta ctg ggc   787
Leu Lys His Phe Asn Asn Ala Val Thr Val Ser Asp Asp Val Leu Gly
    215                 220                 225

tat gtc tac acc tac tcg cag caa ttc aac cca ggc aat aca gca caa   835
Tyr Val Tyr Thr Tyr Ser Gln Gln Phe Asn Pro Gly Asn Thr Ala Gln
230                 235                 240                 245

cct gat gca gca ctg acg ctg ttt gat aag gcg ttg gct tcc cta act   883
Pro Asp Ala Ala Leu Thr Leu Phe Asp Lys Ala Leu Ala Ser Leu Thr
                250                 255                 260

atg gag aaa cag cgt ctg atc aac aac cat gtc att gcg ccg tcg ctc   931
Met Glu Lys Gln Arg Leu Ile Asn Asn His Val Ile Ala Pro Ser Leu
            265                 270                 275

aag ttc cct gtg tca gaa agg cac atc cat aac acc gct cgc aaa ctt   979
Lys Phe Pro Val Ser Glu Arg His Ile His Asn Thr Ala Arg Lys Leu
        280                 285                 290

gcc ttt ggc tct caa gtg cca gcc tcc atc aat act gat gat gct cgt   1027
Ala Phe Gly Ser Gln Val Pro Ala Ser Ile Asn Thr Asp Asp Ala Arg
    295                 300                 305

gac aaa ctc gaa acg ttg ttt ggt caa gat cat att att gag cca gta   1075
Asp Lys Leu Glu Thr Leu Phe Gly Gln Asp His Ile Ile Glu Pro Val
310                 315                 320                 325

ctc acc gct atc aag cgt gaa cag ctt ggt att ttc cct cgc acc aaa   1123
Leu Thr Ala Ile Lys Arg Glu Gln Leu Gly Ile Phe Pro Arg Thr Lys
                330                 335                 340

cca ttg agc tgg gtg ttt gct ggt tca tct ggt gtg ggt aaa aca gaa   1171
Pro Leu Ser Trp Val Phe Ala Gly Ser Ser Gly Val Gly Lys Thr Glu
            345                 350                 355

atg gcg cgt att ctc tct cgc gcc att aat ggc ggc gat ccc atc att   1219
Met Ala Arg Ile Leu Ser Arg Ala Ile Asn Gly Gly Asp Pro Ile Ile
        360                 365                 370

atc aat ggt ccc gaa tac att agt cct gag tcc att act ggc ctt atc   1267
Ile Asn Gly Pro Glu Tyr Ile Ser Pro Glu Ser Ile Thr Gly Leu Ile
    375                 380                 385

gga tca tcc gat ggc tat atc ggc tct aat tct aag cgt gct aaa cca   1315
Gly Ser Ser Asp Gly Tyr Ile Gly Ser Asn Ser Lys Arg Ala Lys Pro
390                 395                 400                 405

ctc gac ccg ctg att tct aat ccg cgt cag gtg att gtg ctc gat gaa   1363
Leu Asp Pro Leu Ile Ser Asn Pro Arg Gln Val Ile Val Leu Asp Glu
                410                 415                 420

ttt gag aag tct cac cct cat ttc cag caa ttg ttc atg gca gct ctt   1411
```

```
Phe Glu Lys Ser His Pro His Phe Gln Gln Leu Phe Met Ala Ala Leu
            425                 430                 435

gat aca ggc act atg gcg atg gct aat ggc acg aca ttg aat ttc tct   1459
Asp Thr Gly Thr Met Ala Met Ala Asn Gly Thr Thr Leu Asn Phe Ser
        440                 445                 450

cag gcc att atc att gcc acc acc aat gca gcc cgc gac aaa atc ggt   1507
Gln Ala Ile Ile Ile Ala Thr Thr Asn Ala Ala Arg Asp Lys Ile Gly
    455                 460                 465

cgt gac agc ttt gga ttc gat tca gat aat tca ggt gtc ctc ggt tct   1555
Arg Asp Ser Phe Gly Phe Asp Ser Asp Asn Ser Gly Val Leu Gly Ser
470                 475                 480                 485

gct caa gca gca act gat ccg cgt gca cag gaa cgc ctc aag tca ctg   1603
Ala Gln Ala Ala Thr Asp Pro Arg Ala Gln Glu Arg Leu Lys Ser Leu
                490                 495                 500

atg tcc aag gat ttc ctg ttg aac tgc tca acc gtt tcc aga ata tct   1651
Met Ser Lys Asp Phe Leu Leu Asn Cys Ser Thr Val Ser Arg Ile Ser
            505                 510                 515

ttg cct tca acc gca ttg atg cag gca cct acc gtg aga ttc tgg aca   1699
Leu Pro Ser Thr Ala Leu Met Gln Ala Pro Thr Val Arg Phe Trp Thr
        520                 525                 530

atc tct acc agc gtc gcc gtg acg ccg tgc tgc tta gcc acc ccg cat   1747
Ile Ser Thr Ser Val Ala Val Thr Pro Cys Cys Leu Ala Thr Pro His
    535                 540                 545

tac gca gca cag atc cct gca gat att gat tca gac act ctt gat cag   1795
Tyr Ala Ala Gln Ile Pro Ala Asp Ile Asp Ser Asp Thr Leu Asp Gln
550                 555                 560                 565

ctg gtg gaa acc acc ttt atc tca gat ttt ggt gca cgt cct gct gca   1843
Leu Val Glu Thr Thr Phe Ile Ser Asp Phe Gly Ala Arg Pro Ala Ala
                570                 575                 580

cgc acc atc gaa gac cac atc gca tcc ttg ctg atg tgaccaacct        1889
Arg Thr Ile Glu Asp His Ile Ala Ser Leu Leu Met
            585                 590

tttaggagta cat                                                   1902


<210> 2050
<211> 593
<212> PRT
<213> Corynebacterium glutamicum

<400> 2050
Met Ile Pro Phe Pro Gly Gln Pro Gln Gln Gln Ser Ala Pro Asn Asp
  1               5                  10                  15

Glu Thr Arg Phe Ile Asp Leu Asn Glu Arg His Lys Asp Asp Glu Pro
             20                  25                  30

Ala Leu Phe Arg Asp Asp Val Ile Asp Gln Thr Leu Ala Ile Leu Ile
         35                  40                  45
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```
Ser Lys Asn Lys Pro Asn Ala Leu Leu Val Gly Pro Ala Gly Thr Gly
     50                  55                  60

Lys Ser Arg Ile Ala Glu Asp Ile Ala Arg Arg Leu Ala Asn Asp Asp
 65                  70                  75                  80

Val Ser Ile Pro Asp Gln Leu Val Gly His Arg Ile Leu Asp Val Ser
                 85                  90                  95

Ile Ala Glu Leu Val Ala Gly Ala Gly Val Val Gly Gln Leu Lys Lys
            100                 105                 110

Arg Ile Leu Asp Leu Ile Lys Tyr Ala Thr Asp Pro Ser Asn Lys Val
        115                 120                 125

Ile Ile Phe Ile Asp Glu Ile His Gln Ile Ala Gly Asp Gln Ser Ser
    130                 135                 140

His Ser Gly Ser Gln Ala Lys Val Ala Gln Ile Leu Lys Pro Tyr Leu
145                 150                 155                 160

Ala Arg Gly Asp Leu Arg Val Ile Gly Ala Thr Thr Thr Gln Glu Ala
                165                 170                 175

Arg Asp Phe Asp His Asp Pro Ala Leu Lys Arg Arg Phe Ser Arg Val
            180                 185                 190

Asn Val Asp Glu Phe Asp Arg Asp Gln Thr Leu Thr Ile Leu His Ala
        195                 200                 205

Ala Arg Asp Gly Tyr Leu Lys His Phe Asn Asn Ala Val Thr Val Ser
    210                 215                 220

Asp Asp Val Leu Gly Tyr Val Tyr Thr Tyr Ser Gln Gln Phe Asn Pro
225                 230                 235                 240

Gly Asn Thr Ala Gln Pro Asp Ala Ala Leu Thr Leu Phe Asp Lys Ala
                245                 250                 255

Leu Ala Ser Leu Thr Met Glu Lys Gln Arg Leu Ile Asn Asn His Val
            260                 265                 270

Ile Ala Pro Ser Leu Lys Phe Pro Val Ser Glu Arg His Ile His Asn
        275                 280                 285

Thr Ala Arg Lys Leu Ala Phe Gly Ser Gln Val Pro Ala Ser Ile Asn
    290                 295                 300

Thr Asp Asp Ala Arg Asp Lys Leu Glu Thr Leu Phe Gly Gln Asp His
305                 310                 315                 320

Ile Ile Glu Pro Val Leu Thr Ala Ile Lys Arg Glu Gln Leu Gly Ile
                325                 330                 335

Phe Pro Arg Thr Lys Pro Leu Ser Trp Val Phe Ala Gly Ser Ser Gly
            340                 345                 350

Val Gly Lys Thr Glu Met Ala Arg Ile Leu Ser Arg Ala Ile Asn Gly
        355                 360                 365

Gly Asp Pro Ile Ile Ile Asn Gly Pro Glu Tyr Ile Ser Pro Glu Ser
```

```
    370                 375                 380

Ile Thr Gly Leu Ile Gly Ser Ser Asp Gly Tyr Ile Gly Ser Asn Ser
385                 390                 395                 400

Lys Arg Ala Lys Pro Leu Asp Pro Leu Ile Ser Asn Pro Arg Gln Val
                405                 410                 415

Ile Val Leu Asp Glu Phe Glu Lys Ser His Pro His Phe Gln Gln Leu
            420                 425                 430

Phe Met Ala Ala Leu Asp Thr Gly Thr Met Ala Met Ala Asn Gly Thr
        435                 440                 445

Thr Leu Asn Phe Ser Gln Ala Ile Ile Ile Ala Thr Thr Asn Ala Ala
    450                 455                 460

Arg Asp Lys Ile Gly Arg Asp Ser Phe Gly Phe Asp Ser Asp Asn Ser
465                 470                 475                 480

Gly Val Leu Gly Ser Ala Gln Ala Ala Thr Asp Pro Arg Ala Gln Glu
                485                 490                 495

Arg Leu Lys Ser Leu Met Ser Lys Asp Phe Leu Leu Asn Cys Ser Thr
            500                 505                 510

Val Ser Arg Ile Ser Leu Pro Ser Thr Ala Leu Met Gln Ala Pro Thr
        515                 520                 525

Val Arg Phe Trp Thr Ile Ser Thr Ser Val Ala Val Thr Pro Cys Cys
    530                 535                 540

Leu Ala Thr Pro His Tyr Ala Ala Gln Ile Pro Ala Asp Ile Asp Ser
545                 550                 555                 560

Asp Thr Leu Asp Gln Leu Val Glu Thr Thr Phe Ile Ser Asp Phe Gly
                565                 570                 575

Ala Arg Pro Ala Ala Arg Thr Ile Glu Asp His Ile Ala Ser Leu Leu
            580                 585                 590

Met
```

<210> 2051
<211> 597
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(574)
<223> RXA01047

<400> 2051
aaccaccttt atctcagatt ttggtgcacg tcctgctgca cgcaccatcg aagaccacat 60

cgcatccttg ctgatgtgac caacctttta ggagtacatc atg att gat acc act 115
                                                Met Ile Asp Thr Thr
                                                  1   5

```
gct aac agc acc tca ggc acc cta cct aca ctc act gct gac caa gct   163
Ala Asn Ser Thr Ser Gly Thr Leu Pro Thr Leu Thr Ala Asp Gln Ala
                 10                  15                  20

gcg ttt atc acc ggt ttt tgc gag gct gct atc ttc aca gcc acc gtc   211
Ala Phe Ile Thr Gly Phe Cys Glu Ala Ala Ile Phe Thr Ala Thr Val
             25                  30                  35

aca ata gat aac gaa cct ata ttt ctt gat gaa gcg ttc ttc tta ggt   259
Thr Ile Asp Asn Glu Pro Ile Phe Leu Asp Glu Ala Phe Phe Leu Gly
         40                  45                  50

caa gaa acc tat acc gac att ctc atg aat caa ctc cgc acc aat gaa   307
Gln Glu Thr Tyr Thr Asp Ile Leu Met Asn Gln Leu Arg Thr Asn Glu
     55                  60                  65

gcc att gtt aaa gac tgt ctc gac ttc ttc ctt gac aac tac acc aca   355
Ala Ile Val Lys Asp Cys Leu Asp Phe Phe Leu Asp Asn Tyr Thr Thr
 70                  75                  80                  85

atg aac aag ctc att gtt gat ggt cta tgc cca gat tgg gag cac cac   403
Met Asn Lys Leu Ile Val Asp Gly Leu Cys Pro Asp Trp Glu His His
                 90                  95                 100

ggc cat gat ttc cta ctc acc cgt gac cat cat ggt gcc gga ttc tgg   451
Gly His Asp Phe Leu Leu Thr Arg Asp His His Gly Ala Gly Phe Trp
            105                 110                 115

gat cgt ggc tac gac gaa tac ggt gcc caa ctc acc gac aat gcc gaa   499
Asp Arg Gly Tyr Asp Glu Tyr Gly Ala Gln Leu Thr Asp Asn Ala Glu
        120                 125                 130

aaa tat tca gaa aac tgt ctc aat ttc tgg att gag cct gat agt gac   547
Lys Tyr Ser Glu Asn Cys Leu Asn Phe Trp Ile Glu Pro Asp Ser Asp
    135                 140                 145

cct ctc att atc aac ttc gag tac cac taacacccct tgaccttatt         594
Pro Leu Ile Ile Asn Phe Glu Tyr His
150                 155

ttt                                                               597
```

<210> 2052
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 2052

```
Met Ile Asp Thr Thr Ala Asn Ser Thr Ser Gly Thr Leu Pro Thr Leu
  1               5                  10                  15

Thr Ala Asp Gln Ala Ala Phe Ile Thr Gly Phe Cys Glu Ala Ala Ile
             20                  25                  30

Phe Thr Ala Thr Val Thr Ile Asp Asn Glu Pro Ile Phe Leu Asp Glu
         35                  40                  45

Ala Phe Phe Leu Gly Gln Glu Thr Tyr Thr Asp Ile Leu Met Asn Gln
     50                  55                  60
```

```
Leu Arg Thr Asn Glu Ala Ile Val Lys Asp Cys Leu Asp Phe Phe Leu
 65                  70                  75                  80

Asp Asn Tyr Thr Thr Met Asn Lys Leu Ile Val Asp Gly Leu Cys Pro
                85                  90                  95

Asp Trp Glu His His Gly His Asp Phe Leu Leu Thr Arg Asp His His
            100                 105                 110

Gly Ala Gly Phe Trp Asp Arg Gly Tyr Asp Glu Tyr Gly Ala Gln Leu
        115                 120                 125

Thr Asp Asn Ala Glu Lys Tyr Ser Glu Asn Cys Leu Asn Phe Trp Ile
    130                 135                 140

Glu Pro Asp Ser Asp Pro Leu Ile Ile Asn Phe Glu Tyr His
145                 150                 155
```

US 20050287652A1

<210> 2053
<211> 444
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(421)
<223> RXA01058

<400> 2053

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ctcccgtaat aggggtaatt ttgcaattaa ctgcgcttaa agtaagaaac attgctaatc 60

tttatctggg taattaacaa tcgattttaa ggatattctc atg cgt aaa ctt cgt   115
                                              Met Arg Lys Leu Arg
                                                1               5

act gct tcc gtt gca ctg ctg acc gca ggt gca ctt gca ctg acc gct   163
Thr Ala Ser Val Ala Leu Leu Thr Ala Gly Ala Leu Ala Leu Thr Ala
                10                  15                  20

act cct gca atg gct cag tcc acc acc ggt tct tct gca tct tct cag   211
Thr Pro Ala Met Ala Gln Ser Thr Thr Gly Ser Ser Ala Ser Ser Gln
            25                  30                  35

gtt ggc gac gca ctc ggt gct agc gac tac gag cgc gac atc tgg ggt   259
Val Gly Asp Ala Leu Gly Ala Ser Asp Tyr Glu Arg Asp Ile Trp Gly
        40                  45                  50

tcc tct aag gac ttc gac gat gta acc cca ttc ggt tcc gct tgg tac   307
Ser Ser Lys Asp Phe Asp Asp Val Thr Pro Phe Gly Ser Ala Trp Tyr
    55                  60                  65

ggc tac acc ctg gcc gca acc gca gtt gct atc tcc ggt ctt gtg tac   355
Gly Tyr Thr Leu Ala Ala Thr Ala Val Ala Ile Ser Gly Leu Val Tyr
70                  75                  80                  85

gca aac ctt cct gca atc gag cag gct gct gca cag gcc ggc atc aag   403
Ala Asn Leu Pro Ala Ile Glu Gln Ala Ala Ala Gln Ala Gly Ile Lys
                90                  95                  100
```

```
ctg gag atc cca cgc tac taattgccac tgcaatctta aat                 444
Leu Glu Ile Pro Arg Tyr
            105


<210> 2054
<211> 107
<212> PRT
<213> Corynebacterium glutamicum

<400> 2054
Met Arg Lys Leu Arg Thr Ala Ser Val Ala Leu Leu Thr Ala Gly Ala
  1               5                  10                  15

Leu Ala Leu Thr Ala Thr Pro Ala Met Ala Gln Ser Thr Thr Gly Ser
             20                  25                  30

Ser Ala Ser Ser Gln Val Gly Asp Ala Leu Gly Ala Ser Asp Tyr Glu
         35                  40                  45

Arg Asp Ile Trp Gly Ser Ser Lys Asp Phe Asp Asp Val Thr Pro Phe
     50                  55                  60

Gly Ser Ala Trp Tyr Gly Tyr Thr Leu Ala Ala Thr Ala Val Ala Ile
 65                  70                  75                  80

Ser Gly Leu Val Tyr Ala Asn Leu Pro Ala Ile Glu Gln Ala Ala Ala
                 85                  90                  95

Gln Ala Gly Ile Lys Leu Glu Ile Pro Arg Tyr
            100                 105


<210> 2055
<211> 453
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(430)
<223> RXA01063

<400> 2055
actttcttgt agaggtctgg gtagtggata agttaatcaa ctatgaaata gactaactta 60

atcattaaca ttaatggatt ttcggagaat agggatagac atg gca gac gag aaa   115
                                            Met Ala Asp Glu Lys
                                              1               5

aag gtt cat gta cgt gcc aca ctg cgc ttt gat tca gac acc cac cag   163
Lys Val His Val Arg Ala Thr Leu Arg Phe Asp Ser Asp Thr His Gln
                 10                  15                  20

cgg gca att tat tgg gca gat cga aaa ggt atc tcg ctg agc gcg tat   211
Arg Ala Ile Tyr Trp Ala Asp Arg Lys Gly Ile Ser Leu Ser Ala Tyr
             25                  30                  35

gca gaa gag gcg atc aga gag aag att gat cgt gat aac ggt gtg cac   259
Ala Glu Glu Ala Ile Arg Glu Lys Ile Asp Arg Asp Asn Gly Val His
         40                  45                  50
```

```
gtt att ccg aat tca ctg ttg gat aac cgc atg aac caa atc att gat   307
Val Ile Pro Asn Ser Leu Leu Asp Asn Arg Met Asn Gln Ile Ile Asp
     55                  60                  65

cag ctc agc tcg ttt ggt cgt gag ttg gcg aac aac acg aca gtt gta   355
Gln Leu Ser Ser Phe Gly Arg Glu Leu Ala Asn Asn Thr Thr Val Val
 70                  75                  80                  85

act agt ggt ttc aac acc att atc ggt atg act cgt ggc gac tcg tat   403
Thr Ser Gly Phe Asn Thr Ile Ile Gly Met Thr Arg Gly Asp Ser Tyr
                 90                  95                 100

ctc tct gat gat ctc gat gac ctg ggt taaacccgat gaacgagcag         450
Leu Ser Asp Asp Leu Asp Asp Leu Gly
            105                 110

gaa                                                               453
```

<210> 2056
<211> 110
<212> PRT
<213> Corynebacterium glutamicum

<400> 2056

```
Met Ala Asp Glu Lys Lys Val His Val Arg Ala Thr Leu Arg Phe Asp
  1               5                  10                  15

Ser Asp Thr His Gln Arg Ala Ile Tyr Trp Ala Asp Arg Lys Gly Ile
             20                  25                  30

Ser Leu Ser Ala Tyr Ala Glu Glu Ala Ile Arg Glu Lys Ile Asp Arg
         35                  40                  45

Asp Asn Gly Val His Val Ile Pro Asn Ser Leu Leu Asp Asn Arg Met
     50                  55                  60

Asn Gln Ile Ile Asp Gln Leu Ser Ser Phe Gly Arg Glu Leu Ala Asn
 65                  70                  75                  80

Asn Thr Thr Val Val Thr Ser Gly Phe Asn Thr Ile Ile Gly Met Thr
                 85                  90                  95

Arg Gly Asp Ser Tyr Leu Ser Asp Asp Leu Asp Asp Leu Gly
            100                 105                 110
```

<210> 2057
<211> 849
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(826)
<223> RXA01066

<400> 2057

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aaacgtattc cttgacctgc gcatcaaggt gctgaagaac tggcaatccg atccaaaggc 60
```

```
tttgaaccgc ctgggcttct agctttaagg gggtgagttc atg cgt agg gac agt   115
                                             Met Arg Arg Asp Ser
                                               1               5

ttt cgg gac cgc gcg cta gta gtc aaa act tat gat ttt ggc gaa gcc   163
Phe Arg Asp Arg Ala Leu Val Val Lys Thr Tyr Asp Phe Gly Glu Ala
                 10                  15                  20

gac cgc att att gtg ctg ctc acc cga gac cac ggc atc gtg cgc gga   211
Asp Arg Ile Ile Val Leu Leu Thr Arg Asp His Gly Ile Val Arg Gly
             25                  30                  35

gtt gcc aaa gga gta cgc cga tcc aaa tcc cgg ttt ggg tca agg ctg   259
Val Ala Lys Gly Val Arg Arg Ser Lys Ser Arg Phe Gly Ser Arg Leu
         40                  45                  50

cag ctt ttt gtg gaa ctc gac gtg cag ctc tac cca ggt aga aaa ctg   307
Gln Leu Phe Val Glu Leu Asp Val Gln Leu Tyr Pro Gly Arg Lys Leu
     55                  60                  65

tcc acc atc tct ggc gcg gac acc gtc ggc tac tac gca tca ggc atc   355
Ser Thr Ile Ser Gly Ala Asp Thr Val Gly Tyr Tyr Ala Ser Gly Ile
 70                  75                  80                  85

atc gag gac ttc act cgg tat tcc tgt gcg tcc gcc atc ctg gaa atc   403
Ile Glu Asp Phe Thr Arg Tyr Ser Cys Ala Ser Ala Ile Leu Glu Ile
                 90                  95                 100

gcc acc cac atc gca gga ctg gaa aac gat ccg cac ctg ttt gaa gaa   451
Ala Thr His Ile Ala Gly Leu Glu Asn Asp Pro His Leu Phe Glu Glu
             105                 110                 115

acc acc cgg gcg ttg aaa aac att cag gac tcc cca gaa ccc atc ctc   499
Thr Thr Arg Ala Leu Lys Asn Ile Gln Asp Ser Pro Glu Pro Ile Leu
         120                 125                 130

aac cta gac gag ttc atg ctc cgc gcc atg aac cac gcc ggc tgg gca   547
Asn Leu Asp Glu Phe Met Leu Arg Ala Met Asn His Ala Gly Trp Ala
     135                 140                 145

cca agc ctt ttc gac tgc gca gcc tgc ggc cga cca gga cct cac aac   595
Pro Ser Leu Phe Asp Cys Ala Ala Cys Gly Arg Pro Gly Pro His Asn
150                 155                 160                 165

gca ttc cac cca ggc gtc ggc ggg gca gtg tgc ctg tac tgc cga ccg   643
Ala Phe His Pro Gly Val Gly Gly Ala Val Cys Leu Tyr Cys Arg Pro
                 170                 175                 180

ccg gga agc gcc gaa gtc cca cca gaa gca cta cac atg atg tgg ttg   691
Pro Gly Ser Ala Glu Val Pro Pro Glu Ala Leu His Met Met Trp Leu
             185                 190                 195

gtc gcc aac ggc caa gca gcc cgc att ccc cgg gaa cac cca gag cag   739
Val Ala Asn Gly Gln Ala Ala Arg Ile Pro Arg Glu His Pro Glu Gln
         200                 205                 210

caa acc acc att cac caa ctg aca acc gcg cat ctg cag tgg cat att   787
Gln Thr Thr Ile His Gln Leu Thr Thr Ala His Leu Gln Trp His Ile
     215                 220                 225

gaa aga aag ctg ccc acg ctg gcg gtg ctg gat cag gcc tagtgcttag    836
```

```
Glu Arg Lys Leu Pro Thr Leu Ala Val Leu Asp Gln Ala
230                 235                 240

gcttaggcgt ccg                                                    849


<210> 2058
<211> 242
<212> PRT
<213> Corynebacterium glutamicum

<400> 2058
Met Arg Arg Asp Ser Phe Arg Asp Arg Ala Leu Val Val Lys Thr Tyr
  1               5                  10                  15

Asp Phe Gly Glu Ala Asp Arg Ile Ile Val Leu Leu Thr Arg Asp His
             20                  25                  30

Gly Ile Val Arg Gly Val Ala Lys Gly Val Arg Arg Ser Lys Ser Arg
         35                  40                  45

Phe Gly Ser Arg Leu Gln Leu Phe Val Glu Leu Asp Val Gln Leu Tyr
     50                  55                  60

Pro Gly Arg Lys Leu Ser Thr Ile Ser Gly Ala Asp Thr Val Gly Tyr
 65                  70                  75                  80

Tyr Ala Ser Gly Ile Ile Glu Asp Phe Thr Arg Tyr Ser Cys Ala Ser
                 85                  90                  95

Ala Ile Leu Glu Ile Ala Thr His Ile Ala Gly Leu Glu Asn Asp Pro
            100                 105                 110

His Leu Phe Glu Glu Thr Thr Arg Ala Leu Lys Asn Ile Gln Asp Ser
        115                 120                 125

Pro Glu Pro Ile Leu Asn Leu Asp Glu Phe Met Leu Arg Ala Met Asn
    130                 135                 140

His Ala Gly Trp Ala Pro Ser Leu Phe Asp Cys Ala Ala Cys Gly Arg
145                 150                 155                 160

Pro Gly Pro His Asn Ala Phe His Pro Gly Val Gly Gly Ala Val Cys
                165                 170                 175

Leu Tyr Cys Arg Pro Pro Gly Ser Ala Glu Val Pro Pro Glu Ala Leu
            180                 185                 190

His Met Met Trp Leu Val Ala Asn Gly Gln Ala Ala Arg Ile Pro Arg
        195                 200                 205

Glu His Pro Glu Gln Gln Thr Thr Ile His Gln Leu Thr Thr Ala His
    210                 215                 220

Leu Gln Trp His Ile Glu Arg Lys Leu Pro Thr Leu Ala Val Leu Asp
225                 230                 235                 240

Gln Ala
```

<210> 2059
<211> 1194
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1171)
<223> RXA01068

<400> 2059
tggtctacca agacaagctg ttccctgatt tcacgcagca agatctgtac gacgcggtcc 60

tggaatacgc caagcgggat cgcagattcg gaagcgcata atg ccc acc aac cag 115
Met Pro Thr Asn Gln
1 5

ccg acg cca gcc caa atc aaa cgc tgg cgc gga tac ctg gcc aat gag 163
Pro Thr Pro Ala Gln Ile Lys Arg Trp Arg Gly Tyr Leu Ala Asn Glu
10 15 20

caa gca gag gcc gca gcc tac cgc gac ctg gcc aaa cga cgc gaa ggc 211
Gln Ala Glu Ala Ala Ala Tyr Arg Asp Leu Ala Lys Arg Arg Glu Gly
25 30 35

gaa gag cga gac atc ctc cta gcg ctc gcc gac gct gaa cac cga cac 259
Glu Glu Arg Asp Ile Leu Leu Ala Leu Ala Asp Ala Glu His Arg His
40 45 50

gcc gct tac tgg gtg gaa aag ctc ggc cct gat gcc gaa aac cca cca 307
Ala Ala Tyr Trp Val Glu Lys Leu Gly Pro Asp Ala Glu Asn Pro Pro
55 60 65

aaa gcc gac gtc aaa acc cgc ctg ctc ggt ttt cta gca cgc cga ttc 355
Lys Ala Asp Val Lys Thr Arg Leu Leu Gly Phe Leu Ala Arg Arg Phe
70 75 80 85

ggc tcc gtg ttc acc ctg gca ctc atg cag tcc gcc gaa acg cgc agc 403
Gly Ser Val Phe Thr Leu Ala Leu Met Gln Ser Ala Glu Thr Arg Ser
90 95 100

ccc tac gac gac gat gcc gac gcc tcc cgc caa atc agc gcc gac gaa 451
Pro Tyr Asp Asp Asp Ala Asp Ala Ser Arg Gln Ile Ser Ala Asp Glu
105 110 115

cgc atc cac gcc gaa gtc gtt cga ggc cta gcc agc cgc ggc aga gaa 499
Arg Ile His Ala Glu Val Val Arg Gly Leu Ala Ser Arg Gly Arg Glu
120 125 130

cgc atg agc ggc aac ttc cgt gcc gcc gta ttc gga atc aac gac ggc 547
Arg Met Ser Gly Asn Phe Arg Ala Ala Val Phe Gly Ile Asn Asp Gly
135 140 145

ctg gtc tcc aac gtc gcc ctc gtc atg ggt gtc atg gcc acc ggc gtg 595
Leu Val Ser Asn Val Ala Leu Val Met Gly Val Met Ala Thr Gly Val
150 155 160 165

ccc gcc caa att gtt ctc atc acc ggc att tcc ggt ctg ctc tcc ggc 643
Pro Ala Gln Ile Val Leu Ile Thr Gly Ile Ser Gly Leu Leu Ser Gly
170 175 180

```
gcg cta tcc atg gcc gcc ggc gaa tac atc tca gtg cgc tcc caa aca   691
Ala Leu Ser Met Ala Ala Gly Glu Tyr Ile Ser Val Arg Ser Gln Thr
            185                 190                 195

gag ctt ctc gac gcc tcc ctc cca gac ccc aaa gcc cgc gaa gcc ctc   739
Glu Leu Leu Asp Ala Ser Leu Pro Asp Pro Lys Ala Arg Glu Ala Leu
        200                 205                 210

cac gcc ctc gac gtc gaa tcc aac gaa ctg gaa ctc gtc tac cga gcc   787
His Ala Leu Asp Val Glu Ser Asn Glu Leu Glu Leu Val Tyr Arg Ala
    215                 220                 225

cgc gga atg agc gaa gac gaa gcg cgg gca aaa gcg tca caa gtt ttc   835
Arg Gly Met Ser Glu Asp Glu Ala Arg Ala Lys Ala Ser Gln Val Phe
230                 235                 240                 245

caa aga atc agc gac caa aaa cgc atc agc gac aac gtc ctc ggc agc   883
Gln Arg Ile Ser Asp Gln Lys Arg Ile Ser Asp Asn Val Leu Gly Ser
                250                 255                 260

acc gaa atc caa agc gcc ggc tcc gct cgt tcg gcc gcc aca ttc agc   931
Thr Glu Ile Gln Ser Ala Gly Ser Ala Arg Ser Ala Ala Thr Phe Ser
            265                 270                 275

ttc ctg tcc ttt gcc atc ggc gca ttc ctc ccg atc gtc cca tac gtc   979
Phe Leu Ser Phe Ala Ile Gly Ala Phe Leu Pro Ile Val Pro Tyr Val
        280                 285                 290

ttc ggc atg gaa ggc ctc gcc ggg gca gtg gtg tcc cta gtc ctc gtc   1027
Phe Gly Met Glu Gly Leu Ala Gly Ala Val Val Ser Leu Val Leu Val
    295                 300                 305

gga cta tca ctg atg gca acg ggc gcg acc acc ggc ctg cta tcg gga   1075
Gly Leu Ser Leu Met Ala Thr Gly Ala Thr Thr Gly Leu Leu Ser Gly
310                 315                 320                 325

aag cca ccg gga atc cgc gcg gtg cgt cag ctg tcg atc ggc tac ggc   1123
Lys Pro Pro Gly Ile Arg Ala Val Arg Gln Leu Ser Ile Gly Tyr Gly
                330                 335                 340

gcg gcg ctg gtc acc tac gtg ctc ggc ctc ctg ttc ggc atg atc ctt   1171
Ala Ala Leu Val Thr Tyr Val Leu Gly Leu Leu Phe Gly Met Ile Leu
            345                 350                 355

taaaagctct tgcttctcga cgt                                        1194


<210> 2060
<211> 357
<212> PRT
<213> Corynebacterium glutamicum

<400> 2060
Met Pro Thr Asn Gln Pro Thr Pro Ala Gln Ile Lys Arg Trp Arg Gly
  1               5                  10                  15

Tyr Leu Ala Asn Glu Gln Ala Glu Ala Ala Ala Tyr Arg Asp Leu Ala
             20                  25                  30

Lys Arg Arg Glu Gly Glu Glu Arg Asp Ile Leu Leu Ala Leu Ala Asp
         35                  40                  45
```

```
Ala Glu His Arg His Ala Ala Tyr Trp Val Glu Lys Leu Gly Pro Asp
     50                  55                  60

Ala Glu Asn Pro Pro Lys Ala Asp Val Lys Thr Arg Leu Leu Gly Phe
 65                  70                  75                  80

Leu Ala Arg Arg Phe Gly Ser Val Phe Thr Leu Ala Leu Met Gln Ser
                 85                  90                  95

Ala Glu Thr Arg Ser Pro Tyr Asp Asp Asp Ala Asp Ala Ser Arg Gln
            100                 105                 110

Ile Ser Ala Asp Glu Arg Ile His Ala Glu Val Val Arg Gly Leu Ala
        115                 120                 125

Ser Arg Gly Arg Glu Arg Met Ser Gly Asn Phe Arg Ala Ala Val Phe
    130                 135                 140

Gly Ile Asn Asp Gly Leu Val Ser Asn Val Ala Leu Val Met Gly Val
145                 150                 155                 160

Met Ala Thr Gly Val Pro Ala Gln Ile Val Leu Ile Thr Gly Ile Ser
                165                 170                 175

Gly Leu Leu Ser Gly Ala Leu Ser Met Ala Ala Gly Glu Tyr Ile Ser
            180                 185                 190

Val Arg Ser Gln Thr Glu Leu Leu Asp Ala Ser Leu Pro Asp Pro Lys
        195                 200                 205

Ala Arg Glu Ala Leu His Ala Leu Asp Val Glu Ser Asn Glu Leu Glu
    210                 215                 220

Leu Val Tyr Arg Ala Arg Gly Met Ser Glu Asp Glu Ala Arg Ala Lys
225                 230                 235                 240

Ala Ser Gln Val Phe Gln Arg Ile Ser Asp Gln Lys Arg Ile Ser Asp
                245                 250                 255

Asn Val Leu Gly Ser Thr Glu Ile Gln Ser Ala Gly Ser Ala Arg Ser
            260                 265                 270

Ala Ala Thr Phe Ser Phe Leu Ser Phe Ala Ile Gly Ala Phe Leu Pro
        275                 280                 285

Ile Val Pro Tyr Val Phe Gly Met Glu Gly Leu Ala Gly Ala Val Val
    290                 295                 300

Ser Leu Val Leu Val Gly Leu Ser Leu Met Ala Thr Gly Ala Thr Thr
305                 310                 315                 320

Gly Leu Leu Ser Gly Lys Pro Pro Gly Ile Arg Ala Val Arg Gln Leu
                325                 330                 335

Ser Ile Gly Tyr Gly Ala Ala Leu Val Thr Tyr Val Leu Gly Leu Leu
            340                 345                 350

Phe Gly Met Ile Leu
        355
```

<210> 2061
<211> 828
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(805)
<223> RXA01074

<400> 2061
cgaatgaaat cactgggcgg gagttcaccc tcggcgagga gcctgagcgc tactagcttt 60

gccacatttc actaaacgcc ccgcacaacc ccaagcagcc ttg gcg gaa gcc gca 115
Leu Ala Glu Ala Ala
1 5

ggt cta cgc tgg ctc gcc gaa gca tct tca gct gtg gca cag gtt gtt 163
Gly Leu Arg Trp Leu Ala Glu Ala Ser Ser Ala Val Ala Gln Val Val
10 15 20

agc gcc gac gca gag cag atc acg act gtt ggc gtc gaa acg caa ttg 211
Ser Ala Asp Ala Glu Gln Ile Thr Thr Val Gly Val Glu Thr Gln Leu
25 30 35

ccc aca ccc gat gcg gcc ttc aag gcc ggc gaa gag ctc gcc cgc atc 259
Pro Thr Pro Asp Ala Ala Phe Lys Ala Gly Glu Glu Leu Ala Arg Ile
40 45 50

cac ctt gcc ggc gcc cca gcg ttc ggc tgt cca cca gcg ggc tgg gcg 307
His Leu Ala Gly Ala Pro Ala Phe Gly Cys Pro Pro Ala Gly Trp Ala
55 60 65

ggg tta aac tac atc ggc acc cag gga caa gca tgc tta tcg acg ccc 355
Gly Leu Asn Tyr Ile Gly Thr Gln Gly Gln Ala Cys Leu Ser Thr Pro
70 75 80 85

acc tgg ggt gtt ttt tac tcc cag caa cgc gta ctc ccg ttt gcg cgc 403
Thr Trp Gly Val Phe Tyr Ser Gln Gln Arg Val Leu Pro Phe Ala Arg
90 95 100

cgg gca cgc agg cga aat cac ctc acc gag cac gca ctc tgg gtc gtg 451
Arg Ala Arg Arg Arg Asn His Leu Thr Glu His Ala Leu Trp Val Val
105 110 115

gaa gcc gct tgt gat ttg att agc gaa ctt ccc gat gac gtt ccc ccc 499
Glu Ala Ala Cys Asp Leu Ile Ser Glu Leu Pro Asp Asp Val Pro Pro
120 125 130

gcc aga atc cac ggc gac ttg tgg ttt ggc aac cta ctt ttt ggc aca 547
Ala Arg Ile His Gly Asp Leu Trp Phe Gly Asn Leu Leu Phe Gly Thr
135 140 145

gac ggg cct gtg ttt att gac ccc gca gct cac ggc ggt cat ccc gaa 595
Asp Gly Pro Val Phe Ile Asp Pro Ala Ala His Gly Gly His Pro Glu
150 155 160 165

act gat ctc gcg atg ctt gat gta ttt ggc gca ccc tat ctc gat gaa 643
Thr Asp Leu Ala Met Leu Asp Val Phe Gly Ala Pro Tyr Leu Asp Glu
170 175 180

```
atc cgg gaa ggt tat ctg tct atc aac ccg ctg cca gac ggg tgg cgt   691
Ile Arg Glu Gly Tyr Leu Ser Ile Asn Pro Leu Pro Asp Gly Trp Arg
            185                 190                 195

gaa cgc acc ccc atg cac caa ctc cac cct ttg gcc gta cat gcg gcg   739
Glu Arg Thr Pro Met His Gln Leu His Pro Leu Ala Val His Ala Ala
        200                 205                 210

tct cat ggg cca agc tac ggc gtg gaa cta ctc cac gcc gcc aaa gcg   787
Ser His Gly Pro Ser Tyr Gly Val Glu Leu Leu His Ala Ala Lys Ala
    215                 220                 225

aca ctc aaa ctg ttg gat taacgccacc aattttcctg cgg                828
Thr Leu Lys Leu Leu Asp
230                 235
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<210> 2062
<211> 235
<212> PRT
<213> Corynebacterium glutamicum

<400> 2062

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Leu Ala Glu Ala Ala Gly Leu Arg Trp Leu Ala Glu Ala Ser Ser Ala
  1               5                  10                  15

Val Ala Gln Val Val Ser Ala Asp Ala Glu Gln Ile Thr Thr Val Gly
             20                  25                  30

Val Glu Thr Gln Leu Pro Thr Pro Asp Ala Ala Phe Lys Ala Gly Glu
         35                  40                  45

Glu Leu Ala Arg Ile His Leu Ala Gly Ala Pro Ala Phe Gly Cys Pro
     50                  55                  60

Pro Ala Gly Trp Ala Gly Leu Asn Tyr Ile Gly Thr Gln Gly Gln Ala
 65                  70                  75                  80

Cys Leu Ser Thr Pro Thr Trp Gly Val Phe Tyr Ser Gln Gln Arg Val
                 85                  90                  95

Leu Pro Phe Ala Arg Arg Ala Arg Arg Arg Asn His Leu Thr Glu His
            100                 105                 110

Ala Leu Trp Val Val Glu Ala Ala Cys Asp Leu Ile Ser Glu Leu Pro
        115                 120                 125

Asp Asp Val Pro Pro Ala Arg Ile His Gly Asp Leu Trp Phe Gly Asn
    130                 135                 140

Leu Leu Phe Gly Thr Asp Gly Pro Val Phe Ile Asp Pro Ala Ala His
145                 150                 155                 160

Gly Gly His Pro Glu Thr Asp Leu Ala Met Leu Asp Val Phe Gly Ala
                165                 170                 175

Pro Tyr Leu Asp Glu Ile Arg Glu Gly Tyr Leu Ser Ile Asn Pro Leu
            180                 185                 190

Pro Asp Gly Trp Arg Glu Arg Thr Pro Met His Gln Leu His Pro Leu
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```
        195                 200                 205

Ala Val His Ala Ala Ser His Gly Pro Ser Tyr Gly Val Glu Leu Leu
    210                 215                 220

His Ala Ala Lys Ala Thr Leu Lys Leu Leu Asp
225                 230                 235


<210> 2063
<211> 1143
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1120)
<223> RXA01076

<400> 2063
tcctcccatt aagcaccttg tcttccggaa gcttccaccc caaattccaa accccaaatt 60

ccatgccccg gatggacatt tttcattaca ctcgggggct atg act cca gct cac   115
                                            Met Thr Pro Ala His
                                              1               5

ata ttt tct gaa ggt cca atc aat agt gtt gtt ctc agc cag gat gag   163
Ile Phe Ser Glu Gly Pro Ile Asn Ser Val Val Leu Ser Gln Asp Glu
                10                  15                  20

gat gga aat ttc acc acc tcc tac cag gac acg ttc tct gat cca tca   211
Asp Gly Asn Phe Thr Thr Ser Tyr Gln Asp Thr Phe Ser Asp Pro Ser
            25                  30                  35

ttt ttg ggg gaa ggt gac gtt cta att gag gtt ggt tgg tcc agc ttg   259
Phe Leu Gly Glu Gly Asp Val Leu Ile Glu Val Gly Trp Ser Ser Leu
        40                  45                  50

aat tac aag gac gca atg gct ctg aag ggt gat aag gga gtg gtg cgt   307
Asn Tyr Lys Asp Ala Met Ala Leu Lys Gly Asp Lys Gly Val Val Arg
    55                  60                  65

act gtg cca ctg att cca ggt atc gat gtg gtg ggc act gtg atc gag   355
Thr Val Pro Leu Ile Pro Gly Ile Asp Val Val Gly Thr Val Ile Glu
70                  75                  80                  85

agc gct gat cct cgc ttt ggt cgt ggt gat gaa gtg gtg ctg aat ggc   403
Ser Ala Asp Pro Arg Phe Gly Arg Gly Asp Glu Val Val Leu Asn Gly
                90                  95                  100

gct ggt ttg ggg gag aac cgg cat gga ggt ttc acg cag cgg ctg aaa   451
Ala Gly Leu Gly Glu Asn Arg His Gly Gly Phe Thr Gln Arg Leu Lys
            105                 110                 115

gtg ccg tct gaa ccg ttg ctg cat att cca ttt aac ttc tcc gcg cag   499
Val Pro Ser Glu Pro Leu Leu His Ile Pro Phe Asn Phe Ser Ala Gln
        120                 125                 130

cag gtg ggt gcg ttg ggt act gca ggt ttc acg gct gcg cta tcg gtg   547
Gln Val Gly Ala Leu Gly Thr Ala Gly Phe Thr Ala Ala Leu Ser Val
    135                 140                 145
```

```
aat gct ctg gtc gat caa ggt atc aaa ccg gag gat ggg gag att ctg   595
Asn Ala Leu Val Asp Gln Gly Ile Lys Pro Glu Asp Gly Glu Ile Leu
150                 155                 160                 165

gta act ggt tcg act ggt ggt gtg ggt tcg att gca ctt cac ctg ctg   643
Val Thr Gly Ser Thr Gly Gly Val Gly Ser Ile Ala Leu His Leu Leu
                170                 175                 180

aat aag ttg gga tat acg acg gtc gcg gtg acg ggg cgt cga gaa gcg   691
Asn Lys Leu Gly Tyr Thr Thr Val Ala Val Thr Gly Arg Arg Glu Ala
            185                 190                 195

cat gcc gaa tac ctg acc agc ctg ggc gca agc gac atc att gat cgc   739
His Ala Glu Tyr Leu Thr Ser Leu Gly Ala Ser Asp Ile Ile Asp Arg
        200                 205                 210

gcg gag ctt tct gaa aag ggc cgg ccg ctg cag aag ggg cgt tgg gcg   787
Ala Glu Leu Ser Glu Lys Gly Arg Pro Leu Gln Lys Gly Arg Trp Ala
    215                 220                 225

ggt gta gtg gat tca gtg gga tcc cac aca ctt gtc aat gcg att gct   835
Gly Val Val Asp Ser Val Gly Ser His Thr Leu Val Asn Ala Ile Ala
230                 235                 240                 245

cag aca aaa tgg ggc gga att gtc acg gcg tgt ggc atg gct cag ggg   883
Gln Thr Lys Trp Gly Gly Ile Val Thr Ala Cys Gly Met Ala Gln Gly
                250                 255                 260

ccg gat ctg ccg gga acg gtg ttg ccg ttt att ctt cgt ggc gtg cat   931
Pro Asp Leu Pro Gly Thr Val Leu Pro Phe Ile Leu Arg Gly Val His
            265                 270                 275

ttg gtt ggc att aac tct gtc gat gca ccc cgt gag ctg cgt cga cgt   979
Leu Val Gly Ile Asn Ser Val Asp Ala Pro Arg Glu Leu Arg Arg Arg
        280                 285                 290

gcg tgg gcg ttg ctg tcc gag cat ctt gat acc gcg gtg cta gat gat   1027
Ala Trp Ala Leu Leu Ser Glu His Leu Asp Thr Ala Val Leu Asp Asp
    295                 300                 305

atg acc act gtg att gat gtc aag gat gtt gct caa gct ggc gaa gat   1075
Met Thr Thr Val Ile Asp Val Lys Asp Val Ala Gln Ala Gly Glu Asp
310                 315                 320                 325

ttg atg gct ggc aag ctt cac gga cgt acc gcg gtg cgt gtt cat       1120
Leu Met Ala Gly Lys Leu His Gly Arg Thr Ala Val Arg Val His
                330                 335                 340

tagcaggtca agcgcgtaat tga                                        1143
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<210> 2064
<211> 340
<212> PRT
<213> Corynebacterium glutamicum

<400> 2064

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Met Thr Pro Ala His Ile Phe Ser Glu Gly Pro Ile Asn Ser Val Val
  1               5                  10                  15
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Leu Ser Gln Asp Glu Asp Gly Asn Phe Thr Thr Ser Tyr Gln Asp Thr
            20                  25                  30

Phe Ser Asp Pro Ser Phe Leu Gly Glu Gly Asp Val Leu Ile Glu Val
        35                  40                  45

Gly Trp Ser Ser Leu Asn Tyr Lys Asp Ala Met Ala Leu Lys Gly Asp
    50                  55                  60

Lys Gly Val Val Arg Thr Val Pro Leu Ile Pro Gly Ile Asp Val Val
65                  70                  75                  80

Gly Thr Val Ile Glu Ser Ala Asp Pro Arg Phe Gly Arg Gly Asp Glu
                85                  90                  95

Val Val Leu Asn Gly Ala Gly Leu Gly Glu Asn Arg His Gly Gly Phe
            100                 105                 110

Thr Gln Arg Leu Lys Val Pro Ser Glu Pro Leu Leu His Ile Pro Phe
        115                 120                 125

Asn Phe Ser Ala Gln Gln Val Gly Ala Leu Gly Thr Ala Gly Phe Thr
    130                 135                 140

Ala Ala Leu Ser Val Asn Ala Leu Val Asp Gln Gly Ile Lys Pro Glu
145                 150                 155                 160

Asp Gly Glu Ile Leu Val Thr Gly Ser Thr Gly Gly Val Gly Ser Ile
                165                 170                 175

Ala Leu His Leu Leu Asn Lys Leu Gly Tyr Thr Thr Val Ala Val Thr
            180                 185                 190

Gly Arg Arg Glu Ala His Ala Glu Tyr Leu Thr Ser Leu Gly Ala Ser
        195                 200                 205

Asp Ile Ile Asp Arg Ala Glu Leu Ser Glu Lys Gly Arg Pro Leu Gln
    210                 215                 220

Lys Gly Arg Trp Ala Gly Val Val Asp Ser Val Gly Ser His Thr Leu
225                 230                 235                 240

Val Asn Ala Ile Ala Gln Thr Lys Trp Gly Gly Ile Val Thr Ala Cys
                245                 250                 255

Gly Met Ala Gln Gly Pro Asp Leu Pro Gly Thr Val Leu Pro Phe Ile
            260                 265                 270

Leu Arg Gly Val His Leu Val Gly Ile Asn Ser Val Asp Ala Pro Arg
        275                 280                 285

Glu Leu Arg Arg Arg Ala Trp Ala Leu Leu Ser Glu His Leu Asp Thr
    290                 295                 300

Ala Val Leu Asp Asp Met Thr Thr Val Ile Asp Val Lys Asp Val Ala
305                 310                 315                 320

Gln Ala Gly Glu Asp Leu Met Ala Gly Lys Leu His Gly Arg Thr Ala
                325                 330                 335

Val Arg Val His
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340

<210> 2065
<211> 957
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(934)
<223> RXA01078

<400> 2065
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tccaccaccc gcagctaaaa ctttttgaaa ggagctcatc atg agc aac gca gta 115
Met Ser Asn Ala Val
1 5

ccc cac aac gtt tcc ttc aac ttt gtt ccc cgc gct tac cgt cca gaa 163
Pro His Asn Val Ser Phe Asn Phe Val Pro Arg Ala Tyr Arg Pro Glu
10 15 20

aag ccc cgc aca ttc ggc atg aca gaa att cgt gca ccg tac tac tcc 211
Lys Pro Arg Thr Phe Gly Met Thr Glu Ile Arg Ala Pro Tyr Tyr Ser
25 30 35

act ttc ggc acc cga cac ctc cag gat gtc ttc gat gtt gca ggc cag 259
Thr Phe Gly Thr Arg His Leu Gln Asp Val Phe Asp Val Ala Gly Gln
40 45 50

tgg gtg gac ggc atc aaa tgg gca ggc ggt tcc ttc tcc ctg gtg ccg 307
Trp Val Asp Gly Ile Lys Trp Ala Gly Gly Ser Phe Ser Leu Val Pro
55 60 65

acc gaa cag gtg cgt gct ttt agc gac atc gcc cat gaa aac aat gcc 355
Thr Glu Gln Val Arg Ala Phe Ser Asp Ile Ala His Glu Asn Asn Ala
70 75 80 85

tat gtg tct tcc ggt ggc tgg att gaa act gtg ctt cgc tac ggc gac 403
Tyr Val Ser Ser Gly Gly Trp Ile Glu Thr Val Leu Arg Tyr Gly Asp
90 95 100

gac gca gtt gat cat tac tta aag gaa gcc aag gaa gtc ggc ttc gat 451
Asp Ala Val Asp His Tyr Leu Lys Glu Ala Lys Glu Val Gly Phe Asp
105 110 115

gtt att gag att tcc acc gga ttc atc atg ctc aac act tca ggt ctt 499
Val Ile Glu Ile Ser Thr Gly Phe Ile Met Leu Asn Thr Ser Gly Leu
120 125 130

cag cgc ctg gta gaa aaa gtg gtc aag gca ggc ctc aaa gca aaa cct 547
Gln Arg Leu Val Glu Lys Val Val Lys Ala Gly Leu Lys Ala Lys Pro
135 140 145

gaa cta gga cta cag att ggt tcc gga ggc gac tct ggt gag gct gaa 595
Glu Leu Gly Leu Gln Ile Gly Ser Gly Gly Asp Ser Gly Glu Ala Glu
150 155 160 165

ctt gca gcc gaa gga aag aaa gac att ggc gat ctg gtt gac cgc ggt 643

```
Leu Ala Ala Glu Gly Lys Lys Asp Ile Gly Asp Leu Val Asp Arg Gly
                170                 175                 180

aaa aaa gct ctc gac gcc ggc gca tcc atc atc atg atc gaa tcc gaa   691
Lys Lys Ala Leu Asp Ala Gly Ala Ser Ile Ile Met Ile Glu Ser Glu
            185                 190                 195

ggc atc acc gaa aac gtc acc gaa tgg gat aca ggc gct gcc gcg tcc   739
Gly Ile Thr Glu Asn Val Thr Glu Trp Asp Thr Gly Ala Ala Ala Ser
        200                 205                 210

atc atc aat gga ctg gga tta gaa aac gtc atg ttc gaa gcc gcc gac   787
Ile Ile Asn Gly Leu Gly Leu Glu Asn Val Met Phe Glu Ala Ala Asp
    215                 220                 225

ggc ccc gtc ttt gag tgg tat gtc aaa aac tac ggc aac gaa tgc aac   835
Gly Pro Val Phe Glu Trp Tyr Val Lys Asn Tyr Gly Asn Glu Cys Asn
230                 235                 240                 245

ctg ttc gtc gac cac agt caa att ctg caa ctt gaa ggg ctg cgc caa   883
Leu Phe Val Asp His Ser Gln Ile Leu Gln Leu Glu Gly Leu Arg Gln
                250                 255                 260

aac atc tgg ggc aac aag agc acc tgg gga cga gta atc aac cct gcg   931
Asn Ile Trp Gly Asn Lys Ser Thr Trp Gly Arg Val Ile Asn Pro Ala
            265                 270                 275

cct taaataccag gtcagggagg gca                                    957
Pro
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<210> 2066
<211> 278
<212> PRT
<213> Corynebacterium glutamicum

<400> 2066

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Met Ser Asn Ala Val Pro His Asn Val Ser Phe Asn Phe Val Pro Arg
  1               5                  10                  15

Ala Tyr Arg Pro Glu Lys Pro Arg Thr Phe Gly Met Thr Glu Ile Arg
             20                  25                  30

Ala Pro Tyr Tyr Ser Thr Phe Gly Thr Arg His Leu Gln Asp Val Phe
         35                  40                  45

Asp Val Ala Gly Gln Trp Val Asp Gly Ile Lys Trp Ala Gly Gly Ser
     50                  55                  60

Phe Ser Leu Val Pro Thr Glu Gln Val Arg Ala Phe Ser Asp Ile Ala
 65                  70                  75                  80

His Glu Asn Asn Ala Tyr Val Ser Ser Gly Gly Trp Ile Glu Thr Val
                 85                  90                  95

Leu Arg Tyr Gly Asp Asp Ala Val Asp His Tyr Leu Lys Glu Ala Lys
            100                 105                 110

Glu Val Gly Phe Asp Val Ile Glu Ile Ser Thr Gly Phe Ile Met Leu
        115                 120                 125
```

```
Asn Thr Ser Gly Leu Gln Arg Leu Val Glu Lys Val Val Lys Ala Gly
    130                 135                 140

Leu Lys Ala Lys Pro Glu Leu Gly Leu Gln Ile Gly Ser Gly Gly Asp
145                 150                 155                 160

Ser Gly Glu Ala Glu Leu Ala Ala Glu Gly Lys Lys Asp Ile Gly Asp
                165                 170                 175

Leu Val Asp Arg Gly Lys Lys Ala Leu Asp Ala Gly Ala Ser Ile Ile
            180                 185                 190

Met Ile Glu Ser Glu Gly Ile Thr Glu Asn Val Thr Glu Trp Asp Thr
        195                 200                 205

Gly Ala Ala Ala Ser Ile Ile Asn Gly Leu Gly Leu Glu Asn Val Met
    210                 215                 220

Phe Glu Ala Ala Asp Gly Pro Val Phe Glu Trp Tyr Val Lys Asn Tyr
225                 230                 235                 240

Gly Asn Glu Cys Asn Leu Phe Val Asp His Ser Gln Ile Leu Gln Leu
                245                 250                 255

Glu Gly Leu Arg Gln Asn Ile Trp Gly Asn Lys Ser Thr Trp Gly Arg
            260                 265                 270

Val Ile Asn Pro Ala Pro
        275


<210> 2067
<211> 399
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(376)
<223> RXA01083

<400> 2067
gtcgacatac tggcacgcaa gatctgtgta cccggcccac gtgcctaaaa ctaggtgagc 60

gagaccttcg agcagttcct cgaaggagag tgatccacct atg ttt ccg cga att   115
                                              Met Phe Pro Arg Ile
                                                1               5

ccg ctg gca atg tgt gct gtc gca gca atc cct gct gtt gtg ctc agg   163
Pro Leu Ala Met Cys Ala Val Ala Ala Ile Pro Ala Val Val Leu Arg
                10                  15                  20

ttt tct gag ctg tcg gcg tca cct gtg gcg acc atg ctg att ttt ggt   211
Phe Ser Glu Leu Ser Ala Ser Pro Val Ala Thr Met Leu Ile Phe Gly
            25                  30                  35

acc gca gtg gtt gct gcc tct ttt gtg ttg gcg tgg gca gct gaa gct   259
Thr Ala Val Val Ala Ala Ser Phe Val Leu Ala Trp Ala Ala Glu Ala
        40                  45                  50
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```
gtg cgc aaa gat att tct ggt gcg ttg gca gtg gcc ttg ctt gcg tta   307
Val Arg Lys Asp Ile Ser Gly Ala Leu Ala Val Ala Leu Leu Ala Leu
     55                  60                  65

gtt gca gtg ctt cct gaa tat gct tct gaa acg gtt gtc gag cac act   355
Val Ala Val Leu Pro Glu Tyr Ala Ser Glu Thr Val Val Glu His Thr
 70                  75                  80                  85

tat caa aca tcg gcg gcg aat taagaaggtg aacagttgac gca             399
Tyr Gln Thr Ser Ala Ala Asn
                 90
```

<210> 2068
<211> 92
<212> PRT
<213> Corynebacterium glutamicum

<400> 2068

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Met Phe Pro Arg Ile Pro Leu Ala Met Cys Ala Val Ala Ala Ile Pro
  1               5                  10                  15

Ala Val Val Leu Arg Phe Ser Glu Leu Ser Ala Ser Pro Val Ala Thr
             20                  25                  30

Met Leu Ile Phe Gly Thr Ala Val Val Ala Ala Ser Phe Val Leu Ala
         35                  40                  45

Trp Ala Ala Glu Ala Val Arg Lys Asp Ile Ser Gly Ala Leu Ala Val
     50                  55                  60

Ala Leu Leu Ala Leu Val Ala Val Leu Pro Glu Tyr Ala Ser Glu Thr
 65                  70                  75                  80

Val Val Glu His Thr Tyr Gln Thr Ser Ala Ala Asn
                 85                  90
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<210> 2069
<211> 1305
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1282)
<223> RXA01088

<400> 2069

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tgccttgagt ctaattctcc cgcccgtgcg atgggtttaa gctggactga taaacctttt 60

gtgaaccgaa ttttttaact gatttgaaga agcgagaata atg gga ctg tgg atc   115
                                              Met Gly Leu Trp Ile
                                                1               5

gat gca acc gct ggc gtt gca ggg gat atg ttg ctg gga gca ctc att   163
Asp Ala Thr Ala Gly Val Ala Gly Asp Met Leu Leu Gly Ala Leu Ile
                 10                  15                  20

gat gca ggt gca gaa cta gaa aaa atc caa cag gtt gtg gaa gca gtc   211
Asp Ala Gly Ala Glu Leu Glu Lys Ile Gln Gln Val Val Glu Ala Val
```

```
                25                  30                  35

atc ccc ggt gac gtg ctc ttg cgc acc gaa gag gta gtg cgc caa ggc   259
Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu Val Val Arg Gln Gly
         40                  45                  50

caa cga ggc atc aag ctg cat gtg gac gca caa cat gaa cac cat cat   307
Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln His Glu His His His
     55                  60                  65

cac cgc cac tta agc acc att aaa gaa ctg ctt gtc aat gct gac atc   355
His Arg His Leu Ser Thr Ile Lys Glu Leu Leu Val Asn Ala Asp Ile
 70                  75                  80                  85

cct gaa caa acc aag cag gat gcc tta ggc gtt ttt gaa ctc atc gct   403
Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val Phe Glu Leu Ile Ala
                 90                  95                 100

atc gct gaa gga aaa gtc cac ggc atc gag ccg gag aaa atc cac ttc   451
Ile Ala Glu Gly Lys Val His Gly Ile Glu Pro Glu Lys Ile His Phe
            105                 110                 115

cat gag gta gga gct tgg gat tcc atc gca gac att gtg ggt gtg tgc   499
His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp Ile Val Gly Val Cys
        120                 125                 130

gaa gcg atc agg cag ctt aac cca ggt ttg att gct gca tct ccg att   547
Glu Ala Ile Arg Gln Leu Asn Pro Gly Leu Ile Ala Ala Ser Pro Ile
    135                 140                 145

gct tta gga ttc gga cgc atc aag gca gct cac gga gat att cca gtg   595
Ala Leu Gly Phe Gly Arg Ile Lys Ala Ala His Gly Asp Ile Pro Val
150                 155                 160                 165

cca gtt cca gcc gtg gca gag ctg gtg aaa ggc tgg ccc acc caa acc   643
Pro Val Pro Ala Val Ala Glu Leu Val Lys Gly Trp Pro Thr Gln Thr
                170                 175                 180

gga gct ctt atg gag agc acc gaa cct gtt ggt gaa tta gcc acc cca   691
Gly Ala Leu Met Glu Ser Thr Glu Pro Val Gly Glu Leu Ala Thr Pro
            185                 190                 195

act ggt gtt gcg ttg atc cgt cac ttt gcc acc caa gat ggc cct ttc   739
Thr Gly Val Ala Leu Ile Arg His Phe Ala Thr Gln Asp Gly Pro Phe
        200                 205                 210

cca ggt ggc atc atc aat gaa gtt ggc att ggt gca gga aca aaa gat   787
Pro Gly Gly Ile Ile Asn Glu Val Gly Ile Gly Ala Gly Thr Lys Asp
    215                 220                 225

aca gaa ggc cgt cca aat ata gtg cgc gca att ttg ttc aac acc tct   835
Thr Glu Gly Arg Pro Asn Ile Val Arg Ala Ile Leu Phe Asn Thr Ser
230                 235                 240                 245

agg agt aac cca gat acc cgc aca ctg gtg caa tta gaa gcc aat gtt   883
Arg Ser Asn Pro Asp Thr Arg Thr Leu Val Gln Leu Glu Ala Asn Val
                250                 255                 260

gat gat caa gac cca cgg ctg tgg cca gga gta ata gag atc ctc ttt   931
Asp Asp Gln Asp Pro Arg Leu Trp Pro Gly Val Ile Glu Ile Leu Phe
            265                 270                 275
```

```
gcc gct ggc gca gta gat gca tgg ctg act cca att ttg atg aag aag   979
Ala Ala Gly Ala Val Asp Ala Trp Leu Thr Pro Ile Leu Met Lys Lys
        280                 285                 290

ggc cgt cct gca cat agg gtg tca gca ttg gtg gat agc tcc gag gtg   1027
Gly Arg Pro Ala His Arg Val Ser Ala Leu Val Asp Ser Ser Glu Val
    295                 300                 305

gaa gca gtg aaa acc gca tta ttt gca gcc acc acg act ttt ggg atc   1075
Glu Ala Val Lys Thr Ala Leu Phe Ala Ala Thr Thr Thr Phe Gly Ile
310                 315                 320                 325

aga tca tgg gaa gtc gaa cga gaa ggc ttg gac cgt cgt ttc gaa caa   1123
Arg Ser Trp Glu Val Glu Arg Glu Gly Leu Asp Arg Arg Phe Glu Gln
                330                 335                 340

gtc gag gtg gac gga cac acc atc aac atc aaa atc ggt tcc cgt gat   1171
Val Glu Val Asp Gly His Thr Ile Asn Ile Lys Ile Gly Ser Arg Asp
            345                 350                 355

gat caa gta atc agt gca cag tcc gag ttt gaa gat att cgg tct gca   1219
Asp Gln Val Ile Ser Ala Gln Ser Glu Phe Glu Asp Ile Arg Ser Ala
        360                 365                 370

gcg gtg gcc ttg gga att tca gag cgg gaa gtt gtg gca aga att ccg   1267
Ala Val Ala Leu Gly Ile Ser Glu Arg Glu Val Val Ala Arg Ile Pro
    375                 380                 385

caa ggc acc acc gag taacaaccaa aaggtcgact gct                    1305
Gln Gly Thr Thr Glu
390
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<210> 2070
<211> 394
<212> PRT
<213> Corynebacterium glutamicum

<400> 2070

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Met Gly Leu Trp Ile Asp Ala Thr Ala Gly Val Ala Gly Asp Met Leu
  1               5                  10                  15

Leu Gly Ala Leu Ile Asp Ala Gly Ala Glu Leu Glu Lys Ile Gln Gln
             20                  25                  30

Val Val Glu Ala Val Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu
         35                  40                  45

Val Val Arg Gln Gly Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln
     50                  55                  60

His Glu His His His His Arg His Leu Ser Thr Ile Lys Glu Leu Leu
 65                  70                  75                  80

Val Asn Ala Asp Ile Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val
                 85                  90                  95

Phe Glu Leu Ile Ala Ile Ala Glu Gly Lys Val His Gly Ile Glu Pro
            100                 105                 110
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Glu Lys Ile His Phe His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp
115 120 125

Ile Val Gly Val Cys Glu Ala Ile Arg Gln Leu Asn Pro Gly Leu Ile
130 135 140

Ala Ala Ser Pro Ile Ala Leu Gly Phe Gly Arg Ile Lys Ala Ala His
145 150 155 160

Gly Asp Ile Pro Val Pro Val Pro Ala Val Ala Glu Leu Val Lys Gly
165 170 175

Trp Pro Thr Gln Thr Gly Ala Leu Met Glu Ser Thr Glu Pro Val Gly
180 185 190

Glu Leu Ala Thr Pro Thr Gly Val Ala Leu Ile Arg His Phe Ala Thr
195 200 205

Gln Asp Gly Pro Phe Pro Gly Gly Ile Ile Asn Glu Val Gly Ile Gly
210 215 220

Ala Gly Thr Lys Asp Thr Glu Gly Arg Pro Asn Ile Val Arg Ala Ile
225 230 235 240

Leu Phe Asn Thr Ser Arg Ser Asn Pro Asp Thr Arg Thr Leu Val Gln
245 250 255

Leu Glu Ala Asn Val Asp Asp Gln Asp Pro Arg Leu Trp Pro Gly Val
260 265 270

Ile Glu Ile Leu Phe Ala Ala Gly Ala Val Asp Ala Trp Leu Thr Pro
275 280 285

Ile Leu Met Lys Lys Gly Arg Pro Ala His Arg Val Ser Ala Leu Val
290 295 300

Asp Ser Ser Glu Val Glu Ala Val Lys Thr Ala Leu Phe Ala Ala Thr
305 310 315 320

Thr Thr Phe Gly Ile Arg Ser Trp Glu Val Glu Arg Glu Gly Leu Asp
325 330 335

Arg Arg Phe Glu Gln Val Glu Val Asp Gly His Thr Ile Asn Ile Lys
340 345 350

Ile Gly Ser Arg Asp Asp Gln Val Ile Ser Ala Gln Ser Glu Phe Glu
355 360 365

Asp Ile Arg Ser Ala Ala Val Ala Leu Gly Ile Ser Glu Arg Glu Val
370 375 380

Val Ala Arg Ile Pro Gln Gly Thr Thr Glu
385 390

<210> 2071
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>

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<221> CDS
<222> (101)..(571)
<223> RXA01091

<400> 2071
tcgtcggaaa aactggcgat actattgata acgggcatgg gttcaccttc gataaagcac 60

ggtctatgct ggactatcgc cttttgacac gagtatcgca atg gtc ccg aac aca 115
Met Val Pro Asn Thr
1 5

gtc ctt atc cat gac gaa acc gcc gat ctg gcg acg cag atc cag cgg 163
Val Leu Ile His Asp Glu Thr Ala Asp Leu Ala Thr Gln Ile Gln Arg
10 15 20

ctg gaa cat atc atg gcg tgc ctg cgc gat ccg gtc agc gga tgc ccg 211
Leu Glu His Ile Met Ala Cys Leu Arg Asp Pro Val Ser Gly Cys Pro
25 30 35

tgg gat att gaa cag acc ttt gcc agc atc gcg ccc cac acg att gag 259
Trp Asp Ile Glu Gln Thr Phe Ala Ser Ile Ala Pro His Thr Ile Glu
40 45 50

gaa ggc tac gag gtt gcc gac gcc atc gcg cag gaa gac tgg ccc gag 307
Glu Gly Tyr Glu Val Ala Asp Ala Ile Ala Gln Glu Asp Trp Pro Glu
55 60 65

cta cgc ggc gag ttg ggc gat ttg ctg ttt cag acc gtg ttt cac gcc 355
Leu Arg Gly Glu Leu Gly Asp Leu Leu Phe Gln Thr Val Phe His Ala
70 75 80 85

caa atg gcg cgc gag gca ggc cat ttc gct ttg gtt gac gtg gtg aag 403
Gln Met Ala Arg Glu Ala Gly His Phe Ala Leu Val Asp Val Val Lys
90 95 100

gca att tcg gac aag atg gtt ttg cgc cat ccg cac gtg ttc ggc gcg 451
Ala Ile Ser Asp Lys Met Val Leu Arg His Pro His Val Phe Gly Ala
105 110 115

cag tcg aac gcg aaa tcc gcc gac cag cag gtg aag att ggg aag tca 499
Gln Ser Asn Ala Lys Ser Ala Asp Gln Gln Val Lys Ile Gly Lys Ser
120 125 130

tca agg cgc ccg agc gcg cgg gca aag cgc aaa agg gcg ttt tgg atg 547
Ser Arg Arg Pro Ser Ala Arg Ala Lys Arg Lys Arg Ala Phe Trp Met
135 140 145

gcg tcg cgc tgg gac tgc ctg ccc tgatgcgcgc gacgaagctg caa 594
Ala Ser Arg Trp Asp Cys Leu Pro
150 155

<210> 2072
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 2072
Met Val Pro Asn Thr Val Leu Ile His Asp Glu Thr Ala Asp Leu Ala
1 5 10 15

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Thr Gln Ile Gln Arg Leu Glu His Ile Met Ala Cys Leu Arg Asp Pro
            20                  25                  30

Val Ser Gly Cys Pro Trp Asp Ile Glu Gln Thr Phe Ala Ser Ile Ala
        35                  40                  45

Pro His Thr Ile Glu Glu Gly Tyr Glu Val Ala Asp Ala Ile Ala Gln
    50                  55                  60

Glu Asp Trp Pro Glu Leu Arg Gly Glu Leu Gly Asp Leu Leu Phe Gln
65                  70                  75                  80

Thr Val Phe His Ala Gln Met Ala Arg Glu Ala Gly His Phe Ala Leu
                85                  90                  95

Val Asp Val Val Lys Ala Ile Ser Asp Lys Met Val Leu Arg His Pro
            100                 105                 110

His Val Phe Gly Ala Gln Ser Asn Ala Lys Ser Ala Asp Gln Gln Val
        115                 120                 125

Lys Ile Gly Lys Ser Ser Arg Arg Pro Ser Ala Arg Ala Lys Arg Lys
    130                 135                 140

Arg Ala Phe Trp Met Ala Ser Arg Trp Asp Cys Leu Pro
145                 150                 155


<210> 2073
<211> 280
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(280)
<223> RXA01092

<400> 2073
tgaacccatg cccgttatca atagtatcgc cagtttttcc gacgagatga cccgctggcg 60

gcgtcacctg catcaaaacc ccgaaatcag ctttgattgt gtg gaa act gcg gcc   115
                                            Val Glu Thr Ala Ala
                                              1               5

ttc gtg gcc gag cag ctg cgc agc ttc ggg gtg gat gaa att cac acc   163
Phe Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp Glu Ile His Thr
                10                  15                  20

ggc atc gcg aaa acc ggt atc atc gcc ctg att cac ggg cgc gag gct   211
Gly Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His Gly Arg Glu Ala
            25                  30                  35

ggc ccc gtc gtc ggc ctg cgc gcc gat atg gac gcg ctg ccg ctg acc   259
Gly Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala Leu Pro Leu Thr
        40                  45                  50

gag att acc ggc gtc tac tat                                      280
Glu Ile Thr Gly Val Tyr Tyr
    55                  60
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<210> 2074
<211> 60
<212> PRT
<213> Corynebacterium glutamicum

<400> 2074
Val Glu Thr Ala Ala Phe Val Ala Glu Gln Leu Arg Ser Phe Gly Val
1 5 10 15

Asp Glu Ile His Thr Gly Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile
20 25 30

His Gly Arg Glu Ala Gly Pro Val Val Gly Leu Arg Ala Asp Met Asp
35 40 45

Ala Leu Pro Leu Thr Glu Ile Thr Gly Val Tyr Tyr
50 55 60

<210> 2075
<211> 280
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(280)
<223> RXA01092

<400> 2075
tgaacccatg cccgttatca atagtatcgc cagtttttcc gacgagatga cccgctggcg 60

gcgtcacctg catcaaaacc ccgaaatcag ctttgattgt gtg gaa act gcg gcc 115
Val Glu Thr Ala Ala
1 5

ttc gtg gcc gag cag ctg cgc agc ttc ggg gtg gat gaa att cac acc 163
Phe Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp Glu Ile His Thr
10 15 20

ggc atc gcg aaa acc ggt atc atc gcc ctg att cac ggg cgc gag gct 211
Gly Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His Gly Arg Glu Ala
25 30 35

ggc ccc gtc gtc ggc ctg cgc gcc gat atg gac gcg ctg ccg ctg acc 259
Gly Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala Leu Pro Leu Thr
40 45 50

gag att acc ggc gtc tac tat 280
Glu Ile Thr Gly Val Tyr Tyr
55 60

<210> 2076
<211> 60
<212> PRT
<213> Corynebacterium glutamicum

<400> 2076
Val Glu Thr Ala Ala Phe Val Ala Glu Gln Leu Arg Ser Phe Gly Val

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  1               5                  10                  15

Asp Glu Ile His Thr Gly Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile
            20                  25                  30

His Gly Arg Glu Ala Gly Pro Val Val Gly Leu Arg Ala Asp Met Asp
        35                  40                  45

Ala Leu Pro Leu Thr Glu Ile Thr Gly Val Tyr Tyr
    50                  55                  60


<210> 2077
<211> 822
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(799)
<223> RXA01096

<400> 2077
accgtgaaac aaaccggcgg tgcgtgccac actggtgccc acacatgttt cgacaatgac 60

gttttgctgt aaaagcaaca acgattaagg aagaaatctt atg aag cca cgc gtg   115
                                               Met Lys Pro Arg Val
                                                 1               5

ctg tca gca tta ggc att gga gct ggc gcc ctg gtt gtc tgg atc agc   163
Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu Val Val Trp Ile Ser
                10                  15                  20

tca cgc atg aac tgg gta acc atc gag gct ttc gac gat aaa tca ggt   211
Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe Asp Asp Lys Ser Gly
            25                  30                  35

agt gtc acc caa tct att gtg ggt gca acc tgg tct aca gaa atc atg   259
Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp Ser Thr Glu Ile Met
        40                  45                  50

gcg ctt gca ctt gct ttg ctc gct gcc ttc gcc gcc gcg ttg gtg ctc   307
Ala Leu Ala Leu Ala Leu Leu Ala Ala Phe Ala Ala Ala Leu Val Leu
    55                  60                  65

aag cgc atg ggt cgg cgc atc att ggt ggt att tcg gcg ctg atc gcg   355
Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile Ser Ala Leu Ile Ala
70                  75                  80                  85

gtg ggt gcc agc ctg tct cca ctc gcg ctt ctc acc caa gac cca gac   403
Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu Thr Gln Asp Pro Asp
                90                  95                  100

gca gaa cgg gcc cga acc ctg ctg acc tcc ggt gtg gcc tca cag aag   451
Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly Val Ala Ser Gln Lys
            105                 110                 115

gct aat tcc gga acc ctg ctg tct gat tgg gcg gag atc atc aat acc   499
Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala Glu Ile Ile Asn Thr
        120                 125                 130
```

```
acc acc cat cca ctg gcg gca gtg gta gcc atg att ggc tgc gcg cta   547
Thr Thr His Pro Leu Ala Ala Val Val Ala Met Ile Gly Cys Ala Leu
    135                 140                 145

gcc cta gtc ggc ggc gtt gtc ctt gcc atg cgc cct gcc gag gac acc   595
Ala Leu Val Gly Gly Val Val Leu Ala Met Arg Pro Ala Glu Asp Thr
150                 155                 160                 165

gcg aaa agc aat cag tat gag cgt aaa cag gct cgc gct gag aaa atc   643
Ala Lys Ser Asn Gln Tyr Glu Arg Lys Gln Ala Arg Ala Glu Lys Ile
                170                 175                 180

cac acc gat ttg gcc caa gat cca gac tcc ggt cgt gtg atg tgg acg   691
His Thr Asp Leu Ala Gln Asp Pro Asp Ser Gly Arg Val Met Trp Thr
            185                 190                 195

cac tcg atg aag aca ttg act tca ccg aga aga ctc aga aat cca aag   739
His Ser Met Lys Thr Leu Thr Ser Pro Arg Arg Leu Arg Asn Pro Lys
        200                 205                 210

aaa ccc cag gtc aaa gct agg gtg tgg cac cct gat ttc ttt cgc cat   787
Lys Pro Gln Val Lys Ala Arg Val Trp His Pro Asp Phe Phe Arg His
    215                 220                 225

gtg tgt tcg gga taaccttaaa cacagcattg gtt                        822
Val Cys Ser Gly
230
```

<210> 2078
<211> 233
<212> PRT
<213> Corynebacterium glutamicum

<400> 2078

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Met Lys Pro Arg Val Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu
  1               5                  10                  15

Val Val Trp Ile Ser Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe
             20                  25                  30

Asp Asp Lys Ser Gly Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp
         35                  40                  45

Ser Thr Glu Ile Met Ala Leu Ala Leu Ala Leu Leu Ala Ala Phe Ala
     50                  55                  60

Ala Ala Leu Val Leu Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile
 65                  70                  75                  80

Ser Ala Leu Ile Ala Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu
                 85                  90                  95

Thr Gln Asp Pro Asp Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly
            100                 105                 110

Val Ala Ser Gln Lys Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala
        115                 120                 125

Glu Ile Ile Asn Thr Thr Thr His Pro Leu Ala Ala Val Val Ala Met
    130                 135                 140
```

```
Ile Gly Cys Ala Leu Ala Leu Val Gly Gly Val Val Leu Ala Met Arg
145                 150                 155                 160

Pro Ala Glu Asp Thr Ala Lys Ser Asn Gln Tyr Glu Arg Lys Gln Ala
                165                 170                 175

Arg Ala Glu Lys Ile His Thr Asp Leu Ala Gln Asp Pro Asp Ser Gly
            180                 185                 190

Arg Val Met Trp Thr His Ser Met Lys Thr Leu Thr Ser Pro Arg Arg
        195                 200                 205

Leu Arg Asn Pro Lys Lys Pro Gln Val Lys Ala Arg Val Trp His Pro
    210                 215                 220

Asp Phe Phe Arg His Val Cys Ser Gly
225                 230


<210> 2079
<211> 1368
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1345)
<223> RXA01102

<400> 2079
attctatggt tgttgggaga gatgacttaa tttggaatca cgggctttaa cacgcgctga 60

cattgagcaa cttcccagca tgtggaaaag cccaggtttc gtg gct gtc ctc gtg   115
                                            Val Ala Val Leu Val
                                              1               5

gcg gtt gca gca gcg ttc ggc agt tgg tca ctc ctt ctt ccc gtc gta   163
Ala Val Ala Ala Ala Phe Gly Ser Trp Ser Leu Leu Leu Pro Val Val
                 10                  15                  20

ccg cta gcg gtc ctc aac aac ggc gga tca agc gct gtc gcc ggt gcc   211
Pro Leu Ala Val Leu Asn Asn Gly Gly Ser Ser Ala Val Ala Gly Ala
             25                  30                  35

acc act ggc atc ttc atg gca gct aca gtg atc act cag att ttc act   259
Thr Thr Gly Ile Phe Met Ala Ala Thr Val Ile Thr Gln Ile Phe Thr
         40                  45                  50

ccc gct gcg ctg cgg aaa att ggc tac acc cca gtg atg gct ttc gcc   307
Pro Ala Ala Leu Arg Lys Ile Gly Tyr Thr Pro Val Met Ala Phe Ala
     55                  60                  65

gca ttc atg ctg ggt gtg cca gcc atc ggg tac atc ttc agc gtc gag   355
Ala Phe Met Leu Gly Val Pro Ala Ile Gly Tyr Ile Phe Ser Val Glu
 70                  75                  80                  85

cca att cca gtg ctg gta gtg tcc gca ctt cga gga att ggg ttc ggt   403
Pro Ile Pro Val Leu Val Val Ser Ala Leu Arg Gly Ile Gly Phe Gly
                 90                  95                 100
```

```
gcg ctc acc gtc gca gaa tct gcg ttg gtg gct gaa ctc gtt ccc gta   451
Ala Leu Thr Val Ala Glu Ser Ala Leu Val Ala Glu Leu Val Pro Val
            105                 110                 115

cgc ttc ttg ggc aaa gct tct gga atg ttg ggc gta ttt att ggc ctt   499
Arg Phe Leu Gly Lys Ala Ser Gly Met Leu Gly Val Phe Ile Gly Leu
        120                 125                 130

tcc caa atg ctt ttc ctg cct gcc ggg ttg gcg tta ggt gac caa ttt   547
Ser Gln Met Leu Phe Leu Pro Ala Gly Leu Ala Leu Gly Asp Gln Phe
    135                 140                 145

ggc tac aac gtg gtc tat gtt tta ggt gcc gtt atc gca cta gtt gca   595
Gly Tyr Asn Val Val Tyr Val Leu Gly Ala Val Ile Ala Leu Val Ala
150                 155                 160                 165

gcg gtg atg tgt ctg cgt att ccg cag gtt aag gca gcg gca aag cag   643
Ala Val Met Cys Leu Arg Ile Pro Gln Val Lys Ala Ala Ala Lys Gln
                170                 175                 180

caa cca cag gtg agc gaa cag gag cgt tct gtt tcc acc tgg aag ttg   691
Gln Pro Gln Val Ser Glu Gln Glu Arg Ser Val Ser Thr Trp Lys Leu
            185                 190                 195

gtg ctg gtt ccc tcc ttg gct gtt acc agt ttg tca atg act ttt ggc   739
Val Leu Val Pro Ser Leu Ala Val Thr Ser Leu Ser Met Thr Phe Gly
        200                 205                 210

gca gtg tct tca ttc ctt cca gct gca gtc att gag tta gat cca gga   787
Ala Val Ser Ser Phe Leu Pro Ala Ala Val Ile Glu Leu Asp Pro Gly
    215                 220                 225

tta ggt gct gca tta gcg ggt att att tta tcc att acc ggt ggt tct   835
Leu Gly Ala Ala Leu Ala Gly Ile Ile Leu Ser Ile Thr Gly Gly Ser
230                 235                 240                 245

tca atg gtg ttc cgc tac ctg tcc ggc gtt atc gct gac cgc cgc ggt   883
Ser Met Val Phe Arg Tyr Leu Ser Gly Val Ile Ala Asp Arg Arg Gly
                250                 255                 260

gtg cct ggt acc acg atg att cct gct cag atc att ggg ttc tta ggt   931
Val Pro Gly Thr Thr Met Ile Pro Ala Gln Ile Ile Gly Phe Leu Gly
            265                 270                 275

gtc gtt tta atc acc gtc aca atc ttc caa ggc tgg tcc gtg tgg ctt   979
Val Val Leu Ile Thr Val Thr Ile Phe Gln Gly Trp Ser Val Trp Leu
        280                 285                 290

ttg att ata ggt gca gtg atg ttt ggt ggt gct ttt ggc atg gtg caa   1027
Leu Ile Ile Gly Ala Val Met Phe Gly Gly Ala Phe Gly Met Val Gln
    295                 300                 305

aac gaa gcg ttg ctt tca atg ttt ttc cgg ctt cct cgc act aga gtc   1075
Asn Glu Ala Leu Leu Ser Met Phe Phe Arg Leu Pro Arg Thr Arg Val
310                 315                 320                 325

tcc gaa gcc tcc gcc atc tgg aat atc gcc ttt gat tcg gga aca gga   1123
Ser Glu Ala Ser Ala Ile Trp Asn Ile Ala Phe Asp Ser Gly Thr Gly
                330                 335                 340

atc gga agc ttc ctc ctt ggc ata gtt gcc gca tcg ctt gct tac agt   1171
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```
Ile Gly Ser Phe Leu Leu Gly Ile Val Ala Ala Ser Leu Ala Tyr Ser
            345                 350                 355

ggt gct ttt ggt tcc gga gcc gtg gtg att ttg ttt gga atc gtt ttg   1219
Gly Ala Phe Gly Ser Gly Ala Val Val Ile Leu Phe Gly Ile Val Leu
        360                 365                 370

acc acc gcc gat cga atc att ggg cgg cac cgc att act gaa tac aac   1267
Thr Thr Ala Asp Arg Ile Ile Gly Arg His Arg Ile Thr Glu Tyr Asn
    375                 380                 385

aac acc cgc gcg cgt ttg cgc cag gtg cca gtc gct cgg cgt gca gtg   1315
Asn Thr Arg Ala Arg Leu Arg Gln Val Pro Val Ala Arg Arg Ala Val
390                 395                 400                 405

caa ggg ctg cgc aac agg cgc aaa gat cgc taaaacgctt ttcgacgcca     1365
Gln Gly Leu Arg Asn Arg Arg Lys Asp Arg
                410                 415

ccc                                                              1368
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<210> 2080
<211> 415
<212> PRT
<213> Corynebacterium glutamicum

<400> 2080

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Val Ala Val Leu Val Ala Val Ala Ala Ala Phe Gly Ser Trp Ser Leu
  1               5                  10                  15

Leu Leu Pro Val Val Pro Leu Ala Val Leu Asn Asn Gly Gly Ser Ser
             20                  25                  30

Ala Val Ala Gly Ala Thr Thr Gly Ile Phe Met Ala Ala Thr Val Ile
         35                  40                  45

Thr Gln Ile Phe Thr Pro Ala Ala Leu Arg Lys Ile Gly Tyr Thr Pro
     50                  55                  60

Val Met Ala Phe Ala Ala Phe Met Leu Gly Val Pro Ala Ile Gly Tyr
 65                  70                  75                  80

Ile Phe Ser Val Glu Pro Ile Pro Val Leu Val Val Ser Ala Leu Arg
                 85                  90                  95

Gly Ile Gly Phe Gly Ala Leu Thr Val Ala Glu Ser Ala Leu Val Ala
            100                 105                 110

Glu Leu Val Pro Val Arg Phe Leu Gly Lys Ala Ser Gly Met Leu Gly
        115                 120                 125

Val Phe Ile Gly Leu Ser Gln Met Leu Phe Leu Pro Ala Gly Leu Ala
    130                 135                 140

Leu Gly Asp Gln Phe Gly Tyr Asn Val Val Tyr Val Leu Gly Ala Val
145                 150                 155                 160

Ile Ala Leu Val Ala Ala Val Met Cys Leu Arg Ile Pro Gln Val Lys
                165                 170                 175
```

```
Ala Ala Ala Lys Gln Gln Pro Gln Val Ser Glu Gln Glu Arg Ser Val
            180                 185                 190

Ser Thr Trp Lys Leu Val Leu Val Pro Ser Leu Ala Val Thr Ser Leu
        195                 200                 205

Ser Met Thr Phe Gly Ala Val Ser Ser Phe Leu Pro Ala Ala Val Ile
    210                 215                 220

Glu Leu Asp Pro Gly Leu Gly Ala Ala Leu Ala Gly Ile Ile Leu Ser
225                 230                 235                 240

Ile Thr Gly Gly Ser Ser Met Val Phe Arg Tyr Leu Ser Gly Val Ile
                245                 250                 255

Ala Asp Arg Arg Gly Val Pro Gly Thr Thr Met Ile Pro Ala Gln Ile
            260                 265                 270

Ile Gly Phe Leu Gly Val Val Leu Ile Thr Val Thr Ile Phe Gln Gly
        275                 280                 285

Trp Ser Val Trp Leu Leu Ile Ile Gly Ala Val Met Phe Gly Gly Ala
    290                 295                 300

Phe Gly Met Val Gln Asn Glu Ala Leu Leu Ser Met Phe Phe Arg Leu
305                 310                 315                 320

Pro Arg Thr Arg Val Ser Glu Ala Ser Ala Ile Trp Asn Ile Ala Phe
                325                 330                 335

Asp Ser Gly Thr Gly Ile Gly Ser Phe Leu Leu Gly Ile Val Ala Ala
            340                 345                 350

Ser Leu Ala Tyr Ser Gly Ala Phe Gly Ser Gly Ala Val Val Ile Leu
        355                 360                 365

Phe Gly Ile Val Leu Thr Thr Ala Asp Arg Ile Ile Gly Arg His Arg
    370                 375                 380

Ile Thr Glu Tyr Asn Asn Thr Arg Ala Arg Leu Arg Gln Val Pro Val
385                 390                 395                 400

Ala Arg Arg Ala Val Gln Gly Leu Arg Asn Arg Arg Lys Asp Arg
                405                 410                 415
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<210> 2081
<211> 348
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(325)
<223> RXA01103

<400> 2081
ccgaagcaga gtacaaggct gttgcccgtg cgctgcgcgg tgccgtagag atggatcctc 60

gtcaaacagg aatcccatcc actaagggag cgctctagac atg aac tct tct ccc 115
Met Asn Ser Ser Pro

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                                                    1               5

atc tct gat atg gtc act gcg gct gtg cag aac gaa cca gat gcg ggc   163
Ile Ser Asp Met Val Thr Ala Ala Val Gln Asn Glu Pro Asp Ala Gly
                 10                  15                  20

gac cga tgg ttt att tat ggt ttg ttc ctc atc gcc ggg ctt ttc ttt   211
Asp Arg Trp Phe Ile Tyr Gly Leu Phe Leu Ile Ala Gly Leu Phe Phe
             25                  30                  35

ggc ggt gcc tgg tct gca tat aaa tca gaa aac aaa atc ctc atg gtt   259
Gly Gly Ala Trp Ser Ala Tyr Lys Ser Glu Asn Lys Ile Leu Met Val
         40                  45                  50

gca gcc ggc ctc atc gca gtg ctg gca gtg gct gga gga att cta tgg   307
Ala Ala Gly Leu Ile Ala Val Leu Ala Val Ala Gly Gly Ile Leu Trp
     55                  60                  65

ttg ttg gga gag atg act taatttggaa tcacgggctt taa                348
Leu Leu Gly Glu Met Thr
 70                  75
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Sequence Listing - 2364 - 20-Jan-2010 - 15:06:20

<210> 2082
<211> 75
<212> PRT
<213> Corynebacterium glutamicum

<400> 2082

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Met Asn Ser Ser Pro Ile Ser Asp Met Val Thr Ala Ala Val Gln Asn
  1               5                  10                  15

Glu Pro Asp Ala Gly Asp Arg Trp Phe Ile Tyr Gly Leu Phe Leu Ile
             20                  25                  30

Ala Gly Leu Phe Phe Gly Gly Ala Trp Ser Ala Tyr Lys Ser Glu Asn
         35                  40                  45

Lys Ile Leu Met Val Ala Ala Gly Leu Ile Ala Val Leu Ala Val Ala
     50                  55                  60

Gly Gly Ile Leu Trp Leu Leu Gly Glu Met Thr
 65                  70                  75
```

<210> 2083
<211> 1323
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1300)
<223> RXA01107

<400> 2083

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gggtacatca gagttcattt gaattagact taaaacttaa aatgaccacc ccagatttac 60

ctgaattaaa cccgctttca cctttgagat actggaagga atg gat ttc acc tct   115
                                               Met Asp Phe Thr Ser
                                                 1               5
```

```
gtg aat gat cga aac gtc cct gca ccc aac acc tcc att cct ttc cca   163
Val Asn Asp Arg Asn Val Pro Ala Pro Asn Thr Ser Ile Pro Phe Pro
                10                  15                  20

gtt gac ctg aat cga gtg acg gag gct gtt gat tcc ttg ggc tac cac   211
Val Asp Leu Asn Arg Val Thr Glu Ala Val Asp Ser Leu Gly Tyr His
            25                  30                  35

tat ttg agc tca gaa gat cgc atc atc gtg ccg tgg caa gat cac cgc   259
Tyr Leu Ser Ser Glu Asp Arg Ile Ile Val Pro Trp Gln Asp His Arg
        40                  45                  50

att tcg atg tac ttc agc cac gaa tca ggg caa atg ctc acc atc ctt   307
Ile Ser Met Tyr Phe Ser His Glu Ser Gly Gln Met Leu Thr Ile Leu
    55                  60                  65

ggt cgc acg cgc ctt aat ttg gac atg ttt gcc atc aac gat gcg gcg   355
Gly Arg Thr Arg Leu Asn Leu Asp Met Phe Ala Ile Asn Asp Ala Ala
70                  75                  80                  85

cga gct gtc acc gaa tgg aat gcc gaa cgc atc ggg cca aca gcc ctc   403
Arg Ala Val Thr Glu Trp Asn Ala Glu Arg Ile Gly Pro Thr Ala Leu
                90                  95                  100

gtc cat ctg ggc aac gac ggc gaa gtg gaa ttg aaa ttc cgc acg acc   451
Val His Leu Gly Asn Asp Gly Glu Val Glu Leu Lys Phe Arg Thr Thr
            105                 110                 115

atc tgc atc gat gaa ggg tta agc acc caa cag cta cgc caa ttc atc   499
Ile Cys Ile Asp Glu Gly Leu Ser Thr Gln Gln Leu Arg Gln Phe Ile
        120                 125                 130

aac ctg tcc ttg gac acc acc gcc atg gct gtg acc tat att ctg gag   547
Asn Leu Ser Leu Asp Thr Thr Ala Met Ala Val Thr Tyr Ile Leu Glu
    135                 140                 145

cgt ttt tca gaa ctt aac ttc agc gac acc gga agc cct gac gac acg   595
Arg Phe Ser Glu Leu Asn Phe Ser Asp Thr Gly Ser Pro Asp Asp Thr
150                 155                 160                 165

aac aat gcc gat gaa ctc agc gac gaa caa gac caa gca gat ctc gta   643
Asn Asn Ala Asp Glu Leu Ser Asp Glu Gln Asp Gln Ala Asp Leu Val
                170                 175                 180

gag aaa atc cgg ggg ctg tac gtt ccc act cca gtt gaa gag ctc atc   691
Glu Lys Ile Arg Gly Leu Tyr Val Pro Thr Pro Val Glu Glu Leu Ile
            185                 190                 195

gaa tcc cta gaa gac gca gag tgg gaa gaa tca gac atg gca gac gag   739
Glu Ser Leu Glu Asp Ala Glu Trp Glu Glu Ser Asp Met Ala Asp Glu
        200                 205                 210

gat gca gaa gac gac tac cta gac gat gac tca gaa atc gaa tgg gaa   787
Asp Ala Glu Asp Asp Tyr Leu Asp Asp Asp Ser Glu Ile Glu Trp Glu
    215                 220                 225

aca gac gat gac tac ttc gaa cct gaa gaa gtc gac atg gac gaa ctc   835
Thr Asp Asp Asp Tyr Phe Glu Pro Glu Glu Val Asp Met Asp Glu Leu
230                 235                 240                 245
```

```
ctc aac ggt ttc ctc gaa gat tct gac atc ccc cag gaa gtc acc ttg   883
Leu Asn Gly Phe Leu Glu Asp Ser Asp Ile Pro Gln Glu Val Thr Leu
                250                 255                 260

gaa cgc att cgg gca caa ctg cat gcc atc ggc gtg gta aaa acc agc   931
Glu Arg Ile Arg Ala Gln Leu His Ala Ile Gly Val Val Lys Thr Ser
            265                 270                 275

ggc gaa gac gat ttc atc atc gcg tgg atc aac gaa gtg ttt tta ggc   979
Gly Glu Asp Asp Phe Ile Ile Ala Trp Ile Asn Glu Val Phe Leu Gly
        280                 285                 290

ttc ttc gtt gat aat ggc ccc act ttc ctg gtg aaa ggt cac tgg gat   1027
Phe Phe Val Asp Asn Gly Pro Thr Phe Leu Val Lys Gly His Trp Asp
    295                 300                 305

ccc agc atg gac ccc aca cgc gac ttc atg aaa ctg ttc atg atg tgc   1075
Pro Ser Met Asp Pro Thr Arg Asp Phe Met Lys Leu Phe Met Met Cys
310                 315                 320                 325

aat cag tgg aac gaa aac tct ctg act acc aaa gct ttt tgc cat act   1123
Asn Gln Trp Asn Glu Asn Ser Leu Thr Thr Lys Ala Phe Cys His Thr
                330                 335                 340

gat gac aag ggt ctc cag gtc cgg gta gag ttc gcg gtc tct gtc gct   1171
Asp Asp Lys Gly Leu Gln Val Arg Val Glu Phe Ala Val Ser Val Ala
            345                 350                 355

gaa ggc ctc aac gac gat caa cta cag cac aac atc gca ctg tca att   1219
Glu Gly Leu Asn Asp Asp Gln Leu Gln His Asn Ile Ala Leu Ser Ile
        360                 365                 370

cat cat att ttg caa gcg att gat tcc atc agc aca gaa gcc act gga   1267
His His Ile Leu Gln Ala Ile Asp Ser Ile Ser Thr Glu Ala Thr Gly
    375                 380                 385

tca tca acg gtg gaa tgg ccg gag aaa aac cgc tgatcattaa ggtcttccaa 1320
Ser Ser Thr Val Glu Trp Pro Glu Lys Asn Arg
390                 395                 400

gaa                                                               1323
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<210> 2084
<211> 400
<212> PRT
<213> Corynebacterium glutamicum

<400> 2084

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Met Asp Phe Thr Ser Val Asn Asp Arg Asn Val Pro Ala Pro Asn Thr
  1               5                  10                  15

Ser Ile Pro Phe Pro Val Asp Leu Asn Arg Val Thr Glu Ala Val Asp
             20                  25                  30

Ser Leu Gly Tyr His Tyr Leu Ser Ser Glu Asp Arg Ile Ile Val Pro
         35                  40                  45

Trp Gln Asp His Arg Ile Ser Met Tyr Phe Ser His Glu Ser Gly Gln
     50                  55                  60
```

```
Met Leu Thr Ile Leu Gly Arg Thr Arg Leu Asn Leu Asp Met Phe Ala
 65                  70                  75                  80

Ile Asn Asp Ala Ala Arg Ala Val Thr Glu Trp Asn Ala Glu Arg Ile
                85                  90                  95

Gly Pro Thr Ala Leu Val His Leu Gly Asn Asp Gly Glu Val Glu Leu
            100                 105                 110

Lys Phe Arg Thr Thr Ile Cys Ile Asp Glu Gly Leu Ser Thr Gln Gln
        115                 120                 125

Leu Arg Gln Phe Ile Asn Leu Ser Leu Asp Thr Thr Ala Met Ala Val
    130                 135                 140

Thr Tyr Ile Leu Glu Arg Phe Ser Glu Leu Asn Phe Ser Asp Thr Gly
145                 150                 155                 160

Ser Pro Asp Asp Thr Asn Asn Ala Asp Glu Leu Ser Asp Glu Gln Asp
                165                 170                 175

Gln Ala Asp Leu Val Glu Lys Ile Arg Gly Leu Tyr Val Pro Thr Pro
            180                 185                 190

Val Glu Glu Leu Ile Glu Ser Leu Glu Asp Ala Glu Trp Glu Glu Ser
        195                 200                 205

Asp Met Ala Asp Glu Asp Ala Glu Asp Asp Tyr Leu Asp Asp Asp Ser
    210                 215                 220

Glu Ile Glu Trp Glu Thr Asp Asp Asp Tyr Phe Glu Pro Glu Glu Val
225                 230                 235                 240

Asp Met Asp Glu Leu Leu Asn Gly Phe Leu Glu Asp Ser Asp Ile Pro
                245                 250                 255

Gln Glu Val Thr Leu Glu Arg Ile Arg Ala Gln Leu His Ala Ile Gly
            260                 265                 270

Val Val Lys Thr Ser Gly Glu Asp Asp Phe Ile Ile Ala Trp Ile Asn
        275                 280                 285

Glu Val Phe Leu Gly Phe Phe Val Asp Asn Gly Pro Thr Phe Leu Val
    290                 295                 300

Lys Gly His Trp Asp Pro Ser Met Asp Pro Thr Arg Asp Phe Met Lys
305                 310                 315                 320

Leu Phe Met Met Cys Asn Gln Trp Asn Glu Asn Ser Leu Thr Thr Lys
                325                 330                 335

Ala Phe Cys His Thr Asp Asp Lys Gly Leu Gln Val Arg Val Glu Phe
            340                 345                 350

Ala Val Ser Val Ala Glu Gly Leu Asn Asp Asp Gln Leu Gln His Asn
        355                 360                 365

Ile Ala Leu Ser Ile His His Ile Leu Gln Ala Ile Asp Ser Ile Ser
    370                 375                 380

Thr Glu Ala Thr Gly Ser Ser Thr Val Glu Trp Pro Glu Lys Asn Arg
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385 390 395 400

<210> 2085
<211> 774
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(751)
<223> RXA01108

<400> 2085
gtggccagtg gaagttctgc gactaatcca cagagcttaa aactccggtt gtcagttcag 60

gttgcaaagt taacagtcaa cggctgtatt ctttagagcc atg aca tac ccc ggc 115
Met Thr Tyr Pro Gly
1 5

atc acc tct gac cac aat cct tat gat gga tac aca ggc gat gac ggg 163
Ile Thr Ser Asp His Asn Pro Tyr Asp Gly Tyr Thr Gly Asp Asp Gly
10 15 20

gcc gga aac aag cgc aac ctc cca aac cga aag aaa ata aac aaa tcg 211
Ala Gly Asn Lys Arg Asn Leu Pro Asn Arg Lys Lys Ile Asn Lys Ser
25 30 35

gtg gga gtt tac gct ggt gtg ttt gcc cta aca ttg gct tta tac gcc 259
Val Gly Val Tyr Ala Gly Val Phe Ala Leu Thr Leu Ala Leu Tyr Ala
40 45 50

att ggg gga gcc gca tgg gga ctg ctc cga ccc act tat acc gct tat 307
Ile Gly Gly Ala Ala Trp Gly Leu Leu Arg Pro Thr Tyr Thr Ala Tyr
55 60 65

gtt gaa gac gct gaa aca gcc tcc ata gcg gtg gaa acc aac act tct 355
Val Glu Asp Ala Glu Thr Ala Ser Ile Ala Val Glu Thr Asn Thr Ser
70 75 80 85

ttt gcc ggc tat gcc tgg ttt gcg atc gcc acc ggt gtg ctt gca gca 403
Phe Ala Gly Tyr Ala Trp Phe Ala Ile Ala Thr Gly Val Leu Ala Ala
90 95 100

gca atc gca tta ttc gtt ttc ctg cgc acc cct caa cat cga ggc cca 451
Ala Ile Ala Leu Phe Val Phe Leu Arg Thr Pro Gln His Arg Gly Pro
105 110 115

gtt atg ctc cta tgg ctg gga att gta tct atc gca ggt tcc gtg gca 499
Val Met Leu Leu Trp Leu Gly Ile Val Ser Ile Ala Gly Ser Val Ala
120 125 130

ttc ctg gtg ttt gga aac gtg gcc tcg acg atg ctt cat ggt tca cca 547
Phe Leu Val Phe Gly Asn Val Ala Ser Thr Met Leu His Gly Ser Pro
135 140 145

tct gat tac gcc tca gcg atc ggt gcg tct ttc cag gta gca ccc act 595
Ser Asp Tyr Ala Ser Ala Ile Gly Ala Ser Phe Gln Val Ala Pro Thr

```
150                 155                 160                 165

att acc cct ggt gtt gcg ttt ggg gtc gct cca ttt ttg agt gtg tgc   643
Ile Thr Pro Gly Val Ala Phe Gly Val Ala Pro Phe Leu Ser Val Cys
                170                 175                 180

atg tat tgg tgc gcg gca ttt gtg aca cct gaa gaa gag ata gac cag   691
Met Tyr Trp Cys Ala Ala Phe Val Thr Pro Glu Glu Glu Ile Asp Gln
            185                 190                 195

gac gac gca ggc cag ggg act tcg aaa gca tcg ggg tct gag atg act   739
Asp Asp Ala Gly Gln Gly Thr Ser Lys Ala Ser Gly Ser Glu Met Thr
        200                 205                 210

ggg gct agt ggc taggggctag atgtgcgcaa aca                        774
Gly Ala Ser Gly
    215


<210> 2086
<211> 217
<212> PRT
<213> Corynebacterium glutamicum

<400> 2086
Met Thr Tyr Pro Gly Ile Thr Ser Asp His Asn Pro Tyr Asp Gly Tyr
  1               5                  10                  15

Thr Gly Asp Asp Gly Ala Gly Asn Lys Arg Asn Leu Pro Asn Arg Lys
             20                  25                  30

Lys Ile Asn Lys Ser Val Gly Val Tyr Ala Gly Val Phe Ala Leu Thr
         35                  40                  45

Leu Ala Leu Tyr Ala Ile Gly Gly Ala Ala Trp Gly Leu Leu Arg Pro
     50                  55                  60

Thr Tyr Thr Ala Tyr Val Glu Asp Ala Glu Thr Ala Ser Ile Ala Val
 65                  70                  75                  80

Glu Thr Asn Thr Ser Phe Ala Gly Tyr Ala Trp Phe Ala Ile Ala Thr
                 85                  90                  95

Gly Val Leu Ala Ala Ala Ile Ala Leu Phe Val Phe Leu Arg Thr Pro
            100                 105                 110

Gln His Arg Gly Pro Val Met Leu Leu Trp Leu Gly Ile Val Ser Ile
        115                 120                 125

Ala Gly Ser Val Ala Phe Leu Val Phe Gly Asn Val Ala Ser Thr Met
    130                 135                 140

Leu His Gly Ser Pro Ser Asp Tyr Ala Ser Ala Ile Gly Ala Ser Phe
145                 150                 155                 160

Gln Val Ala Pro Thr Ile Thr Pro Gly Val Ala Phe Gly Val Ala Pro
                165                 170                 175

Phe Leu Ser Val Cys Met Tyr Trp Cys Ala Ala Phe Val Thr Pro Glu
            180                 185                 190
```

```
Glu Glu Ile Asp Gln Asp Asp Ala Gly Gln Gly Thr Ser Lys Ala Ser
        195                 200                 205

Gly Ser Glu Met Thr Gly Ala Ser Gly
    210                 215


<210> 2087
<211> 765
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(742)
<223> RXA01109

<400> 2087
gggtcgtcag ctagattgct ttgctagggt aatctgcgtg aaccgtccgg gaatttttaa 60

gttttccgga gcatgtcgat gatttatcag gagcagaact ttg tct att agc ctt   115
                                            Leu Ser Ile Ser Leu
                                              1               5

tcc tca aag aag gtt gct ttc gca gca ctc atg gtc acc cca ctt ctc   163
Ser Ser Lys Lys Val Ala Phe Ala Ala Leu Met Val Thr Pro Leu Leu
                10                  15                  20

ttg acc gca tgt ggc agt gat tca tct gat act gaa gca gcc tca tcc   211
Leu Thr Ala Cys Gly Ser Asp Ser Ser Asp Thr Glu Ala Ala Ser Ser
            25                  30                  35

agc gca gcg acg acg aca aat tct tcc tca tcc agc gca gcg acc tcg   259
Ser Ala Ala Thr Thr Thr Asn Ser Ser Ser Ser Ser Ala Ala Thr Ser
        40                  45                  50

gcg gaa gca gca gaa acc acc tcg tcc gaa tct gaa tct tcc gaa gca   307
Ala Glu Ala Ala Glu Thr Thr Ser Ser Glu Ser Glu Ser Ser Glu Ala
    55                  60                  65

aca acc att aac gaa gag cag caa gca cag ctt gat gta ctg tct caa   355
Thr Thr Ile Asn Glu Glu Gln Gln Ala Gln Leu Asp Val Leu Ser Gln
70                  75                  80                  85

gag ctg tct gag aac cca att acc ttc gct gaa gct gcg cca gtt gaa   403
Glu Leu Ser Glu Asn Pro Ile Thr Phe Ala Glu Ala Ala Pro Val Glu
                90                  95                  100

aac ggc gag acc gct tcc cca gaa gac aca gct gcc atc gag gct ctg   451
Asn Gly Glu Thr Ala Ser Pro Glu Asp Thr Ala Ala Ile Glu Ala Leu
            105                 110                 115

gtt cgc gga tac act gac acc aac acc ttg cgt agc tcc ctt gcg tac   499
Val Arg Gly Tyr Thr Asp Thr Asn Thr Leu Arg Ser Ser Leu Ala Tyr
        120                 125                 130

acc atc aac aac acc tgc acc cgc gtt ctt gaa gcc agc ggc gct gac   547
Thr Ile Asn Asn Thr Cys Thr Arg Val Leu Glu Ala Ser Gly Ala Asp
    135                 140                 145

gct acc cag ctt gat ctc aac acc atc cct gat atc cca ctg ggt ggc   595
```

```
Ala Thr Gln Leu Asp Leu Asn Thr Ile Pro Asp Ile Pro Leu Gly Gly
150                 155                 160                 165

gaa ggc acc gga act gtt gat tcc atc acc gat gtt gtg gtc aac ggc   643
Glu Gly Thr Gly Thr Val Asp Ser Ile Thr Asp Val Val Val Asn Gly
                170                 175                 180

cag gaa gca tcc gca tgg gtc gta gca acc gcc ggt gga acc acc gac   691
Gln Glu Ala Ser Ala Trp Val Val Ala Thr Ala Gly Gly Thr Thr Asp
            185                 190                 195

tct gca acc cag cgc ttc ttc aac gaa ggt ggc cag tgg aag ttc tgc   739
Ser Ala Thr Gln Arg Phe Phe Asn Glu Gly Gly Gln Trp Lys Phe Cys
        200                 205                 210

gac taatccacag agcttaaaac tcc                                    765
Asp
```

<210> 2088
<211> 214
<212> PRT
<213> Corynebacterium glutamicum

<400> 2088

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Leu Ser Ile Ser Leu Ser Ser Lys Lys Val Ala Phe Ala Ala Leu Met
  1               5                  10                  15

Val Thr Pro Leu Leu Leu Thr Ala Cys Gly Ser Asp Ser Ser Asp Thr
             20                  25                  30

Glu Ala Ala Ser Ser Ser Ala Ala Thr Thr Thr Asn Ser Ser Ser Ser
         35                  40                  45

Ser Ala Ala Thr Ser Ala Glu Ala Ala Glu Thr Thr Ser Ser Glu Ser
     50                  55                  60

Glu Ser Ser Glu Ala Thr Thr Ile Asn Glu Glu Gln Gln Ala Gln Leu
 65                  70                  75                  80

Asp Val Leu Ser Gln Glu Leu Ser Glu Asn Pro Ile Thr Phe Ala Glu
                 85                  90                  95

Ala Ala Pro Val Glu Asn Gly Glu Thr Ala Ser Pro Glu Asp Thr Ala
            100                 105                 110

Ala Ile Glu Ala Leu Val Arg Gly Tyr Thr Asp Thr Asn Thr Leu Arg
        115                 120                 125

Ser Ser Leu Ala Tyr Thr Ile Asn Asn Thr Cys Thr Arg Val Leu Glu
    130                 135                 140

Ala Ser Gly Ala Asp Ala Thr Gln Leu Asp Leu Asn Thr Ile Pro Asp
145                 150                 155                 160

Ile Pro Leu Gly Gly Glu Gly Thr Gly Thr Val Asp Ser Ile Thr Asp
                165                 170                 175

Val Val Val Asn Gly Gln Glu Ala Ser Ala Trp Val Val Ala Thr Ala
            180                 185                 190
```

```
Gly Gly Thr Thr Asp Ser Ala Thr Gln Arg Phe Phe Asn Glu Gly Gly
        195                 200                 205

Gln Trp Lys Phe Cys Asp
    210


<210> 2089
<211> 1053
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1030)
<223> RXA01119

<400> 2089
ccgtaaagac gttggcgaag tcatcatcaa cggtgccgtt gcccgtggcg aagccgaacc 60

agagatgttg gaagctgtcg cagaagaaaa gaccgcgtag ttg gca gga gtt atc   115
                                              Leu Ala Gly Val Ile
                                                1               5

acc ggc ttt gcc atc atc ctg tcg gtt atc ggc gtt gga ttt ctt ctg   163
Thr Gly Phe Ala Ile Ile Leu Ser Val Ile Gly Val Gly Phe Leu Leu
                10                  15                  20

gca aag ctg ggg gtc atc aat gat gac aaa cag cgc ttg gtg tta aac   211
Ala Lys Leu Gly Val Ile Asn Asp Asp Lys Gln Arg Leu Val Leu Asn
            25                  30                  35

cgc att gct ttt tat gcg gca act cca gcg ctg ctt ttc aat gtc gtt   259
Arg Ile Ala Phe Tyr Ala Ala Thr Pro Ala Leu Leu Phe Asn Val Val
        40                  45                  50

gcc cga tca gat ccc agc gcg ttg atc tca ccg gtc att gtg gtg aca   307
Ala Arg Ser Asp Pro Ser Ala Leu Ile Ser Pro Val Ile Val Val Thr
    55                  60                  65

ttt gtg gcc acg atc gtc aca gca gct gtg tac tgc gtg att tcg gcg   355
Phe Val Ala Thr Ile Val Thr Ala Ala Val Tyr Cys Val Ile Ser Ala
70                  75                  80                  85

att ttc ttt aag aag gat atc gcc act acg gcg aca gga gct gcg gct   403
Ile Phe Phe Lys Lys Asp Ile Ala Thr Thr Ala Thr Gly Ala Ala Ala
                90                  95                  100

tct gcc tac gtg aac tcc aac aac att ggc ctg ccg gtg tct att tat   451
Ser Ala Tyr Val Asn Ser Asn Asn Ile Gly Leu Pro Val Ser Ile Tyr
            105                 110                 115

gtg ctg gga aca ggc gca tat gtg gca ccg att ctg gtc atg cag atg   499
Val Leu Gly Thr Gly Ala Tyr Val Ala Pro Ile Leu Val Met Gln Met
        120                 125                 130

gtg att ttc gcg ccc atg atc ctg gcc gcg ctg acc tct ggt gat gtg   547
Val Ile Phe Ala Pro Met Ile Leu Ala Ala Leu Thr Ser Gly Asp Val
    135                 140                 145
```

```
aaa ggc tcg cgc ggg caa aaa ata tgg gct gcg gtg aaa ggt tca ctg   595
Lys Gly Ser Arg Gly Gln Lys Ile Trp Ala Ala Val Lys Gly Ser Leu
150                 155                 160                 165

ctc agc cca att gtg ttg gcc tct atc gcg ggc ctg atc gtg tgt ctg   643
Leu Ser Pro Ile Val Leu Ala Ser Ile Ala Gly Leu Ile Val Cys Leu
                170                 175                 180

tta gaa att cag ctg cca gcc gca gtc atg gaa ccc acc atc att ttg   691
Leu Glu Ile Gln Leu Pro Ala Ala Val Met Glu Pro Thr Ile Ile Leu
            185                 190                 195

ggc ggc gca tcc att ccg ttg att ctg atg agc ttc ggc gca tca ttg   739
Gly Gly Ala Ser Ile Pro Leu Ile Leu Met Ser Phe Gly Ala Ser Leu
        200                 205                 210

ccc tca acc aac gtg ctg gct tcc aag gcg gat cgc ccc agc gtt ctt   787
Pro Ser Thr Asn Val Leu Ala Ser Lys Ala Asp Arg Pro Ser Val Leu
    215                 220                 225

act gct act gcg ata aaa att gtg ggt atg ccc gcc atc act tgg ctg   835
Thr Ala Thr Ala Ile Lys Ile Val Gly Met Pro Ala Ile Thr Trp Leu
230                 235                 240                 245

atc gcc aag gcg ttt ggt ctg gag ggc gat tac ctc tac gcc gct gtt   883
Ile Ala Lys Ala Phe Gly Leu Glu Gly Asp Tyr Leu Tyr Ala Ala Val
                250                 255                 260

att ttg gcg gcg ctg ccc gcc gcg cag aat gtg tac aac tac gcg gcg   931
Ile Leu Ala Ala Leu Pro Ala Ala Gln Asn Val Tyr Asn Tyr Ala Ala
            265                 270                 275

acg tac cgc aag ggc gag atc gtc gcc cgc gat acg gtc ttc ctc acc   979
Thr Tyr Arg Lys Gly Glu Ile Val Ala Arg Asp Thr Val Phe Leu Thr
        280                 285                 290

acg ttc cta gcg ctg ctg ggc atg cta gga atc gcg gcc cta ttt ggt   1027
Thr Phe Leu Ala Leu Leu Gly Met Leu Gly Ile Ala Ala Leu Phe Gly
    295                 300                 305

cgc tagggcttca ggctgctttt cga                                    1053
Arg
310
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US 60/[illegible] filed on [illegible]

<210> 2090
<211> 310
<212> PRT
<213> Corynebacterium glutamicum

<400> 2090

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Leu Ala Gly Val Ile Thr Gly Phe Ala Ile Ile Leu Ser Val Ile Gly
  1               5                  10                  15

Val Gly Phe Leu Leu Ala Lys Leu Gly Val Ile Asn Asp Asp Lys Gln
             20                  25                  30

Arg Leu Val Leu Asn Arg Ile Ala Phe Tyr Ala Ala Thr Pro Ala Leu
         35                  40                  45

Leu Phe Asn Val Val Ala Arg Ser Asp Pro Ser Ala Leu Ile Ser Pro
```

```
     50                  55                  60

Val Ile Val Val Thr Phe Val Ala Thr Ile Val Thr Ala Ala Val Tyr
 65                  70                  75                  80

Cys Val Ile Ser Ala Ile Phe Phe Lys Lys Asp Ile Ala Thr Thr Ala
                85                  90                  95

Thr Gly Ala Ala Ala Ser Ala Tyr Val Asn Ser Asn Asn Ile Gly Leu
            100                 105                 110

Pro Val Ser Ile Tyr Val Leu Gly Thr Gly Ala Tyr Val Ala Pro Ile
        115                 120                 125

Leu Val Met Gln Met Val Ile Phe Ala Pro Met Ile Leu Ala Ala Leu
    130                 135                 140

Thr Ser Gly Asp Val Lys Gly Ser Arg Gly Gln Lys Ile Trp Ala Ala
145                 150                 155                 160

Val Lys Gly Ser Leu Leu Ser Pro Ile Val Leu Ala Ser Ile Ala Gly
                165                 170                 175

Leu Ile Val Cys Leu Leu Glu Ile Gln Leu Pro Ala Ala Val Met Glu
            180                 185                 190

Pro Thr Ile Ile Leu Gly Gly Ala Ser Ile Pro Leu Ile Leu Met Ser
        195                 200                 205

Phe Gly Ala Ser Leu Pro Ser Thr Asn Val Leu Ala Ser Lys Ala Asp
    210                 215                 220

Arg Pro Ser Val Leu Thr Ala Thr Ala Ile Lys Ile Val Gly Met Pro
225                 230                 235                 240

Ala Ile Thr Trp Leu Ile Ala Lys Ala Phe Gly Leu Glu Gly Asp Tyr
                245                 250                 255

Leu Tyr Ala Ala Val Ile Leu Ala Ala Leu Pro Ala Ala Gln Asn Val
            260                 265                 270

Tyr Asn Tyr Ala Ala Thr Tyr Arg Lys Gly Glu Ile Val Ala Arg Asp
        275                 280                 285

Thr Val Phe Leu Thr Thr Phe Leu Ala Leu Leu Gly Met Leu Gly Ile
    290                 295                 300

Ala Ala Leu Phe Gly Arg
305                 310
```

<210> 2091
<211> 645
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(622)
<223> RXA01122

<400> 2091
tattcgacca aggctgagca aaaaggcgct aagctgtggg gagatcgcaa gcccctatcc 60

ggcctctact aagccccgaa gttgaaggga aactccccca atg ccg ttt cca gca 115
Met Pro Phe Pro Ala
1 5

ctg ttg ttg ccg ctg att ttc tgg aca gga att gca gct ttg tcc tct 163
Leu Leu Leu Pro Leu Ile Phe Trp Thr Gly Ile Ala Ala Leu Ser Ser
10 15 20

tgg gcg gtc agc cgt gca ctt ccg ctg cgc gcc gat aat tcc att gag 211
Trp Ala Val Ser Arg Ala Leu Pro Leu Arg Ala Asp Asn Ser Ile Glu
25 30 35

att gat gcg ccg gtg gaa aag gtc tgg gat ttc atc gag gag acc aac 259
Ile Asp Ala Pro Val Glu Lys Val Trp Asp Phe Ile Glu Glu Thr Asn
40 45 50

cgc gtg ccg gag tgg aat gag cac att ctg tac gtg cag gcg cct ggt 307
Arg Val Pro Glu Trp Asn Glu His Ile Leu Tyr Val Gln Ala Pro Gly
55 60 65

gag atc gag cag ggc atg aag ctc aag atg aaa aca agg cac cca gag 355
Glu Ile Glu Gln Gly Met Lys Leu Lys Met Lys Thr Arg His Pro Glu
70 75 80 85

acc aat cgc ctc act ttg aag ttt cgc ccc acc atc gac gtg ctg cgt 403
Thr Asn Arg Leu Thr Leu Lys Phe Arg Pro Thr Ile Asp Val Leu Arg
90 95 100

cca cac cgt gaa ttg acg tgg tcc acc aaa att gtt gcg cgt tgg ctg 451
Pro His Arg Glu Leu Thr Trp Ser Thr Lys Ile Val Ala Arg Trp Leu
105 110 115

ctc acc gtc acc gac acg atc gag ctg aag cct ttg gaa gat ggt cgc 499
Leu Thr Val Thr Asp Thr Ile Glu Leu Lys Pro Leu Glu Asp Gly Arg
120 125 130

act gag gtg gat caa tca atg tcc ttt agt ggc gta cta tcc ccc gga 547
Thr Glu Val Asp Gln Ser Met Ser Phe Ser Gly Val Leu Ser Pro Gly
135 140 145

gtg ccc ttt ttg gcc agc atc agc agg atc aaa gag aac tca aac cgc 595
Val Pro Phe Leu Ala Ser Ile Ser Arg Ile Lys Glu Asn Ser Asn Arg
150 155 160 165

cag ttg aaa gca ctg atc gaa gcc gag taaacctcca acccctacat 642
Gln Leu Lys Ala Leu Ile Glu Ala Glu
170

aac 645

<210> 2092
<211> 174
<212> PRT
<213> Corynebacterium glutamicum

<400> 2092
Met Pro Phe Pro Ala Leu Leu Leu Pro Leu Ile Phe Trp Thr Gly Ile

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  1               5                  10                  15

Ala Ala Leu Ser Ser Trp Ala Val Ser Arg Ala Leu Pro Leu Arg Ala
             20                  25                  30

Asp Asn Ser Ile Glu Ile Asp Ala Pro Val Glu Lys Val Trp Asp Phe
         35                  40                  45

Ile Glu Glu Thr Asn Arg Val Pro Glu Trp Asn Glu His Ile Leu Tyr
     50                  55                  60

Val Gln Ala Pro Gly Glu Ile Glu Gln Gly Met Lys Leu Lys Met Lys
 65                  70                  75                  80

Thr Arg His Pro Glu Thr Asn Arg Leu Thr Leu Lys Phe Arg Pro Thr
                 85                  90                  95

Ile Asp Val Leu Arg Pro His Arg Glu Leu Thr Trp Ser Thr Lys Ile
            100                 105                 110

Val Ala Arg Trp Leu Leu Thr Val Thr Asp Thr Ile Glu Leu Lys Pro
        115                 120                 125

Leu Glu Asp Gly Arg Thr Glu Val Asp Gln Ser Met Ser Phe Ser Gly
    130                 135                 140

Val Leu Ser Pro Gly Val Pro Phe Leu Ala Ser Ile Ser Arg Ile Lys
145                 150                 155                 160

Glu Asn Ser Asn Arg Gln Leu Lys Ala Leu Ile Glu Ala Glu
                165                 170
```

US 20050153417 A1

<210> 2093
<211> 570
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(547)
<223> RXA01123

<400> 2093
aaagagcagt gatttttccc gatccccccc tggccgccta gcggaaatta ttgataccgc 60

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gtggcggttg gtggaaacac gtggctgggc gaatgtgagc atg cga acc ctg gcc   115
                                              Met Arg Thr Leu Ala
                                                1               5

gcg gag cta aat atc aag gcg ccg tcg ctg tac aag cat gta aaa acg   163
Ala Glu Leu Asn Ile Lys Ala Pro Ser Leu Tyr Lys His Val Lys Thr
                10                  15                  20

cgc gag gat atc gcc gca cac atc gcc acg aag gca ttt att cag ctg   211
Arg Glu Asp Ile Ala Ala His Ile Ala Thr Lys Ala Phe Ile Gln Leu
            25                  30                  35

ggg caa agc ctg cat gaa cat tgt gaa agt gtg gag gat ttg ctt gcg   259
Gly Gln Ser Leu His Glu His Cys Glu Ser Val Glu Asp Leu Leu Ala
        40                  45                  50
```

```
gaa tac cgc tcc atg gct cgg gaa aat cca aat att tac cgg ctt ctc   307
Glu Tyr Arg Ser Met Ala Arg Glu Asn Pro Asn Ile Tyr Arg Leu Leu
     55                  60                  65

acc agt tca gag ttc ccc cgc gag cta ctt cca gaa ggc cta gaa act   355
Thr Ser Ser Glu Phe Pro Arg Glu Leu Leu Pro Glu Gly Leu Glu Thr
 70                  75                  80                  85

tgg gca gga acg cca ttc tac ctg gtc acc ggc cac gat ccg atc aag   403
Trp Ala Gly Thr Pro Phe Tyr Leu Val Thr Gly His Asp Pro Ile Lys
                 90                  95                 100

ggt caa gca ctg tgg gca ttc gcg cac ggc atg gcc atc ctg gaa atc   451
Gly Gln Ala Leu Trp Ala Phe Ala His Gly Met Ala Ile Leu Glu Ile
            105                 110                 115

gac gcc cga ttc gcc ggc ccc aac aat gga tcc ccc gcg gat ggc gtg   499
Asp Ala Arg Phe Ala Gly Pro Asn Asn Gly Ser Pro Ala Asp Gly Val
        120                 125                 130

tgg gag atc ggc gcg cgg gca ttt gac aca caa gta ttc gac caa ggc   547
Trp Glu Ile Gly Ala Arg Ala Phe Asp Thr Gln Val Phe Asp Gln Gly
    135                 140                 145

tgagcaaaaa ggcgctaagc tgt                                        570


<210> 2094
<211> 149
<212> PRT
<213> Corynebacterium glutamicum

<400> 2094
Met Arg Thr Leu Ala Ala Glu Leu Asn Ile Lys Ala Pro Ser Leu Tyr
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Lys His Val Lys Thr Arg Glu Asp Ile Ala Ala His Ile Ala Thr Lys
             20                  25                  30

Ala Phe Ile Gln Leu Gly Gln Ser Leu His Glu His Cys Glu Ser Val
         35                  40                  45

Glu Asp Leu Leu Ala Glu Tyr Arg Ser Met Ala Arg Glu Asn Pro Asn
     50                  55                  60

Ile Tyr Arg Leu Leu Thr Ser Ser Glu Phe Pro Arg Glu Leu Leu Pro
 65                  70                  75                  80

Glu Gly Leu Glu Thr Trp Ala Gly Thr Pro Phe Tyr Leu Val Thr Gly
                 85                  90                  95

His Asp Pro Ile Lys Gly Gln Ala Leu Trp Ala Phe Ala His Gly Met
            100                 105                 110

Ala Ile Leu Glu Ile Asp Ala Arg Phe Ala Gly Pro Asn Asn Gly Ser
        115                 120                 125

Pro Ala Asp Gly Val Trp Glu Ile Gly Ala Arg Ala Phe Asp Thr Gln
    130                 135                 140
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Val Phe Asp Gln Gly
145

<210> 2095
<211> 302
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(279)
<223> RXA01127

<400> 2095
gga att ggc ctc gca gca tcc ggc aac atc gat gcc acg ggc acc aac 48
Gly Ile Gly Leu Ala Ala Ser Gly Asn Ile Asp Ala Thr Gly Thr Asn
1 5 10 15

cct tcc atg ttc gag cca gtc cac ggc tct gca cca gat atc gca ggc 96
Pro Ser Met Phe Glu Pro Val His Gly Ser Ala Pro Asp Ile Ala Gly
20 25 30

cag gga atc gca gac cca acg gca gca atc cta tcc gct gcg atg ctg 144
Gln Gly Ile Ala Asp Pro Thr Ala Ala Ile Leu Ser Ala Ala Met Leu
35 40 45

ctg cgt cac tta ggt gat gaa gac aac gca gta cgt att gaa aca gcc 192
Leu Arg His Leu Gly Asp Glu Asp Asn Ala Val Arg Ile Glu Thr Ala
50 55 60

atc gca gct gat gtg gct ggc cga gat aac tct cag ccg att tct acc 240
Ile Ala Ala Asp Val Ala Gly Arg Asp Asn Ser Gln Pro Ile Ser Thr
65 70 75 80

act gag gtg gga gac cgc atc gtc aag gcg ctg caa agc taaatttcaa 289
Thr Glu Val Gly Asp Arg Ile Val Lys Ala Leu Gln Ser
85 90

cgccgacccc ctt 302

<210> 2096
<211> 93
<212> PRT
<213> Corynebacterium glutamicum

<400> 2096
Gly Ile Gly Leu Ala Ala Ser Gly Asn Ile Asp Ala Thr Gly Thr Asn
1 5 10 15

Pro Ser Met Phe Glu Pro Val His Gly Ser Ala Pro Asp Ile Ala Gly
20 25 30

Gln Gly Ile Ala Asp Pro Thr Ala Ala Ile Leu Ser Ala Ala Met Leu
35 40 45

Leu Arg His Leu Gly Asp Glu Asp Asn Ala Val Arg Ile Glu Thr Ala
50 55 60

Ile Ala Ala Asp Val Ala Gly Arg Asp Asn Ser Gln Pro Ile Ser Thr

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 65                  70                  75                  80

Thr Glu Val Gly Asp Arg Ile Val Lys Ala Leu Gln Ser
                 85                  90


<210> 2097
<211> 1989
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1966)
<223> RXA01129

<400> 2097
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cgaatgcagg atttcgagac aatgaggcag tttttctttt atg gtt aat ctc atg   115
                                            Met Val Asn Leu Met
                                              1               5

tcg gtc gaa ctc gaa gaa atc cgc gat ttc tta gca gga ttt gaa cct   163
Ser Val Glu Leu Glu Glu Ile Arg Asp Phe Leu Ala Gly Phe Glu Pro
                10                  15                  20

ttc gcg cag cta cca gcc gag gaa cta gat cag tta cct gga aaa atg   211
Phe Ala Gln Leu Pro Ala Glu Glu Leu Asp Gln Leu Pro Gly Lys Met
            25                  30                  35

agc ttg cgc tat ttt cgg cgt ggg gaa gag atc atc cca att ggt gtg   259
Ser Leu Arg Tyr Phe Arg Arg Gly Glu Glu Ile Ile Pro Ile Gly Val
        40                  45                  50

ccc aat cat tac atg ggg gta atc aga tcg ggt gcc att gat gtt ctt   307
Pro Asn His Tyr Met Gly Val Ile Arg Ser Gly Ala Ile Asp Val Leu
    55                  60                  65

gat cag gag ggc gta ctg ctg gat cgc cgt gac gcg ggg cgc tcg ttt   355
Asp Gln Glu Gly Val Leu Leu Asp Arg Arg Asp Ala Gly Arg Ser Phe
70                  75                  80                  85

ggc tat tcc acg atg ggg cca gaa cga aat tct cgg tac cgt atg gtt   403
Gly Tyr Ser Thr Met Gly Pro Glu Arg Asn Ser Arg Tyr Arg Met Val
                90                  95                  100

gcc gtg gaa gat tcc ttg gtg ttg cgt ctg ggg cgt gat gat ttt gat   451
Ala Val Glu Asp Ser Leu Val Leu Arg Leu Gly Arg Asp Asp Phe Asp
            105                 110                 115

gag tta gcc aag cgc aac cct gat ctg aac cgt tac tac tcc agc tgg   499
Glu Leu Ala Lys Arg Asn Pro Asp Leu Asn Arg Tyr Tyr Ser Ser Trp
        120                 125                 130

tcg aag cgt atc cgc gcc gct gct gat caa ttg cgc caa gaa tct agt   547
Ser Lys Arg Ile Arg Ala Ala Ala Asp Gln Leu Arg Gln Glu Ser Ser
    135                 140                 145

tcg aag gtg ctg cgc acg aag ttg ggg gag ttc aag atc gcc aac ccg   595
Ser Lys Val Leu Arg Thr Lys Leu Gly Glu Phe Lys Ile Ala Asn Pro
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150                 155                 160                 165

att tcc tgc agc ccg gac acc acg atc atg gat gct gcc atc aag atg   643
Ile Ser Cys Ser Pro Asp Thr Thr Ile Met Asp Ala Ala Ile Lys Met
                170                 175                 180

cat gag ttc ggg gtg tct tcg ttg ctg gtg cag atc gat ggg gaa ctc   691
His Glu Phe Gly Val Ser Ser Leu Leu Val Gln Ile Asp Gly Glu Leu
            185                 190                 195

aaa ggc atc atc acc gat cac tat atg cgc agc agg gtg gtg gcg aag   739
Lys Gly Ile Ile Thr Asp His Tyr Met Arg Ser Arg Val Val Ala Lys
        200                 205                 210

cat ttg gat att cag ctg ccg gtc tct gag gtc atg acg gtg gat ccg   787
His Leu Asp Ile Gln Leu Pro Val Ser Glu Val Met Thr Val Asp Pro
    215                 220                 225

cgt tgc gcg acc tcg cag ggg ttg gct ttt gag gcc atg ttg ttg atg   835
Arg Cys Ala Thr Ser Gln Gly Leu Ala Phe Glu Ala Met Leu Leu Met
230                 235                 240                 245

tcg gag ctg cgc att cac cac ttg ccg att gtg gat gat ggc caa atc   883
Ser Glu Leu Arg Ile His His Leu Pro Ile Val Asp Asp Gly Gln Ile
                250                 255                 260

tcc ggc atc gtc act gca gct gac atc atg cgc ttg ctg cgc cac gat   931
Ser Gly Ile Val Thr Ala Ala Asp Ile Met Arg Leu Leu Arg His Asp
            265                 270                 275

ccg att tac ctc act gcg gat ctg tcg cga aaa aat acc gtg gag gaa   979
Pro Ile Tyr Leu Thr Ala Asp Leu Ser Arg Lys Asn Thr Val Glu Glu
        280                 285                 290

ttg gcc aac acc ttc cag tcg gca gcg gag gtg gct tcg aga ttt att   1027
Leu Ala Asn Thr Phe Gln Ser Ala Ala Glu Val Ala Ser Arg Phe Ile
    295                 300                 305

gat cgg gga gct tct gcg gaa gaa gtc agt agc ttg ctc acc gtg gct   1075
Asp Arg Gly Ala Ser Ala Glu Glu Val Ser Ser Leu Leu Thr Val Ala
310                 315                 320                 325

gcg gat tct ttg gca aga agg ctc ctt gtg ctg gcg gag cgg aaa ttt   1123
Ala Asp Ser Leu Ala Arg Arg Leu Leu Val Leu Ala Glu Arg Lys Phe
                330                 335                 340

ggt gca ccg cca gtt ccg tat tgc ttt gtg gtg gtg ggc tcg cag ggc   1171
Gly Ala Pro Pro Val Pro Tyr Cys Phe Val Val Val Gly Ser Gln Gly
            345                 350                 355

agg aaa gaa atg gga ctg gcc tct gat caa gac aat gcc ctt gtt ctg   1219
Arg Lys Glu Met Gly Leu Ala Ser Asp Gln Asp Asn Ala Leu Val Leu
        360                 365                 370

gac aat tcc tac aat gac cgc gag cat gga cag tat ttt gca gcg ctg   1267
Asp Asn Ser Tyr Asn Asp Arg Glu His Gly Gln Tyr Phe Ala Ala Leu
    375                 380                 385

agt gaa ttc gtg tgc cag ggc ctc gac cgc gca gga cag gtg ctg tgt   1315
Ser Glu Phe Val Cys Gln Gly Leu Asp Arg Ala Gly Gln Val Leu Cys
390                 395                 400                 405
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ccg ggt gac atg atg gca tcc aat ccg gag tgg cgg aaa act gct gac   1363
Pro Gly Asp Met Met Ala Ser Asn Pro Glu Trp Arg Lys Thr Ala Asp
                410                 415                 420

cag tgg atc tcc acc ttc cat tcc tgg att act gcg ccg gag ccg gat   1411
Gln Trp Ile Ser Thr Phe His Ser Trp Ile Thr Ala Pro Glu Pro Asp
            425                 430                 435

gcg ttg ctg cat gcc cag aca ttc ttt gat ttc agg gga att tac ggc   1459
Ala Leu Leu His Ala Gln Thr Phe Phe Asp Phe Arg Gly Ile Tyr Gly
        440                 445                 450

gac acc gag atg gct aag gat gtc cac caa aat gcg gtg aat atg gcc   1507
Asp Thr Glu Met Ala Lys Asp Val His Gln Asn Ala Val Asn Met Ala
    455                 460                 465

agg ggt gcg cgt cgc atg cat gca cac ttg gct agt ctt gcg gcc cgg   1555
Arg Gly Ala Arg Arg Met His Ala His Leu Ala Ser Leu Ala Ala Arg
470                 475                 480                 485

cgc gat cct ccg ctg ggg ttt ttc cgt ggt ctt gtg gtg gag cgt tct   1603
Arg Asp Pro Pro Leu Gly Phe Phe Arg Gly Leu Val Val Glu Arg Ser
                490                 495                 500

ggt gaa tac ggc gcg acg atg gat att aag aag ggt ggc acc gcg ggc   1651
Gly Glu Tyr Gly Ala Thr Met Asp Ile Lys Lys Gly Gly Thr Ala Gly
            505                 510                 515

atc gtg cag atg gcg agg ctg tat gcg ctg gcc acg ggt agt gat gcg   1699
Ile Val Gln Met Ala Arg Leu Tyr Ala Leu Ala Thr Gly Ser Asp Ala
        520                 525                 530

att ggg act cgg gag cgg ttg att gct gcg tcg ggc cat ggt cag gtg   1747
Ile Gly Thr Arg Glu Arg Leu Ile Ala Ala Ser Gly His Gly Gln Val
    535                 540                 545

tcg cgt aag ggt gcg cag gat ttg ttg gat gcc ttt gat ttc tta gcg   1795
Ser Arg Lys Gly Ala Gln Asp Leu Leu Asp Ala Phe Asp Phe Leu Ala
550                 555                 560                 565

gcg atg gcg ttc cag cac cag gcg cgg ttg atc aag gtg ggg gag aag   1843
Ala Met Ala Phe Gln His Gln Ala Arg Leu Ile Lys Val Gly Glu Lys
                570                 575                 580

ccg aac tat cac att gat ccc aag acg ttg ggc aag atg gat cgg gag   1891
Pro Asn Tyr His Ile Asp Pro Lys Thr Leu Gly Lys Met Asp Arg Glu
            585                 590                 595

cat ttg cgc gat gca ttt tcc att att aaa gat atg cag tcg gcg tta   1939
His Leu Arg Asp Ala Phe Ser Ile Ile Lys Asp Met Gln Ser Ala Leu
        600                 605                 610

gct act aaa tat ccg gtg agg aac atc tagtgttggg gcgtcgaaaa         1986
Ala Thr Lys Tyr Pro Val Arg Asn Ile
    615                 620

gcg                                                              1989
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<210> 2098

<211> 622
<212> PRT
<213> Corynebacterium glutamicum

<400> 2098

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Met Val Asn Leu Met Ser Val Glu Leu Glu Glu Ile Arg Asp Phe Leu
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Ala Gly Phe Glu Pro Phe Ala Gln Leu Pro Ala Glu Glu Leu Asp Gln
             20                  25                  30

Leu Pro Gly Lys Met Ser Leu Arg Tyr Phe Arg Arg Gly Glu Glu Ile
         35                  40                  45

Ile Pro Ile Gly Val Pro Asn His Tyr Met Gly Val Ile Arg Ser Gly
     50                  55                  60

Ala Ile Asp Val Leu Asp Gln Glu Gly Val Leu Leu Asp Arg Arg Asp
 65                  70                  75                  80

Ala Gly Arg Ser Phe Gly Tyr Ser Thr Met Gly Pro Glu Arg Asn Ser
                 85                  90                  95

Arg Tyr Arg Met Val Ala Val Glu Asp Ser Leu Val Leu Arg Leu Gly
            100                 105                 110

Arg Asp Asp Phe Asp Glu Leu Ala Lys Arg Asn Pro Asp Leu Asn Arg
        115                 120                 125

Tyr Tyr Ser Ser Trp Ser Lys Arg Ile Arg Ala Ala Ala Asp Gln Leu
    130                 135                 140

Arg Gln Glu Ser Ser Ser Lys Val Leu Arg Thr Lys Leu Gly Glu Phe
145                 150                 155                 160

Lys Ile Ala Asn Pro Ile Ser Cys Ser Pro Asp Thr Thr Ile Met Asp
                165                 170                 175

Ala Ala Ile Lys Met His Glu Phe Gly Val Ser Ser Leu Leu Val Gln
            180                 185                 190

Ile Asp Gly Glu Leu Lys Gly Ile Ile Thr Asp His Tyr Met Arg Ser
        195                 200                 205

Arg Val Val Ala Lys His Leu Asp Ile Gln Leu Pro Val Ser Glu Val
    210                 215                 220

Met Thr Val Asp Pro Arg Cys Ala Thr Ser Gln Gly Leu Ala Phe Glu
225                 230                 235                 240

Ala Met Leu Leu Met Ser Glu Leu Arg Ile His His Leu Pro Ile Val
                245                 250                 255

Asp Asp Gly Gln Ile Ser Gly Ile Val Thr Ala Ala Asp Ile Met Arg
            260                 265                 270

Leu Leu Arg His Asp Pro Ile Tyr Leu Thr Ala Asp Leu Ser Arg Lys
        275                 280                 285

Asn Thr Val Glu Glu Leu Ala Asn Thr Phe Gln Ser Ala Ala Glu Val
    290                 295                 300
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Ala Ser Arg Phe Ile Asp Arg Gly Ala Ser Ala Glu Glu Val Ser Ser
305                 310                 315                 320

Leu Leu Thr Val Ala Ala Asp Ser Leu Ala Arg Arg Leu Leu Val Leu
                325                 330                 335

Ala Glu Arg Lys Phe Gly Ala Pro Pro Val Pro Tyr Cys Phe Val Val
            340                 345                 350

Val Gly Ser Gln Gly Arg Lys Glu Met Gly Leu Ala Ser Asp Gln Asp
        355                 360                 365

Asn Ala Leu Val Leu Asp Asn Ser Tyr Asn Asp Arg Glu His Gly Gln
    370                 375                 380

Tyr Phe Ala Ala Leu Ser Glu Phe Val Cys Gln Gly Leu Asp Arg Ala
385                 390                 395                 400

Gly Gln Val Leu Cys Pro Gly Asp Met Met Ala Ser Asn Pro Glu Trp
                405                 410                 415

Arg Lys Thr Ala Asp Gln Trp Ile Ser Thr Phe His Ser Trp Ile Thr
            420                 425                 430

Ala Pro Glu Pro Asp Ala Leu Leu His Ala Gln Thr Phe Phe Asp Phe
        435                 440                 445

Arg Gly Ile Tyr Gly Asp Thr Glu Met Ala Lys Asp Val His Gln Asn
    450                 455                 460

Ala Val Asn Met Ala Arg Gly Ala Arg Arg Met His Ala His Leu Ala
465                 470                 475                 480

Ser Leu Ala Ala Arg Arg Asp Pro Pro Leu Gly Phe Phe Arg Gly Leu
                485                 490                 495

Val Val Glu Arg Ser Gly Glu Tyr Gly Ala Thr Met Asp Ile Lys Lys
            500                 505                 510

Gly Gly Thr Ala Gly Ile Val Gln Met Ala Arg Leu Tyr Ala Leu Ala
        515                 520                 525

Thr Gly Ser Asp Ala Ile Gly Thr Arg Glu Arg Leu Ile Ala Ala Ser
    530                 535                 540

Gly His Gly Gln Val Ser Arg Lys Gly Ala Gln Asp Leu Leu Asp Ala
545                 550                 555                 560

Phe Asp Phe Leu Ala Ala Met Ala Phe Gln His Gln Ala Arg Leu Ile
                565                 570                 575

Lys Val Gly Glu Lys Pro Asn Tyr His Ile Asp Pro Lys Thr Leu Gly
            580                 585                 590

Lys Met Asp Arg Glu His Leu Arg Asp Ala Phe Ser Ile Ile Lys Asp
        595                 600                 605

Met Gln Ser Ala Leu Ala Thr Lys Tyr Pro Val Arg Asn Ile
    610                 615                 620
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<210> 2099
<211> 990
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(967)
<223> RXA01131

<400> 2099
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tgggagagaa gatttccctt aagaaaggtt cttaacaacc atg ccg cct gcg acg 115
Met Pro Pro Ala Thr
1 5

ctg ttc aat gtt ttg act tca gct gga ctt gac cct cac cag tca ggt 163
Leu Phe Asn Val Leu Thr Ser Ala Gly Leu Asp Pro His Gln Ser Gly
10 15 20

gat gcc att gtt gtc gag tct gcc cat ttc aca ttg acg ttc acg tgg 211
Asp Ala Ile Val Val Glu Ser Ala His Phe Thr Leu Thr Phe Thr Trp
25 30 35

gat gag tgg ctg cga gct caa gcg acg tgg gtg ggg gag ttg agt gcg 259
Asp Glu Trp Leu Arg Ala Gln Ala Thr Trp Val Gly Glu Leu Ser Ala
40 45 50

tcg gat tat gtg cgt tct att gtg gcg att aac tct gcc cat gat gca 307
Ser Asp Tyr Val Arg Ser Ile Val Ala Ile Asn Ser Ala His Asp Ala
55 60 65

cgg gca acg ccg aag atg atg ttg gat gcc ccg act ggt ctg aca acg 355
Arg Ala Thr Pro Lys Met Met Leu Asp Ala Pro Thr Gly Leu Thr Thr
70 75 80 85

gtg ctt aag gcg gat aag ggt cag ttg cag gcg ttt gcc gtg gag gcg 403
Val Leu Lys Ala Asp Lys Gly Gln Leu Gln Ala Phe Ala Val Glu Ala
90 95 100

ctg ccg att ggc gat ggc ctc agc gag gct cag ttg gcg ggg ttt gtg 451
Leu Pro Ile Gly Asp Gly Leu Ser Glu Ala Gln Leu Ala Gly Phe Val
105 110 115

gct gcc gcg ttt gat ggc gcc atc gac ctc act cgt gag ttt cat gca 499
Ala Ala Ala Phe Asp Gly Ala Ile Asp Leu Thr Arg Glu Phe His Ala
120 125 130

ctt tac ccg gag cgc tcg ccg cag gag cgc ggc gca atg ctc aac att 547
Leu Tyr Pro Glu Arg Ser Pro Gln Glu Arg Gly Ala Met Leu Asn Ile
135 140 145

aag ctt gtc gac gcc tcc ccc tct caa aca gtt acg ccc gtg cga gta 595
Lys Leu Val Asp Ala Ser Pro Ser Gln Thr Val Thr Pro Val Arg Val
150 155 160 165

gct aac tgg ttc atg gat cag ggg gtg gag gaa gtt cct tat gat gca 643
Ala Asn Trp Phe Met Asp Gln Gly Val Glu Glu Val Pro Tyr Asp Ala
170 175 180

```
gct tct ggg cgc atc agc ttt gag ctg ggt gac acc cca gtg gat gtg   691
Ala Ser Gly Arg Ile Ser Phe Glu Leu Gly Asp Thr Pro Val Asp Val
            185                 190                 195

att ttg gat gat ccc gag ttg ttg aag atc caa gcc gtg gtg gtt gct   739
Ile Leu Asp Asp Pro Glu Leu Leu Lys Ile Gln Ala Val Val Val Ala
        200                 205                 210

gac cgc gat gtg gaa gcc act gaa gtt tta cat ttg tgt aat cga gcg   787
Asp Arg Asp Val Glu Ala Thr Glu Val Leu His Leu Cys Asn Arg Ala
    215                 220                 225

aac ctg gat tct gat cac tcc acc att ttt atg cgt tcg gat ggg gat   835
Asn Leu Asp Ser Asp His Ser Thr Ile Phe Met Arg Ser Asp Gly Asp
230                 235                 240                 245

gat gtg gat ttc gtc gcc acg gtt gcg gtg ccg att cgt gct ggt ctg   883
Asp Val Asp Phe Val Ala Thr Val Ala Val Pro Ile Arg Ala Gly Leu
                250                 255                 260

aac gat ttc cag ttg agt caa gcc ctg cat gat ggg gta gtg ggg gtt   931
Asn Asp Phe Gln Leu Ser Gln Ala Leu His Asp Gly Val Val Gly Val
            265                 270                 275

gtt ggg cag gta cga gct gtg atc aat cag cta cac tagtgaagtc        977
Val Gly Gln Val Arg Ala Val Ile Asn Gln Leu His
        280                 285

catatagtga gaa                                                   990


<210> 2100
<211> 289
<212> PRT
<213> Corynebacterium glutamicum

<400> 2100
Met Pro Pro Ala Thr Leu Phe Asn Val Leu Thr Ser Ala Gly Leu Asp
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Pro His Gln Ser Gly Asp Ala Ile Val Val Glu Ser Ala His Phe Thr
             20                  25                  30

Leu Thr Phe Thr Trp Asp Glu Trp Leu Arg Ala Gln Ala Thr Trp Val
         35                  40                  45

Gly Glu Leu Ser Ala Ser Asp Tyr Val Arg Ser Ile Val Ala Ile Asn
     50                  55                  60

Ser Ala His Asp Ala Arg Ala Thr Pro Lys Met Met Leu Asp Ala Pro
 65                  70                  75                  80

Thr Gly Leu Thr Thr Val Leu Lys Ala Asp Lys Gly Gln Leu Gln Ala
                 85                  90                  95

Phe Ala Val Glu Ala Leu Pro Ile Gly Asp Gly Leu Ser Glu Ala Gln
            100                 105                 110

Leu Ala Gly Phe Val Ala Ala Ala Phe Asp Gly Ala Ile Asp Leu Thr
        115                 120                 125
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Arg Glu Phe His Ala Leu Tyr Pro Glu Arg Ser Pro Gln Glu Arg Gly
    130                 135                 140

Ala Met Leu Asn Ile Lys Leu Val Asp Ala Ser Pro Ser Gln Thr Val
145                 150                 155                 160

Thr Pro Val Arg Val Ala Asn Trp Phe Met Asp Gln Gly Val Glu Glu
                165                 170                 175

Val Pro Tyr Asp Ala Ala Ser Gly Arg Ile Ser Phe Glu Leu Gly Asp
            180                 185                 190

Thr Pro Val Asp Val Ile Leu Asp Asp Pro Glu Leu Leu Lys Ile Gln
        195                 200                 205

Ala Val Val Val Ala Asp Arg Asp Val Glu Ala Thr Glu Val Leu His
    210                 215                 220

Leu Cys Asn Arg Ala Asn Leu Asp Ser Asp His Ser Thr Ile Phe Met
225                 230                 235                 240

Arg Ser Asp Gly Asp Asp Val Asp Phe Val Ala Thr Val Ala Val Pro
                245                 250                 255

Ile Arg Ala Gly Leu Asn Asp Phe Gln Leu Ser Gln Ala Leu His Asp
            260                 265                 270

Gly Val Val Gly Val Val Gly Gln Val Arg Ala Val Ile Asn Gln Leu
        275                 280                 285

His
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<210> 2101
<211> 483
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(460)
<223> RXA01137

<400> 2101

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tcggtttgaa cgcaactgct tgcgcttggg tgagctttga ggatgtcttc attcctgggg 60

ctcagattct aagccacgat ttccttacct tgtggcatcg gtg cgc cca acc ttc   115
                                                Val Arg Pro Thr Phe
                                                  1               5

gtg atc cta cgg atc tcc gaa tac ttc ggt gtc gct gaa gct gcg att   163
Val Ile Leu Arg Ile Ser Glu Tyr Phe Gly Val Ala Glu Ala Ala Ile
                 10                  15                  20

aat gca gcc act gga cgt ctg acc agc ctc agc gaa gtg ttt atc gac   211
Asn Ala Ala Thr Gly Arg Leu Thr Ser Leu Ser Glu Val Phe Ile Asp
             25                  30                  35

aac gct gcc gag atc caa gac aac ctt tct tcg ctg gtc gcg ctt cag   259
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Asn Ala Ala Glu Ile Gln Asp Asn Leu Ser Ser Leu Val Ala Leu Gln
40 45 50

aaa gat ttg gca gag cga gtc aac gtt gaa gga gtc aat cct gtt act 307
Lys Asp Leu Ala Glu Arg Val Asn Val Glu Gly Val Asn Pro Val Thr
55 60 65

cca gtt gat cta ctg gaa ctt cgc ctc ggt tcc gcg cag ctg gcc gtt 355
Pro Val Asp Leu Leu Glu Leu Arg Leu Gly Ser Ala Gln Leu Ala Val
70 75 80 85

gct gca act gcc att gag gtt cgt gtt gct gga gga gca ggt tat gta 403
Ala Ala Thr Ala Ile Glu Val Arg Val Ala Gly Gly Ala Gly Tyr Val
90 95 100

aag tct tca tca acg tct cgt cgt ttc cgt gtt gaa atg gga gct tgc 451
Lys Ser Ser Ser Thr Ser Arg Arg Phe Arg Val Glu Met Gly Ala Cys
105 110 115

acg ggt ccg tgatctacag gccacgcaaa act 483
Thr Gly Pro
120

<210> 2102
<211> 120
<212> PRT
<213> Corynebacterium glutamicum

<400> 2102
Val Arg Pro Thr Phe Val Ile Leu Arg Ile Ser Glu Tyr Phe Gly Val
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Ala Glu Ala Ala Ile Asn Ala Ala Thr Gly Arg Leu Thr Ser Leu Ser
20 25 30

Glu Val Phe Ile Asp Asn Ala Ala Glu Ile Gln Asp Asn Leu Ser Ser
35 40 45

Leu Val Ala Leu Gln Lys Asp Leu Ala Glu Arg Val Asn Val Glu Gly
50 55 60

Val Asn Pro Val Thr Pro Val Asp Leu Leu Glu Leu Arg Leu Gly Ser
65 70 75 80

Ala Gln Leu Ala Val Ala Ala Thr Ala Ile Glu Val Arg Val Ala Gly
85 90 95

Gly Ala Gly Tyr Val Lys Ser Ser Ser Thr Ser Arg Arg Phe Arg Val
100 105 110

Glu Met Gly Ala Cys Thr Gly Pro
115 120

<210> 2103
<211> 257
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (34)..(234)
<223> RXA01156

<400> 2103
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Val Ser Val Val Asn Ala Lys
1 5

caa acc caa att atg ggt ggc ggc gga cgt gac gag gac aac gcc gag 102
Gln Thr Gln Ile Met Gly Gly Gly Gly Arg Asp Glu Asp Asn Ala Glu
10 15 20

gat tcc gca cag gca tct gga cag gtt cag atc aac acc gaa ggt gtg 150
Asp Ser Ala Gln Ala Ser Gly Gln Val Gln Ile Asn Thr Glu Gly Val
25 30 35

gac agc ttg ctg gat gaa atc gac gga ctg ttg gaa aac aac gcc gag 198
Asp Ser Leu Leu Asp Glu Ile Asp Gly Leu Leu Glu Asn Asn Ala Glu
40 45 50 55

gaa ttc gtt cgt tcc tat gta caa aag ggt ggc gaa tagtcactgt 244
Glu Phe Val Arg Ser Tyr Val Gln Lys Gly Gly Glu
60 65

gagtaccgtg gaa 257

<210> 2104
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<212> PRT
<213> Corynebacterium glutamicum

<400> 2104
Val Ser Val Val Asn Ala Lys Gln Thr Gln Ile Met Gly Gly Gly Gly
1 5 10 15

Arg Asp Glu Asp Asn Ala Glu Asp Ser Ala Gln Ala Ser Gly Gln Val
20 25 30

Gln Ile Asn Thr Glu Gly Val Asp Ser Leu Leu Asp Glu Ile Asp Gly
35 40 45

Leu Leu Glu Asn Asn Ala Glu Glu Phe Val Arg Ser Tyr Val Gln Lys
50 55 60

Gly Gly Glu
65

<210> 2105
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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1042)
<223> RXA01158

<400> 2105

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taggacgttc aaggaattgg ctgaatcaac aagcgccaag gtggttaagc gccctcggcg 60

agttatctca aaaaagaaga agaagtctcc tacgggagag atg tcc att gtt gag   115
                                            Met Ser Ile Val Glu
                                              1               5

cac atc aaa gag ttt cga cgc cga ctt ctt atc gct ctg gcg ggc atc   163
His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile Ala Leu Ala Gly Ile
                 10                  15                  20

ctc gtg ggc acc att atc ggc ttt att tgg tac gat ttc tca ttt tgg   211
Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr Asp Phe Ser Phe Trp
             25                  30                  35

cag atc ccc act ttg ggc gag ctg ctg agg gat ccg tac tgt tct ctg   259
Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp Pro Tyr Cys Ser Leu
         40                  45                  50

cct gct gaa tcc cgc tgg gcc atg agc gac tca gag gaa tgt cga ctg   307
Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser Glu Glu Cys Arg Leu
     55                  60                  65

ctc gca acc ggc ccg ttt gat cca ttc atg ctt cgc ctt aaa gta gcg   355
Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu Arg Leu Lys Val Ala
 70                  75                  80                  85

gcg ttg gtg ggt atg gtt ctt ggc tca ccc gtg tgg ctg agc cag ctg   403
Ala Leu Val Gly Met Val Leu Gly Ser Pro Val Trp Leu Ser Gln Leu
                 90                  95                 100

tgg ggc ttt atc acc cca ggt ttg atg aag aat gag cgc cgt tac acc   451
Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn Glu Arg Arg Tyr Thr
            105                 110                 115

gca atc ttc gtc acg att gct gtt gtg ctg ttt gtc ggc ggt gct gtt   499
Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe Val Gly Gly Ala Val
        120                 125                 130

ctt gcg tac ttc gtc gtt gca tat ggt ttg gag ttc ctc ctt acc att   547
Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu Phe Leu Leu Thr Ile
    135                 140                 145

ggt gga gac acc cag gca gcg gcc ctg act ggt gat aag tac ttc gga   595
Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly Asp Lys Tyr Phe Gly
150                 155                 160                 165

ttc ttg ctc gcg ttg ttg gcg att ttc ggc gtg agc ttc gaa gtt cca   643
Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val Ser Phe Glu Val Pro
                170                 175                 180

ctg gtg atc ggc atg ctc aac att gtg ggt atc ttg cct tac gat gcc   691
Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile Leu Pro Tyr Asp Ala
            185                 190                 195

att aaa gat aag cga cgc atg atc atc atg att ttg ttc gtg ttc gct   739
Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile Leu Phe Val Phe Ala
        200                 205                 210

gct ttc atg aca ccc ggc cag gat cct ttc acc atg ttg gtg ttg gcg   787
Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr Met Leu Val Leu Ala
    215                 220                 225
```

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ctt tca ctc acc gtt ctg gta gag ctt gcc ctg cag ttc tgt cgc ttc   835
Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu Gln Phe Cys Arg Phe
230                 235                 240                 245

aac gac aaa cgc cgg gac aag aag cgc cca gaa tgg ctt gat ggc gat   883
Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu Trp Leu Asp Gly Asp
                250                 255                 260

gac ctc tct gca tca cca ctg gat act tct gct ggt gga gaa gat gct   931
Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala Gly Gly Glu Asp Ala
            265                 270                 275

cca agc cca gtc gaa acc cca gag gcg gtg gag cct tcg cgg atg ctg   979
Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu Pro Ser Arg Met Leu
        280                 285                 290

aac cca agt ggg gag gcg tcg ata agc tat aaa ccc ggg cgc gcc gac   1027
Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys Pro Gly Arg Ala Asp
    295                 300                 305

ttc ggt gac gtg ctc tagggcctag ccaggtaccc tta                    1065
Phe Gly Asp Val Leu
310
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Sequence Listing

<210> 2106
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<213> Corynebacterium glutamicum

<400> 2106

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Met Ser Ile Val Glu His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile
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Ala Leu Ala Gly Ile Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr
             20                  25                  30

Asp Phe Ser Phe Trp Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp
         35                  40                  45

Pro Tyr Cys Ser Leu Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser
     50                  55                  60

Glu Glu Cys Arg Leu Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu
 65                  70                  75                  80

Arg Leu Lys Val Ala Ala Leu Val Gly Met Val Leu Gly Ser Pro Val
                 85                  90                  95

Trp Leu Ser Gln Leu Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn
            100                 105                 110

Glu Arg Arg Tyr Thr Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe
        115                 120                 125

Val Gly Gly Ala Val Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu
    130                 135                 140

Phe Leu Leu Thr Ile Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly
145                 150                 155                 160
```

```
Asp Lys Tyr Phe Gly Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val
                165                 170                 175

Ser Phe Glu Val Pro Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile
            180                 185                 190

Leu Pro Tyr Asp Ala Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile
        195                 200                 205

Leu Phe Val Phe Ala Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr
    210                 215                 220

Met Leu Val Leu Ala Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu
225                 230                 235                 240

Gln Phe Cys Arg Phe Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu
                245                 250                 255

Trp Leu Asp Gly Asp Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala
            260                 265                 270

Gly Gly Glu Asp Ala Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu
        275                 280                 285

Pro Ser Arg Met Leu Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys
    290                 295                 300

Pro Gly Arg Ala Asp Phe Gly Asp Val Leu
305                 310


<210> 2107
<211> 438
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(415)
<223> RXA01159

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catcaatcaa tgtgcaaggg tttcatttct ggaaatcgtg gtcaccccac attcaccagt 60

catgaacaag cttgtttaat gtgaatttgg agtagaccac atg tcc ctc gga cca   115
                                              Met Ser Leu Gly Pro
                                                1               5

tgg gaa att gga atc att gtc ctg ctg atc atc gtg ctg ttc ggc gcg   163
Trp Glu Ile Gly Ile Ile Val Leu Leu Ile Ile Val Leu Phe Gly Ala
                  10                  15                  20

aag aag ctg cct gat gca gct cgt tcc atc ggc cgt tcc atg cgc atc   211
Lys Lys Leu Pro Asp Ala Ala Arg Ser Ile Gly Arg Ser Met Arg Ile
              25                  30                  35

ttc aag tct gaa gtc aaa gaa atg aac aag gac ggc gat acc cca gaa   259
Phe Lys Ser Glu Val Lys Glu Met Asn Lys Asp Gly Asp Thr Pro Glu
          40                  45                  50
```

```
caa cag cag cag cct cag cag cag att gcg ccc aac cag atc gag gct   307
Gln Gln Gln Gln Pro Gln Gln Gln Ile Ala Pro Asn Gln Ile Glu Ala
     55                  60                  65

cct cag cca aac ttt gag cag cac tac cag gga cag cag gtt cag cag   355
Pro Gln Pro Asn Phe Glu Gln His Tyr Gln Gly Gln Gln Val Gln Gln
 70                  75                  80                  85

cct cag aac cct cag acc cct gac tac cgt cag aac tac gag gat cca   403
Pro Gln Asn Pro Gln Thr Pro Asp Tyr Arg Gln Asn Tyr Glu Asp Pro
                 90                  95                 100

aac cgc acc tct taaagttggg cagtttgcat cta                         438
Asn Arg Thr Ser
            105


<210> 2108
<211> 105
<212> PRT
<213> Corynebacterium glutamicum

<400> 2108
Met Ser Leu Gly Pro Trp Glu Ile Gly Ile Ile Val Leu Leu Ile Ile
  1               5                  10                  15

Val Leu Phe Gly Ala Lys Lys Leu Pro Asp Ala Ala Arg Ser Ile Gly
             20                  25                  30

Arg Ser Met Arg Ile Phe Lys Ser Glu Val Lys Glu Met Asn Lys Asp
         35                  40                  45

Gly Asp Thr Pro Glu Gln Gln Gln Gln Pro Gln Gln Gln Ile Ala Pro
     50                  55                  60

Asn Gln Ile Glu Ala Pro Gln Pro Asn Phe Glu Gln His Tyr Gln Gly
 65                  70                  75                  80

Gln Gln Val Gln Gln Pro Gln Asn Pro Gln Thr Pro Asp Tyr Arg Gln
                 85                  90                  95

Asn Tyr Glu Asp Pro Asn Arg Thr Ser
            100                 105


<210> 2109
<211> 998
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(975)
<223> RXA01160

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aaa tca tcc aac aaa atc agc gac ctt gcc cgc cag ctt aat ctg ttg    48
Lys Ser Ser Asn Lys Ile Ser Asp Leu Ala Arg Gln Leu Asn Leu Leu
  1               5                  10                  15

ccg tat ttc acc agg tat aaa ggc cgt acc gtc atg gaa gca gcg cgc    96
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Pro Tyr Phe Thr Arg Tyr Lys Gly Arg Thr Val Met Glu Ala Ala Arg
             20                  25                  30

gat ctt ggc caa ccc tcc tcc caa atc atg gaa gac ctc aac aga tta   144
Asp Leu Gly Gln Pro Ser Ser Gln Ile Met Glu Asp Leu Asn Arg Leu
         35                  40                  45

tgg atg tgt ggt ctg cca gga ctt ctt cca ggt gac ttg gtg gag ctt   192
Trp Met Cys Gly Leu Pro Gly Leu Leu Pro Gly Asp Leu Val Glu Leu
     50                  55                  60

gat cat tcc ttt aag gaa gta aaa atc cac aat gct caa ggc atg gat   240
Asp His Ser Phe Lys Glu Val Lys Ile His Asn Ala Gln Gly Met Asp
 65                  70                  75                  80

aaa ccc ttg cgc ctc aca cca act gaa gcc ggt gtt ttg ctg ctg aca   288
Lys Pro Leu Arg Leu Thr Pro Thr Glu Ala Gly Val Leu Leu Leu Thr
                 85                  90                  95

ctt gaa tcc ctg gaa tcc ctc ccc ggt att gcg aaa cag gaa gcg gtc   336
Leu Glu Ser Leu Glu Ser Leu Pro Gly Ile Ala Lys Gln Glu Ala Val
            100                 105                 110

gta tct gct gcg aac aag cta cgc gcc atc atg ggg gag tat tcc tcg   384
Val Ser Ala Ala Asn Lys Leu Arg Ala Ile Met Gly Glu Tyr Ser Ser
        115                 120                 125

act gtt ttc gac tcc act gga gaa gac ctc gat gct gaa gtt cta gag   432
Thr Val Phe Asp Ser Thr Gly Glu Asp Leu Asp Ala Glu Val Leu Glu
    130                 135                 140

atc atc cgc gac gcc atg gat tta cac cag cag gtc agt ttt gaa tac   480
Ile Ile Arg Asp Ala Met Asp Leu His Gln Gln Val Ser Phe Glu Tyr
145                 150                 155                 160

cac tcg cac aga tca gac aac acc agc ctg agg caa gtc agc cct gct   528
His Ser His Arg Ser Asp Asn Thr Ser Leu Arg Gln Val Ser Pro Ala
                165                 170                 175

cat atc ttc acc cat gaa ggc gaa acc tac atc aaa gcc tgg gaa gaa   576
His Ile Phe Thr His Glu Gly Glu Thr Tyr Ile Lys Ala Trp Glu Glu
            180                 185                 190

gct gtg aac caa tgg cgg acg ttt agg ctt gat cgc atc cga agc att   624
Ala Val Asn Gln Trp Arg Thr Phe Arg Leu Asp Arg Ile Arg Ser Ile
        195                 200                 205

gtg ctt ctt gac agc aaa gca gtg cac ccg gcg cga ggg gtt tca gta   672
Val Leu Leu Asp Ser Lys Ala Val His Pro Ala Arg Gly Val Ser Val
    210                 215                 220

tcc acg gac gat cct ttt gag ttc gca aaa tct tcc gat att gcc acg   720
Ser Thr Asp Asp Pro Phe Glu Phe Ala Lys Ser Ser Asp Ile Ala Thr
225                 230                 235                 240

tta ttg ctg cgt gag gac gca atg tgg tta ggc aat tac atg gcc atg   768
Leu Leu Leu Arg Glu Asp Ala Met Trp Leu Gly Asn Tyr Met Ala Met
                245                 250                 255

gag gtg gat gaa acg gtg gaa ccg att cgc gat agc gac gga ttc agc   816
Glu Val Asp Glu Thr Val Glu Pro Ile Arg Asp Ser Asp Gly Phe Ser
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```
            260                 265                 270

tgg cac aca gtc cac ttt ccg ctg ctt tct agg gat tgg ttc gtc cga   864
Trp His Thr Val His Phe Pro Leu Leu Ser Arg Asp Trp Phe Val Arg
        275                 280                 285

ttc gcg att ggc cat gct gag cat ttg aaa gta act agt ccc gaa gat   912
Phe Ala Ile Gly His Ala Glu His Leu Lys Val Thr Ser Pro Glu Asp
    290                 295                 300

ctt cgg aaa tgc ata aag caa aag gct ttt agt ggt ttg tca gcg tat   960
Leu Arg Lys Cys Ile Lys Gln Lys Ala Phe Ser Gly Leu Ser Ala Tyr
305                 310                 315                 320

gat cat cac gta gag taacacccaa gagtaagacg caa                     998
Asp His His Val Glu
                325
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<210> 2110
<211> 325
<212> PRT
<213> Corynebacterium glutamicum

<400> 2110
Lys Ser Ser Asn Lys Ile Ser Asp Leu Ala Arg Gln Leu Asn Leu Leu
  1               5                  10                  15

Pro Tyr Phe Thr Arg Tyr Lys Gly Arg Thr Val Met Glu Ala Ala Arg
             20                  25                  30

Asp Leu Gly Gln Pro Ser Ser Gln Ile Met Glu Asp Leu Asn Arg Leu
         35                  40                  45

Trp Met Cys Gly Leu Pro Gly Leu Leu Pro Gly Asp Leu Val Glu Leu
     50                  55                  60

Asp His Ser Phe Lys Glu Val Lys Ile His Asn Ala Gln Gly Met Asp
 65                  70                  75                  80

Lys Pro Leu Arg Leu Thr Pro Thr Glu Ala Gly Val Leu Leu Leu Thr
                 85                  90                  95

Leu Glu Ser Leu Glu Ser Leu Pro Gly Ile Ala Lys Gln Glu Ala Val
            100                 105                 110

Val Ser Ala Ala Asn Lys Leu Arg Ala Ile Met Gly Glu Tyr Ser Ser
        115                 120                 125

Thr Val Phe Asp Ser Thr Gly Glu Asp Leu Asp Ala Glu Val Leu Glu
    130                 135                 140

Ile Ile Arg Asp Ala Met Asp Leu His Gln Gln Val Ser Phe Glu Tyr
145                 150                 155                 160

His Ser His Arg Ser Asp Asn Thr Ser Leu Arg Gln Val Ser Pro Ala
                165                 170                 175

His Ile Phe Thr His Glu Gly Glu Thr Tyr Ile Lys Ala Trp Glu Glu
            180                 185                 190
```

```
Ala Val Asn Gln Trp Arg Thr Phe Arg Leu Asp Arg Ile Arg Ser Ile
        195                 200                 205

Val Leu Leu Asp Ser Lys Ala Val His Pro Ala Arg Gly Val Ser Val
    210                 215                 220

Ser Thr Asp Asp Pro Phe Glu Phe Ala Lys Ser Ser Asp Ile Ala Thr
225                 230                 235                 240

Leu Leu Leu Arg Glu Asp Ala Met Trp Leu Gly Asn Tyr Met Ala Met
                245                 250                 255

Glu Val Asp Glu Thr Val Glu Pro Ile Arg Asp Ser Asp Gly Phe Ser
            260                 265                 270

Trp His Thr Val His Phe Pro Leu Leu Ser Arg Asp Trp Phe Val Arg
        275                 280                 285

Phe Ala Ile Gly His Ala Glu His Leu Lys Val Thr Ser Pro Glu Asp
    290                 295                 300

Leu Arg Lys Cys Ile Lys Gln Lys Ala Phe Ser Gly Leu Ser Ala Tyr
305                 310                 315                 320

Asp His His Val Glu
                325
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Sequence Total Quantity: 2395 Sequence Quantity: 2111 Sequence Quantity: 2111

<210> 2111
<211> 805
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(805)
<223> RXA01163

<400> 2111

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accgtaccca cagacacacc agaattaaca gaaacagact gaaaaacaac atcgctcgac 60

atgcgcgtaa tcctaacccg cgcacactaa tgtggccgat atg ggc tac acc aac   115
                                              Met Gly Tyr Thr Asn
                                                1               5

ctc aac gac aca cgg gtc ttg cgc gcc ggg tca tgt gat gcc tgg tgg   163
Leu Asn Asp Thr Arg Val Leu Arg Ala Gly Ser Cys Asp Ala Trp Trp
                10                  15                  20

cgc acg atg tct ccg cta gtg cag cag gga agt gag gca gtc ttt cgg   211
Arg Thr Met Ser Pro Leu Val Gln Gln Gly Ser Glu Ala Val Phe Arg
            25                  30                  35

cgc atc atg ggt ctc tcg cgg cgt cct gat cgg aaa cct ggc ttt gac   259
Arg Ile Met Gly Leu Ser Arg Arg Pro Asp Arg Lys Pro Gly Phe Asp
        40                  45                  50

gat gtc cca cat ttc ggc gca gct gtt cga gtt ccc ggt cta aaa cac   307
Asp Val Pro His Phe Gly Ala Ala Val Arg Val Pro Gly Leu Lys His
    55                  60                  65
```

```
ggc acg ttg gtc aat gct gca ccc ttg aaa gtt ttg ggc gca cgg ggc   355
Gly Thr Leu Val Asn Ala Ala Pro Leu Lys Val Leu Gly Ala Arg Gly
 70                  75                  80                  85

gag ccc aac ccc gcg agt tcg tac cgt ttt gaa tac atc acc ggt gat   403
Glu Pro Asn Pro Ala Ser Ser Tyr Arg Phe Glu Tyr Ile Thr Gly Asp
                90                  95                 100

tcc gca ggt cga gcc atc act gcg acc ggc gct gtc ctc ttt tcc aca   451
Ser Ala Gly Arg Ala Ile Thr Ala Thr Gly Ala Val Leu Phe Ser Thr
            105                 110                 115

cgc ccc tgg aca acc ggc ccg cgt ccc gcg atc gcc atg gct cca tcc   499
Arg Pro Trp Thr Thr Gly Pro Arg Pro Ala Ile Ala Met Ala Pro Ser
        120                 125                 130

acc caa ggc gtc gca cag cac tgc gat ccc tcc cac acc tgc gcc atc   547
Thr Gln Gly Val Ala Gln His Cys Asp Pro Ser His Thr Cys Ala Ile
    135                 140                 145

gga ctc aac gca ttc tat gac aaa ccc ttc gac gca atc att gct tac   595
Gly Leu Asn Ala Phe Tyr Asp Lys Pro Phe Asp Ala Ile Ile Ala Tyr
150                 155                 160                 165

gaa ctc ccc gtc atc ctc tgg ttt cta gct cac gga ctt gac gtt gtg   643
Glu Leu Pro Val Ile Leu Trp Phe Leu Ala His Gly Leu Asp Val Val
                170                 175                 180

ttc atc gat tac ccc cgc gac ccc gca acc ggc gtc caa tac tat tgc   691
Phe Ile Asp Tyr Pro Arg Asp Pro Ala Thr Gly Val Gln Tyr Tyr Cys
            185                 190                 195

gat tcc atc gct gca gct aaa tcg ctt ctc gac gcc gtc ctc gcc tcc   739
Asp Ser Ile Ala Ala Ala Lys Ser Leu Leu Asp Ala Val Leu Ala Ser
        200                 205                 210

aga caa ctc ggc ctt tca ccg gaa gca ccg ctt ggc ctg tgg gga ttc   787
Arg Gln Leu Gly Leu Ser Pro Glu Ala Pro Leu Gly Leu Trp Gly Phe
    215                 220                 225

tcc caa gga ggc ggc gcc                                          805
Ser Gln Gly Gly Gly Ala
230                 235
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<210> 2112
<211> 235
<212> PRT
<213> Corynebacterium glutamicum

<400> 2112

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Met Gly Tyr Thr Asn Leu Asn Asp Thr Arg Val Leu Arg Ala Gly Ser
  1               5                  10                  15

Cys Asp Ala Trp Trp Arg Thr Met Ser Pro Leu Val Gln Gln Gly Ser
             20                  25                  30

Glu Ala Val Phe Arg Arg Ile Met Gly Leu Ser Arg Arg Pro Asp Arg
         35                  40                  45

Lys Pro Gly Phe Asp Asp Val Pro His Phe Gly Ala Ala Val Arg Val
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```
     50                  55                  60

Pro Gly Leu Lys His Gly Thr Leu Val Asn Ala Ala Pro Leu Lys Val
 65                  70                  75                  80

Leu Gly Ala Arg Gly Glu Pro Asn Pro Ala Ser Ser Tyr Arg Phe Glu
                 85                  90                  95

Tyr Ile Thr Gly Asp Ser Ala Gly Arg Ala Ile Thr Ala Thr Gly Ala
            100                 105                 110

Val Leu Phe Ser Thr Arg Pro Trp Thr Thr Gly Pro Arg Pro Ala Ile
        115                 120                 125

Ala Met Ala Pro Ser Thr Gln Gly Val Ala Gln His Cys Asp Pro Ser
    130                 135                 140

His Thr Cys Ala Ile Gly Leu Asn Ala Phe Tyr Asp Lys Pro Phe Asp
145                 150                 155                 160

Ala Ile Ile Ala Tyr Glu Leu Pro Val Ile Leu Trp Phe Leu Ala His
                165                 170                 175

Gly Leu Asp Val Val Phe Ile Asp Tyr Pro Arg Asp Pro Ala Thr Gly
            180                 185                 190

Val Gln Tyr Tyr Cys Asp Ser Ile Ala Ala Ala Lys Ser Leu Leu Asp
        195                 200                 205

Ala Val Leu Ala Ser Arg Gln Leu Gly Leu Ser Pro Glu Ala Pro Leu
    210                 215                 220

Gly Leu Trp Gly Phe Ser Gln Gly Gly Gly Ala
225                 230                 235


<210> 2113
<211> 696
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(673)
<223> RXA01165

<400> 2113
agaccactca cattgcacat ctgcagctgc caggaagtct ccacccaaca gttttctagg 60

tcacagggat ccattagcca tttggtcctt gtcgaaaggt atg gtg ggg cat gtg   115
                                              Met Val Gly His Val
                                                1               5

cct gca gca ata gca atc cca tat ttc att att gag atc ctc gcc ttc   163
Pro Ala Ala Ile Ala Ile Pro Tyr Phe Ile Ile Glu Ile Leu Ala Phe
                10                  15                  20

att ggt gtc gtc atg tgg ctc ggt ttc ggc tgg gct ttg ggt ctc ctc   211
Ile Gly Val Val Met Trp Leu Gly Phe Gly Trp Ala Leu Gly Leu Leu
            25                  30                  35
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```
gta ttg ttc ttc gtc ggt gga ctt ctt cta gcc ggc gtg gag ctt cgt   259
Val Leu Phe Phe Val Gly Gly Leu Leu Leu Ala Gly Val Glu Leu Arg
         40                  45                  50

cgc att agt aag agt gcc gcc att cat cag gct tcg ggc cag gga agt   307
Arg Ile Ser Lys Ser Ala Ala Ile His Gln Ala Ser Gly Gln Gly Ser
     55                  60                  65

gcg gga gcg atc gcc gga aac att ggg ctg acc gca gct ggt gcc att   355
Ala Gly Ala Ile Ala Gly Asn Ile Gly Leu Thr Ala Ala Gly Ala Ile
 70                  75                  80                  85

ttg gtg gcc atg ccg ggg ttt gtg tct tcg att atc ggt ttg ttg ttc   403
Leu Val Ala Met Pro Gly Phe Val Ser Ser Ile Ile Gly Leu Leu Phe
                 90                  95                 100

att ttt gca cca acc agg gcg ctg ttc cgc aag gtt ttg gcc aag cgc   451
Ile Phe Ala Pro Thr Arg Ala Leu Phe Arg Lys Val Leu Ala Lys Arg
            105                 110                 115

atg cgc agt gcc atc gag aac cta ggt gtg cgt ggt ttt gaa gcc gtt   499
Met Arg Ser Ala Ile Glu Asn Leu Gly Val Arg Gly Phe Glu Ala Val
        120                 125                 130

aat ggt tac cgc acc cag gca tcc tac gga aac ttc gga gcg gca ttc   547
Asn Gly Tyr Arg Thr Gln Ala Ser Tyr Gly Asn Phe Gly Ala Ala Phe
    135                 140                 145

aat ggt ggt gcg caa caa cca tca aat gag ccg atc gtg att gat gaa   595
Asn Gly Gly Ala Gln Gln Pro Ser Asn Glu Pro Ile Val Ile Asp Glu
150                 155                 160                 165

gac gag atc caa gcc tgg act tct gat ctc aaa cct gaa gat ttc acc   643
Asp Glu Ile Gln Ala Trp Thr Ser Asp Leu Lys Pro Glu Asp Phe Thr
                170                 175                 180

aaa ggt aaa gat gaa tcc gac ggt gag aaa taagtgacac tgtttgttcg     693
Lys Gly Lys Asp Glu Ser Asp Gly Glu Lys
            185                 190

gct                                                               696


<210> 2114
<211> 191
<212> PRT
<213> Corynebacterium glutamicum

<400> 2114
Met Val Gly His Val Pro Ala Ala Ile Ala Ile Pro Tyr Phe Ile Ile
  1               5                  10                  15

Glu Ile Leu Ala Phe Ile Gly Val Val Met Trp Leu Gly Phe Gly Trp
             20                  25                  30

Ala Leu Gly Leu Leu Val Leu Phe Phe Val Gly Gly Leu Leu Leu Ala
         35                  40                  45

Gly Val Glu Leu Arg Arg Ile Ser Lys Ser Ala Ala Ile His Gln Ala
     50                  55                  60
```

```
Ser Gly Gln Gly Ser Ala Gly Ala Ile Ala Gly Asn Ile Gly Leu Thr
 65                  70                  75                  80

Ala Ala Gly Ala Ile Leu Val Ala Met Pro Gly Phe Val Ser Ser Ile
                 85                  90                  95

Ile Gly Leu Leu Phe Ile Phe Ala Pro Thr Arg Ala Leu Phe Arg Lys
            100                 105                 110

Val Leu Ala Lys Arg Met Arg Ser Ala Ile Glu Asn Leu Gly Val Arg
        115                 120                 125

Gly Phe Glu Ala Val Asn Gly Tyr Arg Thr Gln Ala Ser Tyr Gly Asn
    130                 135                 140

Phe Gly Ala Ala Phe Asn Gly Gly Ala Gln Gln Pro Ser Asn Glu Pro
145                 150                 155                 160

Ile Val Ile Asp Glu Asp Glu Ile Gln Ala Trp Thr Ser Asp Leu Lys
                165                 170                 175

Pro Glu Asp Phe Thr Lys Gly Lys Asp Glu Ser Asp Gly Glu Lys
            180                 185                 190
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<210> 2115
<211> 506
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(483)
<223> RXA01166

<400> 2115

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ctc acc gga gtg att gcc tac gcc atc gcg gga ctt gca gtg aac tct   48
Leu Thr Gly Val Ile Ala Tyr Ala Ile Ala Gly Leu Ala Val Asn Ser
  1               5                  10                  15

tca gag atg ttt gag gaa atc atg tcg gtg tta aat gaa cgc gga gtc   96
Ser Glu Met Phe Glu Glu Ile Met Ser Val Leu Asn Glu Arg Gly Val
             20                  25                  30

agt gat gtg ctg aaa aat atc acc agc tgc gcg gga ggt tcc ttg ttg   144
Ser Asp Val Leu Lys Asn Ile Thr Ser Cys Ala Gly Gly Ser Leu Leu
         35                  40                  45

gcc agt ggc tac tcg tct tcc cgc ggg tgg aca cat cag ggc acg ccg   192
Ala Ser Gly Tyr Ser Ser Ser Arg Gly Trp Thr His Gln Gly Thr Pro
     50                  55                  60

ctg gca gac att ctg gac gat ctg cca ctt gtt gtc gct gag ttt ggg   240
Leu Ala Asp Ile Leu Asp Asp Leu Pro Leu Val Val Ala Glu Phe Gly
 65                  70                  75                  80

aag caa aag ctg ggt cgt gtg gcg cca gaa atc cca gtg ctg ttg tgg   288
Lys Gln Lys Leu Gly Arg Val Ala Pro Glu Ile Pro Val Leu Leu Trp
                 85                  90                  95

ggc tct aaa aat gat gat gtc att ccc att gat ccc att agg gaa ttg   336
```

```
Gly Ser Lys Asn Asp Asp Val Ile Pro Ile Asp Pro Ile Arg Glu Leu
          100                 105                 110

cgt gat agc tgg gcg gac aag ggt acg cca ttg acc tgg cat gaa tcc   384
Arg Asp Ser Trp Ala Asp Lys Gly Thr Pro Leu Thr Trp His Glu Ser
        115                 120                 125

caa gcg ccg cgt gtg cca gga cgc aca ggt ctc aac cat ttc ggg ccc   432
Gln Ala Pro Arg Val Pro Gly Arg Thr Gly Leu Asn His Phe Gly Pro
    130                 135                 140

tat ttt aga aac ctg gaa aag tac tcg gga tgg ctc ata gat cat ctt   480
Tyr Phe Arg Asn Leu Glu Lys Tyr Ser Gly Trp Leu Ile Asp His Leu
145                 150                 155                 160

gtc tgagtgccgt tttaaaggct cgg                                    506
Val
```

<210> 2116
<211> 161
<212> PRT
<213> Corynebacterium glutamicum

<400> 2116

```
Leu Thr Gly Val Ile Ala Tyr Ala Ile Ala Gly Leu Ala Val Asn Ser
  1               5                  10                  15

Ser Glu Met Phe Glu Glu Ile Met Ser Val Leu Asn Glu Arg Gly Val
             20                  25                  30

Ser Asp Val Leu Lys Asn Ile Thr Ser Cys Ala Gly Gly Ser Leu Leu
         35                  40                  45

Ala Ser Gly Tyr Ser Ser Ser Arg Gly Trp Thr His Gln Gly Thr Pro
     50                  55                  60

Leu Ala Asp Ile Leu Asp Asp Leu Pro Leu Val Val Ala Glu Phe Gly
 65                  70                  75                  80

Lys Gln Lys Leu Gly Arg Val Ala Pro Glu Ile Pro Val Leu Leu Trp
                 85                  90                  95

Gly Ser Lys Asn Asp Asp Val Ile Pro Ile Asp Pro Ile Arg Glu Leu
            100                 105                 110

Arg Asp Ser Trp Ala Asp Lys Gly Thr Pro Leu Thr Trp His Glu Ser
        115                 120                 125

Gln Ala Pro Arg Val Pro Gly Arg Thr Gly Leu Asn His Phe Gly Pro
    130                 135                 140

Tyr Phe Arg Asn Leu Glu Lys Tyr Ser Gly Trp Leu Ile Asp His Leu
145                 150                 155                 160

Val
```

<210> 2117

<211> 606
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(583)
<223> RXA01170

<400> 2117
tacaggaaac tttcaggcat aggggagtca tgaaacagaa cggcaagcta aggtgacata 60

gtcacttaaa ctaaacaaga agggtggagg acccaagcac gtg agt ctt tca aac 115
Val Ser Leu Ser Asn
1 5

aaa gct aaa gga atc gtt gca gta atc atc gtc gcc tgg atc gtc gcg 163
Lys Ala Lys Gly Ile Val Ala Val Ile Ile Val Ala Trp Ile Val Ala
10 15 20

atg gct ggc atg gtc gca tac gcg tca agc aat aat gct gat aag aca 211
Met Ala Gly Met Val Ala Tyr Ala Ser Ser Asn Asn Ala Asp Lys Thr
25 30 35

ttt cca act gca ggt gcg cta gaa caa acc gtc gca gca ttt gat agg 259
Phe Pro Thr Ala Gly Ala Leu Glu Gln Thr Val Ala Ala Phe Asp Arg
40 45 50

caa ggc ctt cag gtc tct gca gtc gca ctg gca gac atc tac ggc gat 307
Gln Gly Leu Gln Val Ser Ala Val Ala Leu Ala Asp Ile Tyr Gly Asp
55 60 65

gaa tac gtc tcc gcg gcg att ctg tgc gaa gga act cca acc gca aca 355
Glu Tyr Val Ser Ala Ala Ile Leu Cys Glu Gly Thr Pro Thr Ala Thr
70 75 80 85

ctc gag cag tca ctg ggc gta gac ctg tct gag ctg aac ctg gac gag 403
Leu Glu Gln Ser Leu Gly Val Asp Leu Ser Glu Leu Asn Leu Asp Glu
90 95 100

tct ggt gtt cct tcg ggc gtg tcc tac ttg gct ctg tcc aat cag gat 451
Ser Gly Val Pro Ser Gly Val Ser Tyr Leu Ala Leu Ser Asn Gln Asp
105 110 115

ggg gaa gtt gtc tac gac aag att gat cgt gcc aac gtt gat ctc tgc 499
Gly Glu Val Val Tyr Asp Lys Ile Asp Arg Ala Asn Val Asp Leu Cys
120 125 130

gca acg cca ctc aat ggt gct ttc agc gct tat tca ttg atg cca gtt 547
Ala Thr Pro Leu Asn Gly Ala Phe Ser Ala Tyr Ser Leu Met Pro Val
135 140 145

gcc aag gtt ggc gag aac tcc tgg gcg atc gcc gct tagggtttta 593
Ala Lys Val Gly Glu Asn Ser Trp Ala Ile Ala Ala
150 155 160

agggtcaatc cgc 606

<210> 2118
<211> 161

<212> PRT
<213> Corynebacterium glutamicum

<400> 2118
Val Ser Leu Ser Asn Lys Ala Lys Gly Ile Val Ala Val Ile Ile Val
1 5 10 15

Ala Trp Ile Val Ala Met Ala Gly Met Val Ala Tyr Ala Ser Ser Asn
20 25 30

Asn Ala Asp Lys Thr Phe Pro Thr Ala Gly Ala Leu Glu Gln Thr Val
35 40 45

Ala Ala Phe Asp Arg Gln Gly Leu Gln Val Ser Ala Val Ala Leu Ala
50 55 60

Asp Ile Tyr Gly Asp Glu Tyr Val Ser Ala Ala Ile Leu Cys Glu Gly
65 70 75 80

Thr Pro Thr Ala Thr Leu Glu Gln Ser Leu Gly Val Asp Leu Ser Glu
85 90 95

Leu Asn Leu Asp Glu Ser Gly Val Pro Ser Gly Val Ser Tyr Leu Ala
100 105 110

Leu Ser Asn Gln Asp Gly Glu Val Val Tyr Asp Lys Ile Asp Arg Ala
115 120 125

Asn Val Asp Leu Cys Ala Thr Pro Leu Asn Gly Ala Phe Ser Ala Tyr
130 135 140

Ser Leu Met Pro Val Ala Lys Val Gly Glu Asn Ser Trp Ala Ile Ala
145 150 155 160

Ala

<210> 2119
<211> 816
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(793)
<223> RXA01171

<400> 2119
gtagaaattt tccatgcaga ggaaagccga taatggggca gaacccctttc ccgccaaaat 60

gacataatgt acattatcgg acaattatcc atatctggcc atg tcg cag gcc gct 115
Met Ser Gln Ala Ala
1 5

ggt aag ttt aag ccc atg act tca acg ctc gcc gaa tca aca ctt aca 163
Gly Lys Phe Lys Pro Met Thr Ser Thr Leu Ala Glu Ser Thr Leu Thr
10 15 20

tcc ctt aaa gaa ctt gag gat cca aag atc ctt tcc gtc aat gaa cgc 211
Ser Leu Lys Glu Leu Glu Asp Pro Lys Ile Leu Ser Val Asn Glu Arg

```
            25                  30                  35

cac ggc gat gat cac gca gtg aac ctc acc aag ctt cgc gcc gtt gcc   259
His Gly Asp Asp His Ala Val Asn Leu Thr Lys Leu Arg Ala Val Ala
         40                  45                  50

aaa gag ctg aaa aag aac cag ccg ctg gct cgt gag ctt tgg gca acc   307
Lys Glu Leu Lys Lys Asn Gln Pro Leu Ala Arg Glu Leu Trp Ala Thr
     55                  60                  65

gac gat aca gcc gca cgt ttg gtg gcg ttg ctt att tgc cga ccc aag   355
Asp Asp Thr Ala Ala Arg Leu Val Ala Leu Leu Ile Cys Arg Pro Lys
 70                  75                  80                  85

gaa ttt gat cag tct gaa ctc gac tcg atg atc cat gag gct cgc acg   403
Glu Phe Asp Gln Ser Glu Leu Asp Ser Met Ile His Glu Ala Arg Thr
                 90                  95                 100

ccg aag gtt ctt gat tgg ttg atc aat tat gtg gtc aag aag aat cct   451
Pro Lys Val Leu Asp Trp Leu Ile Asn Tyr Val Val Lys Lys Asn Pro
            105                 110                 115

cat tgg aac gat ctc cgt gtg ctc tgg ctt gaa gat ccc gcc gag aat   499
His Trp Asn Asp Leu Arg Val Leu Trp Leu Glu Asp Pro Ala Glu Asn
        120                 125                 130

gtt gcg gcc gcc ggc tgg gct ctc aac act cat gcc gtt atc aca aag   547
Val Ala Ala Ala Gly Trp Ala Leu Asn Thr His Ala Val Ile Thr Lys
    135                 140                 145

ccg gac gca ttg gac gat tcc gaa atc ctt gac acc att gaa gct cag   595
Pro Asp Ala Leu Asp Asp Ser Glu Ile Leu Asp Thr Ile Glu Ala Gln
150                 155                 160                 165

atg aaa act gcc gag cct cgc gta cag tgg tca atg aat gaa tgt ttg   643
Met Lys Thr Ala Glu Pro Arg Val Gln Trp Ser Met Asn Glu Cys Leu
                170                 175                 180

gcg caa atc ggc atc cat cgt cca gag ctt cgt gat cgt gcc att gcc   691
Ala Gln Ile Gly Ile His Arg Pro Glu Leu Arg Asp Arg Ala Ile Ala
            185                 190                 195

att ggt gag cgc ctg gaa gtt ctc aaa gat tat ccg acc cct cca aat   739
Ile Gly Glu Arg Leu Glu Val Leu Lys Asp Tyr Pro Thr Pro Pro Asn
        200                 205                 210

tgc acc tcg cct ttt gct ccg att tgg atc gaa gag atg gtt cgc agg   787
Cys Thr Ser Pro Phe Ala Pro Ile Trp Ile Glu Glu Met Val Arg Arg
    215                 220                 225

aaa aaa taaccgacct gttccctatc ttt                                816
Lys Lys
230
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<210> 2120
<211> 231
<212> PRT
<213> Corynebacterium glutamicum

<400> 2120

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Met Ser Gln Ala Ala Gly Lys Phe Lys Pro Met Thr Ser Thr Leu Ala
  1               5                  10                  15

Glu Ser Thr Leu Thr Ser Leu Lys Glu Leu Glu Asp Pro Lys Ile Leu
             20                  25                  30

Ser Val Asn Glu Arg His Gly Asp Asp His Ala Val Asn Leu Thr Lys
         35                  40                  45

Leu Arg Ala Val Ala Lys Glu Leu Lys Lys Asn Gln Pro Leu Ala Arg
     50                  55                  60

Glu Leu Trp Ala Thr Asp Asp Thr Ala Ala Arg Leu Val Ala Leu Leu
 65                  70                  75                  80

Ile Cys Arg Pro Lys Glu Phe Asp Gln Ser Glu Leu Asp Ser Met Ile
                 85                  90                  95

His Glu Ala Arg Thr Pro Lys Val Leu Asp Trp Leu Ile Asn Tyr Val
            100                 105                 110

Val Lys Lys Asn Pro His Trp Asn Asp Leu Arg Val Leu Trp Leu Glu
        115                 120                 125

Asp Pro Ala Glu Asn Val Ala Ala Ala Gly Trp Ala Leu Asn Thr His
    130                 135                 140

Ala Val Ile Thr Lys Pro Asp Ala Leu Asp Asp Ser Glu Ile Leu Asp
145                 150                 155                 160

Thr Ile Glu Ala Gln Met Lys Thr Ala Glu Pro Arg Val Gln Trp Ser
                165                 170                 175

Met Asn Glu Cys Leu Ala Gln Ile Gly Ile His Arg Pro Glu Leu Arg
            180                 185                 190

Asp Arg Ala Ile Ala Ile Gly Glu Arg Leu Glu Val Leu Lys Asp Tyr
        195                 200                 205

Pro Thr Pro Pro Asn Cys Thr Ser Pro Phe Ala Pro Ile Trp Ile Glu
    210                 215                 220

Glu Met Val Arg Arg Lys Lys
225                 230
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<210> 2121
<211> 627
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(604)
<223> RXA01176

<400> 2121
gagctgtgca ccttgtgacc ttttgtgaca ctgctcaatg ctttacggct acgatgaaca 60

acaaaccgac gttttcgacg ctgtgaagga ctaattgcta gtg cgt tat ttt tac 115
Val Arg Tyr Phe Tyr

```
                                                    1               5

gat act gag ttc att gaa gat ggg cgc acg atc gaa ttg gtc tct att   163
Asp Thr Glu Phe Ile Glu Asp Gly Arg Thr Ile Glu Leu Val Ser Ile
                10                  15                  20

gga atc gtc gca gaa gac ggt cgc gag tat tac gca gtt agc aca cag   211
Gly Ile Val Ala Glu Asp Gly Arg Glu Tyr Tyr Ala Val Ser Thr Gln
            25                  30                  35

ttt gat tcc tcc aag gcg aac gct tgg gtg cgc gcc aac gtg ttg gac   259
Phe Asp Ser Ser Lys Ala Asn Ala Trp Val Arg Ala Asn Val Leu Asp
        40                  45                  50

aaa ttg cct aat cct tcc tcc aaa gtg tgg aaa tct gca gac act ata   307
Lys Leu Pro Asn Pro Ser Ser Lys Val Trp Lys Ser Ala Asp Thr Ile
    55                  60                  65

aag cgc gaa gtt tat gag ttt ctc acc tcc acc gga cca acc cct gaa   355
Lys Arg Glu Val Tyr Glu Phe Leu Thr Ser Thr Gly Pro Thr Pro Glu
70                  75                  80                  85

ctg tgg gcc tgg gtg ggc gca tat gac cac gtg ttg ttg gca caa atg   403
Leu Trp Ala Trp Val Gly Ala Tyr Asp His Val Leu Leu Ala Gln Met
                90                  95                  100

tgg ggc gat atg gcg ggg ctt cct cgg gag atc cct cgt ttt acc cgc   451
Trp Gly Asp Met Ala Gly Leu Pro Arg Glu Ile Pro Arg Phe Thr Arg
            105                 110                 115

gag ctt cgc cag tat tgg gac atg gct ggc cgc cca acg ctg cca gag   499
Glu Leu Arg Gln Tyr Trp Asp Met Ala Gly Arg Pro Thr Leu Pro Glu
        120                 125                 130

ctg ccg aac ggc aac cac gat gcg ttg att gat gcg cgt cat aat tta   547
Leu Pro Asn Gly Asn His Asp Ala Leu Ile Asp Ala Arg His Asn Leu
    135                 140                 145

gcc aag ttc aaa gtg tgc atg gca gcg ctg cct ttg ggt aaa agg gat   595
Ala Lys Phe Lys Val Cys Met Ala Ala Leu Pro Leu Gly Lys Arg Asp
150                 155                 160                 165

cgc gtc tct tagtcgatct gctcccattc cat                            627
Arg Val Ser
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<210> 2122
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 2122

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Val Arg Tyr Phe Tyr Asp Thr Glu Phe Ile Glu Asp Gly Arg Thr Ile
  1               5                  10                  15

Glu Leu Val Ser Ile Gly Ile Val Ala Glu Asp Gly Arg Glu Tyr Tyr
            20                  25                  30

Ala Val Ser Thr Gln Phe Asp Ser Ser Lys Ala Asn Ala Trp Val Arg
        35                  40                  45
```

```
Ala Asn Val Leu Asp Lys Leu Pro Asn Pro Ser Ser Lys Val Trp Lys
     50                  55                  60

Ser Ala Asp Thr Ile Lys Arg Glu Val Tyr Glu Phe Leu Thr Ser Thr
 65                  70                  75                  80

Gly Pro Thr Pro Glu Leu Trp Ala Trp Val Gly Ala Tyr Asp His Val
                85                  90                  95

Leu Leu Ala Gln Met Trp Gly Asp Met Ala Gly Leu Pro Arg Glu Ile
            100                 105                 110

Pro Arg Phe Thr Arg Glu Leu Arg Gln Tyr Trp Asp Met Ala Gly Arg
        115                 120                 125

Pro Thr Leu Pro Glu Leu Pro Asn Gly Asn His Asp Ala Leu Ile Asp
    130                 135                 140

Ala Arg His Asn Leu Ala Lys Phe Lys Val Cys Met Ala Ala Leu Pro
145                 150                 155                 160

Leu Gly Lys Arg Asp Arg Val Ser
                165
```

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<210> 2123
<211> 2109
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2086)
<223> RXA01177

<400> 2123

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tgttcatcgt agccgtaaag cattgagcag tgtcacaaaa ggtcacaagg tgcacagctc 60

agttccttaa aaaccgctgg atacggatac actatttttc atg cac ggt gaa aaa   115
                                            Met His Gly Glu Lys
                                              1               5

ctt gtg gat ggc act gag gga aat ctc agt caa ttc caa tgg cgc gat   163
Leu Val Asp Gly Thr Glu Gly Asn Leu Ser Gln Phe Gln Trp Arg Asp
                  10                  15                  20

atg gct aca aat cag acg ctg aga aaa gca ctg tta gtg ctt tct acc   211
Met Ala Thr Asn Gln Thr Leu Arg Lys Ala Leu Leu Val Leu Ser Thr
              25                  30                  35

atc gct cta ctc ttg act tta tgg cct tca att ttc aat gtt cgg gcc   259
Ile Ala Leu Leu Leu Thr Leu Trp Pro Ser Ile Phe Asn Val Arg Ala
          40                  45                  50

atc gag tct ttt gtt ttc ttc ttc cat att gat act gac gtg tac cgc   307
Ile Glu Ser Phe Val Phe Phe Phe His Ile Asp Thr Asp Val Tyr Arg
     55                  60                  65

gcc ggt gct aat gca ttc ttg cat ggc gag aat ctg tat acc cag gac   355
Ala Gly Ala Asn Ala Phe Leu His Gly Glu Asn Leu Tyr Thr Gln Asp
```

```
 70                  75                  80                  85

tac caa gtt ggt agc att caa ctt ccc ttc acg tac cca ccg att tct   403
Tyr Gln Val Gly Ser Ile Gln Leu Pro Phe Thr Tyr Pro Pro Ile Ser
                90                  95                 100

gct gcg ctg ttt gtt cca ctt gca atc ctt gca agc agt gta gcc gga   451
Ala Ala Leu Phe Val Pro Leu Ala Ile Leu Ala Ser Ser Val Ala Gly
            105                 110                 115

ata gca tta acg ctt att tcc acg gtg ttg ctg tgg tgg agc gta gct   499
Ile Ala Leu Thr Leu Ile Ser Thr Val Leu Leu Trp Trp Ser Val Ala
        120                 125                 130

atc gtc ttg cgc cga gtg ctc aag ggt ctc acg gat gct gat tcc agg   547
Ile Val Leu Arg Arg Val Leu Lys Gly Leu Thr Asp Ala Asp Ser Arg
    135                 140                 145

ttt gtg tcc tat ttg att ctg cct atg gca ttg tcc acg gaa cct gta   595
Phe Val Ser Tyr Leu Ile Leu Pro Met Ala Leu Ser Thr Glu Pro Val
150                 155                 160                 165

ttc cag acc ctg cag ttt ggc cag gtc aac atc att ttg atg gcg ctg   643
Phe Gln Thr Leu Gln Phe Gly Gln Val Asn Ile Ile Leu Met Ala Leu
                170                 175                 180

gtt ctc atg gat acc ttc acc aaa aag ccc tgg ttg cca cgt ggt ttt   691
Val Leu Met Asp Thr Phe Thr Lys Lys Pro Trp Leu Pro Arg Gly Phe
            185                 190                 195

tgg att ggt ttg gcg gca tcc atc aag ctg acc ccc gca gtc ttt ggc   739
Trp Ile Gly Leu Ala Ala Ser Ile Lys Leu Thr Pro Ala Val Phe Gly
        200                 205                 210

ctt tac ttc cta gtg aag aag gac tgg aag ggc gct gga gta gca att   787
Leu Tyr Phe Leu Val Lys Lys Asp Trp Lys Gly Ala Gly Val Ala Ile
    215                 220                 225

gct tct ggc gta ggt ttt tcc gcc ttg gcg ttt atc ctc tca cct tca   835
Ala Ser Gly Val Gly Phe Ser Ala Leu Ala Phe Ile Leu Ser Pro Ser
230                 235                 240                 245

agt tcc aag att tac tgg act gaa aca ctc aac gac cct tct cgc atc   883
Ser Ser Lys Ile Tyr Trp Thr Glu Thr Leu Asn Asp Pro Ser Arg Ile
                250                 255                 260

ggc aac cta tct tat att gct aac caa tct gtg cgt gga acg ctc agc   931
Gly Asn Leu Ser Tyr Ile Ala Asn Gln Ser Val Arg Gly Thr Leu Ser
            265                 270                 275

cga atg atg cat gaa cag cag gat ctc gtc gaa aag ctt tgg ctt gtg   979
Arg Met Met His Glu Gln Gln Asp Leu Val Glu Lys Leu Trp Leu Val
        280                 285                 290

gca gtt gtc ttg tgc ctt gcc gct gtc gcc gtc gcc atg tgg cgc gtg   1027
Ala Val Val Leu Cys Leu Ala Ala Val Ala Val Ala Met Trp Arg Val
    295                 300                 305

gta cgc gcc ggc aac ccg tac ggc gcc gtc atg ctc aac tcg ttg att   1075
Val Arg Ala Gly Asn Pro Tyr Gly Ala Val Met Leu Asn Ser Leu Ile
310                 315                 320                 325
```

```
gct ctg ctg tgc tcc cct gtt tca tgg tct cac cac tgg gta tgg ctg   1123
Ala Leu Leu Cys Ser Pro Val Ser Trp Ser His His Trp Val Trp Leu
                330                 335                 340

att cca atc gct att ggt ttg ggg gca agt gcg tgg aac cag cgg cgg   1171
Ile Pro Ile Ala Ile Gly Leu Gly Ala Ser Ala Trp Asn Gln Arg Arg
            345                 350                 355

act gct cca gga att gcc gcg acg gct gga gtc ttg gcg ctt ctg acc   1219
Thr Ala Pro Gly Ile Ala Ala Thr Ala Gly Val Leu Ala Leu Leu Thr
        360                 365                 370

acg att ccg atg ttc atc aca aca ttt tgg aac atg cca tac gat tca   1267
Thr Ile Pro Met Phe Ile Thr Thr Phe Trp Asn Met Pro Tyr Asp Ser
    375                 380                 385

gag tct tac cca ttt tgg cca ttg att ctg cag ccg tcg ggc aac gcg   1315
Glu Ser Tyr Pro Phe Trp Pro Leu Ile Leu Gln Pro Ser Gly Asn Ala
390                 395                 400                 405

tat gta gta gtg gtc atc gct att ttg atc gtc gcg att gtg aat cca   1363
Tyr Val Val Val Val Ile Ala Ile Leu Ile Val Ala Ile Val Asn Pro
                410                 415                 420

aca gtt ttg ggc agt ggc aat aaa gct gtt tca ggc cag gca gag aag   1411
Thr Val Leu Gly Ser Gly Asn Lys Ala Val Ser Gly Gln Ala Glu Lys
            425                 430                 435

aag tcc tcc cct gcg ttg ctt gtt gtt tta gcg att gcc att ttc tac   1459
Lys Ser Ser Pro Ala Leu Leu Val Val Leu Ala Ile Ala Ile Phe Tyr
        440                 445                 450

ctc ttt gcc aat att tgg ttt aag gga aac aat caa aac aaa gcg ctc   1507
Leu Phe Ala Asn Ile Trp Phe Lys Gly Asn Asn Gln Asn Lys Ala Leu
    455                 460                 465

att cag tac cca ctg cag act atg gaa ggt cgc ggt ctc act gac ttc   1555
Ile Gln Tyr Pro Leu Gln Thr Met Glu Gly Arg Gly Leu Thr Asp Phe
470                 475                 480                 485

ggc gag ctt att ttt gaa ttc gcg gct tcc tcc aac cag ctt gtt tcc   1603
Gly Glu Leu Ile Phe Glu Phe Ala Ala Ser Ser Asn Gln Leu Val Ser
                490                 495                 500

ctc tgg ata atc ggc gcc ctc aac gcc atc gca ttg gct att acc ctg   1651
Leu Trp Ile Ile Gly Ala Leu Asn Ala Ile Ala Leu Ala Ile Thr Leu
            505                 510                 515

tgg ttc ctc ctt cag cgt ttt gct ggg aag aag agc tcc tgg ctg att   1699
Trp Phe Leu Leu Gln Arg Phe Ala Gly Lys Lys Ser Ser Trp Leu Ile
        520                 525                 530

tat ctc agc acc gtg gct gtt gcg ctg atg atg ttc tca gtg cag gat   1747
Tyr Leu Ser Thr Val Ala Val Ala Leu Met Met Phe Ser Val Gln Asp
    535                 540                 545

gcc ttg cag ttt ggt tcg ctg act ctc gtt gca ctc gca ttg atc act   1795
Ala Leu Gln Phe Gly Ser Leu Thr Leu Val Ala Leu Ala Leu Ile Thr
550                 555                 560                 565
```

```
gtt gat gtg ttg agt gtc aga gag att ggc cgc cgc ggg ctg ctc aca   1843
Val Asp Val Leu Ser Val Arg Glu Ile Gly Arg Arg Gly Leu Leu Thr
                570                 575                 580

gga ctt gca gca gcc ctg ttt gga tgg cca att ctg att gtt atc gga   1891
Gly Leu Ala Ala Ala Leu Phe Gly Trp Pro Ile Leu Ile Val Ile Gly
            585                 590                 595

ttc ctc att cac cga cgt tat gca gca aca atc aca acc act gtc acc   1939
Phe Leu Ile His Arg Arg Tyr Ala Ala Thr Ile Thr Thr Thr Val Thr
        600                 605                 610

gca gct gtg ctg tgg atc tta gga att ctg ctc aat cca gac gcc ttc   1987
Ala Ala Val Leu Trp Ile Leu Gly Ile Leu Leu Asn Pro Asp Ala Phe
    615                 620                 625

aac ctc aac ctg ctg cgt caa tgg ttc aac ggg cgc gat ggt cgg gac   2035
Asn Leu Asn Leu Leu Arg Gln Trp Phe Asn Gly Arg Asp Gly Arg Asp
630                 635                 640                 645

aat ttg tcc ttc tat gct ttc ctt gcc agg tgg gtc agc gaa tcc cca   2083
Asn Leu Ser Phe Tyr Ala Phe Leu Ala Arg Trp Val Ser Glu Ser Pro
                650                 655                 660

gca tgatgttcgt atggttcatc gtc                                    2109
Ala
```

Application Data Sheet - Page 2409 of 2444

<210> 2124
<211> 662
<212> PRT
<213> Corynebacterium glutamicum

<400> 2124

```
Met His Gly Glu Lys Leu Val Asp Gly Thr Glu Gly Asn Leu Ser Gln
  1               5                  10                  15

Phe Gln Trp Arg Asp Met Ala Thr Asn Gln Thr Leu Arg Lys Ala Leu
             20                  25                  30

Leu Val Leu Ser Thr Ile Ala Leu Leu Leu Thr Leu Trp Pro Ser Ile
         35                  40                  45

Phe Asn Val Arg Ala Ile Glu Ser Phe Val Phe Phe Phe His Ile Asp
     50                  55                  60

Thr Asp Val Tyr Arg Ala Gly Ala Asn Ala Phe Leu His Gly Glu Asn
 65                  70                  75                  80

Leu Tyr Thr Gln Asp Tyr Gln Val Gly Ser Ile Gln Leu Pro Phe Thr
                 85                  90                  95

Tyr Pro Pro Ile Ser Ala Ala Leu Phe Val Pro Leu Ala Ile Leu Ala
            100                 105                 110

Ser Ser Val Ala Gly Ile Ala Leu Thr Leu Ile Ser Thr Val Leu Leu
        115                 120                 125

Trp Trp Ser Val Ala Ile Val Leu Arg Arg Val Leu Lys Gly Leu Thr
    130                 135                 140
```

```
Asp Ala Asp Ser Arg Phe Val Ser Tyr Leu Ile Leu Pro Met Ala Leu
145                 150                 155                 160

Ser Thr Glu Pro Val Phe Gln Thr Leu Gln Phe Gly Gln Val Asn Ile
                165                 170                 175

Ile Leu Met Ala Leu Val Leu Met Asp Thr Phe Thr Lys Lys Pro Trp
            180                 185                 190

Leu Pro Arg Gly Phe Trp Ile Gly Leu Ala Ala Ser Ile Lys Leu Thr
        195                 200                 205

Pro Ala Val Phe Gly Leu Tyr Phe Leu Val Lys Lys Asp Trp Lys Gly
    210                 215                 220

Ala Gly Val Ala Ile Ala Ser Gly Val Gly Phe Ser Ala Leu Ala Phe
225                 230                 235                 240

Ile Leu Ser Pro Ser Ser Ser Lys Ile Tyr Trp Thr Glu Thr Leu Asn
                245                 250                 255

Asp Pro Ser Arg Ile Gly Asn Leu Ser Tyr Ile Ala Asn Gln Ser Val
            260                 265                 270

Arg Gly Thr Leu Ser Arg Met Met His Glu Gln Gln Asp Leu Val Glu
        275                 280                 285

Lys Leu Trp Leu Val Ala Val Val Leu Cys Leu Ala Ala Val Ala Val
    290                 295                 300

Ala Met Trp Arg Val Val Arg Ala Gly Asn Pro Tyr Gly Ala Val Met
305                 310                 315                 320

Leu Asn Ser Leu Ile Ala Leu Leu Cys Ser Pro Val Ser Trp Ser His
                325                 330                 335

His Trp Val Trp Leu Ile Pro Ile Ala Ile Gly Leu Gly Ala Ser Ala
            340                 345                 350

Trp Asn Gln Arg Arg Thr Ala Pro Gly Ile Ala Ala Thr Ala Gly Val
        355                 360                 365

Leu Ala Leu Leu Thr Thr Ile Pro Met Phe Ile Thr Thr Phe Trp Asn
    370                 375                 380

Met Pro Tyr Asp Ser Glu Ser Tyr Pro Phe Trp Pro Leu Ile Leu Gln
385                 390                 395                 400

Pro Ser Gly Asn Ala Tyr Val Val Val Val Ile Ala Ile Leu Ile Val
                405                 410                 415

Ala Ile Val Asn Pro Thr Val Leu Gly Ser Gly Asn Lys Ala Val Ser
            420                 425                 430

Gly Gln Ala Glu Lys Lys Ser Ser Pro Ala Leu Leu Val Val Leu Ala
        435                 440                 445

Ile Ala Ile Phe Tyr Leu Phe Ala Asn Ile Trp Phe Lys Gly Asn Asn
    450                 455                 460
```

```
Gln Asn Lys Ala Leu Ile Gln Tyr Pro Leu Gln Thr Met Glu Gly Arg
465                 470                 475                 480

Gly Leu Thr Asp Phe Gly Glu Leu Ile Phe Glu Phe Ala Ala Ser Ser
                485                 490                 495

Asn Gln Leu Val Ser Leu Trp Ile Ile Gly Ala Leu Asn Ala Ile Ala
            500                 505                 510

Leu Ala Ile Thr Leu Trp Phe Leu Leu Gln Arg Phe Ala Gly Lys Lys
        515                 520                 525

Ser Ser Trp Leu Ile Tyr Leu Ser Thr Val Ala Val Ala Leu Met Met
    530                 535                 540

Phe Ser Val Gln Asp Ala Leu Gln Phe Gly Ser Leu Thr Leu Val Ala
545                 550                 555                 560

Leu Ala Leu Ile Thr Val Asp Val Leu Ser Val Arg Glu Ile Gly Arg
                565                 570                 575

Arg Gly Leu Leu Thr Gly Leu Ala Ala Ala Leu Phe Gly Trp Pro Ile
            580                 585                 590

Leu Ile Val Ile Gly Phe Leu Ile His Arg Arg Tyr Ala Ala Thr Ile
        595                 600                 605

Thr Thr Thr Val Thr Ala Ala Val Leu Trp Ile Leu Gly Ile Leu Leu
    610                 615                 620

Asn Pro Asp Ala Phe Asn Leu Asn Leu Leu Arg Gln Trp Phe Asn Gly
625                 630                 635                 640

Arg Asp Gly Arg Asp Asn Leu Ser Phe Tyr Ala Phe Leu Ala Arg Trp
                645                 650                 655

Val Ser Glu Ser Pro Ala
            660
```

Sequence Listing.ST25.txt

<210> 2125
<211> 573
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(550)
<223> RXA01178

<400> 2125
tcaacctcaa cctgctgcgt caatggttca acgggcgcga tggtcgggac aatttgtcct 60

```
tctatgcttt ccttgccagg tgggtcagcg aatccccagc atg atg ttc gta tgg   115
                                               Met Met Phe Val Trp
                                                 1               5

ttc atc gtc gcc cta gga ctt ggt gcc tgg gca atc cac cgc acc tgg   163
Phe Ile Val Ala Leu Gly Leu Gly Ala Trp Ala Ile His Arg Thr Trp
                 10                  15                  20
```

```
tca cat gga ttc aag gac ctc tcc gtt gca ctg agc atc gca cta cca   211
Ser His Gly Phe Lys Asp Leu Ser Val Ala Leu Ser Ile Ala Leu Pro
             25                  30                  35

acc ttg gtg ctc ccc ata gtg gaa ctc cac cac ctc gtg cta ctt ctt   259
Thr Leu Val Leu Pro Ile Val Glu Leu His His Leu Val Leu Leu Leu
         40                  45                  50

cca ctg atc gca gtg ttg ctt cgt caa gga cgc gtg gca att tcc tac   307
Pro Leu Ile Ala Val Leu Leu Arg Gln Gly Arg Val Ala Ile Ser Tyr
     55                  60                  65

ctc atc gga ttt atc tac cta gtc tca tgg act ccg caa cac ctg tcc   355
Leu Ile Gly Phe Ile Tyr Leu Val Ser Trp Thr Pro Gln His Leu Ser
 70                  75                  80                  85

tac tcc acg gta ttc cca ctt aat gat cca gca cca gaa ggg tac gtc   403
Tyr Ser Thr Val Phe Pro Leu Asn Asp Pro Ala Pro Glu Gly Tyr Val
                 90                  95                 100

gcc cac ttt gga tgg tat tta ctc gtt gaa cca atg gcg gta gca ccg   451
Ala His Phe Gly Trp Tyr Leu Leu Val Glu Pro Met Ala Val Ala Pro
            105                 110                 115

gca gct ata atc ctc gga gca ttt att gcc tgt gct gca acc aca cct   499
Ala Ala Ile Ile Leu Gly Ala Phe Ile Ala Cys Ala Ala Thr Thr Pro
        120                 125                 130

aaa aca agt cag ctc gtg cag gtc gac aag tca agc gcg gaa aac acc   547
Lys Thr Ser Gln Leu Val Gln Val Asp Lys Ser Ser Ala Glu Asn Thr
    135                 140                 145

aag taagccttac agtccgacag cct                                    573
Lys
150
```

[illegible]

<210> 2126
<211> 150
<212> PRT
<213> Corynebacterium glutamicum

<400> 2126

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Met Met Phe Val Trp Phe Ile Val Ala Leu Gly Leu Gly Ala Trp Ala
  1               5                  10                  15

Ile His Arg Thr Trp Ser His Gly Phe Lys Asp Leu Ser Val Ala Leu
             20                  25                  30

Ser Ile Ala Leu Pro Thr Leu Val Leu Pro Ile Val Glu Leu His His
         35                  40                  45

Leu Val Leu Leu Leu Pro Leu Ile Ala Val Leu Leu Arg Gln Gly Arg
     50                  55                  60

Val Ala Ile Ser Tyr Leu Ile Gly Phe Ile Tyr Leu Val Ser Trp Thr
 65                  70                  75                  80

Pro Gln His Leu Ser Tyr Ser Thr Val Phe Pro Leu Asn Asp Pro Ala
                 85                  90                  95
```

```
Pro Glu Gly Tyr Val Ala His Phe Gly Trp Tyr Leu Leu Val Glu Pro
            100                 105                 110

Met Ala Val Ala Pro Ala Ala Ile Ile Leu Gly Ala Phe Ile Ala Cys
        115                 120                 125

Ala Ala Thr Thr Pro Lys Thr Ser Gln Leu Val Gln Val Asp Lys Ser
    130                 135                 140

Ser Ala Glu Asn Thr Lys
145                 150


<210> 2127
<211> 1589
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1573)
<223> RXA01184

<400> 2127
taaaacactt ctgaaactac agctgacgtt gtggggaaga actattaaag gaaataaagc 60

ggcaatagtg atgatgtcgc tgatatcttt ttacgccttg atg ggt ttg ttt ggt   115
                                            Met Gly Leu Phe Gly
                                              1               5

ttc ggc atc ttt ttg gct ctt ggg ctt ggg caa gac cac atg ggc atc   163
Phe Gly Ile Phe Leu Ala Leu Gly Leu Gly Gln Asp His Met Gly Ile
                10                  15                  20

ctt gct ggt gtt gtc tcg gtc ggc atg gtg gct tat tgc att gct gcg   211
Leu Ala Gly Val Val Ser Val Gly Met Val Ala Tyr Cys Ile Ala Ala
            25                  30                  35

ttt atg tgg ccg tca ggt gag ggg cag ctg gat ccg act gca ttt tcc   259
Phe Met Trp Pro Ser Gly Glu Gly Gln Leu Asp Pro Thr Ala Phe Ser
        40                  45                  50

acc atg ccg cta tcg gcg aag caa tta ttg cct gga ttc gct atc ggt   307
Thr Met Pro Leu Ser Ala Lys Gln Leu Leu Pro Gly Phe Ala Ile Gly
    55                  60                  65

acg ctc ctg cag tca cgg ggg att att gcg gtg att tgt acg gtg gcg   355
Thr Leu Leu Gln Ser Arg Gly Ile Ile Ala Val Ile Cys Thr Val Ala
70                  75                  80                  85

aca tcc att att gct gcg gtg ttt tta cct gtt ggt tcg tgg ccg atg   403
Thr Ser Ile Ile Ala Ala Val Phe Leu Pro Val Gly Ser Trp Pro Met
                90                  95                  100

atc gtg ttc atg atg gcg gta tcg ctg gtt act acg ttg ctt ttg ggt   451
Ile Val Phe Met Met Ala Val Ser Leu Val Thr Thr Leu Leu Leu Gly
            105                 110                 115

gag ttg ctt ggg gcg ttg acc tcg ggt tct tct tct agg gtg agt aat   499
Glu Leu Leu Gly Ala Leu Thr Ser Gly Ser Ser Ser Arg Val Ser Asn
        120                 125                 130
```

```
gat cgc cgt aca gtt ctt act tcc gtt gtc ttc atg gtg ttt gtt gtt   547
Asp Arg Arg Thr Val Leu Thr Ser Val Val Phe Met Val Phe Val Val
    135                 140                 145

ggc tat aac atg ctg att ggc gcg gat gga atg agt cga atc gat gcc   595
Gly Tyr Asn Met Leu Ile Gly Ala Asp Gly Met Ser Arg Ile Asp Ala
150                 155                 160                 165

att ggg gct tat aca aag tgg aca cca ttt ggg gcg ggt gca ggt gct   643
Ile Gly Ala Tyr Thr Lys Trp Thr Pro Phe Gly Ala Gly Ala Gly Ala
                170                 175                 180

att gag gct ttt gct gtt ggt ttg tgg ggt gag gca ggc ctg tta aca   691
Ile Glu Ala Phe Ala Val Gly Leu Trp Gly Glu Ala Gly Leu Leu Thr
            185                 190                 195

ttg ctg gct ttt gtt tat gtt gct gct ggt ttc tgg tta tgg tca cag   739
Leu Leu Ala Phe Val Tyr Val Ala Ala Gly Phe Trp Leu Trp Ser Gln
        200                 205                 210

ctg att aat cgc gcg ctc act gcg ccg ctg gac caa ggt ggg caa ggg   787
Leu Ile Asn Arg Ala Leu Thr Ala Pro Leu Asp Gln Gly Gly Gln Gly
    215                 220                 225

caa agc gct aaa gac agc gcc ggt gaa ggc aag aag gtt ctc ttt ctg   835
Gln Ser Ala Lys Asp Ser Ala Gly Glu Gly Lys Lys Val Leu Phe Leu
230                 235                 240                 245

cca ggt att cct tgg tca gtt gga ggt gcc att ttc tcg agg tcg ctg   883
Pro Gly Ile Pro Trp Ser Val Gly Gly Ala Ile Phe Ser Arg Ser Leu
                250                 255                 260

cgt tat atg ttc agg gac tcc agg ttg ttg gga tca atg att gtg ttc   931
Arg Tyr Met Phe Arg Asp Ser Arg Leu Leu Gly Ser Met Ile Val Phe
            265                 270                 275

ccg ctt ctt ggc gtg ctg ttt att ttc cag agc ttc acc gtt gag ttt   979
Pro Leu Leu Gly Val Leu Phe Ile Phe Gln Ser Phe Thr Val Glu Phe
        280                 285                 290

ttc atg atc tat gtt ggg ttg atc atg atg gca gtg ttc gca gga tcc   1027
Phe Met Ile Tyr Val Gly Leu Ile Met Met Ala Val Phe Ala Gly Ser
    295                 300                 305

gtt gct acc aat gat ttt ggc tat gac ggc cct tcg ttg tgg cta aat   1075
Val Ala Thr Asn Asp Phe Gly Tyr Asp Gly Pro Ser Leu Trp Leu Asn
310                 315                 320                 325

atc gtt gct ggt gtc aaa gcc cga acg ttg ttg atg ccc agg cac tgg   1123
Ile Val Ala Gly Val Lys Ala Arg Thr Leu Leu Met Pro Arg His Trp
                330                 335                 340

gca tca atg ctg ccg gga agt gtg tca att gtg gtg ttt atg atc atc   1171
Ala Ser Met Leu Pro Gly Ser Val Ser Ile Val Val Phe Met Ile Ile
            345                 350                 355

acc att gtg ctc gcg gag aat aag acc acc gct gtg ctg atc tgt ttt   1219
Thr Ile Val Leu Ala Glu Asn Lys Thr Thr Ala Val Leu Ile Cys Phe
        360                 365                 370
```

```
att ggc ctg ggg atc ttt atc tcc agt gcg gct gta gcg ttg ttg gtc   1267
Ile Gly Leu Gly Ile Phe Ile Ser Ser Ala Ala Val Ala Leu Leu Val
    375                 380                 385

acc aca ttt aat ccg tat ccg act tct aag cca ggc acg agt cct tgg   1315
Thr Thr Phe Asn Pro Tyr Pro Thr Ser Lys Pro Gly Thr Ser Pro Trp
390                 395                 400                 405

ggc gat cga agt ggc tat tcc ggt gct gcg ttc gtg gga gca ttt gcc   1363
Gly Asp Arg Ser Gly Tyr Ser Gly Ala Ala Phe Val Gly Ala Phe Ala
                410                 415                 420

gca ctg tta ctg gga tgg atc ccg acg att cct act atc gca ttg ggt   1411
Ala Leu Leu Leu Gly Trp Ile Pro Thr Ile Pro Thr Ile Ala Leu Gly
            425                 430                 435

atc ttt ggt ctg gtt acc gat cag atg tgg atg atc atc ctc gcg gag   1459
Ile Phe Gly Leu Val Thr Asp Gln Met Trp Met Ile Ile Leu Ala Glu
        440                 445                 450

gtg ctg gcc att att ctc cca gta gct gtg tac atc ggc gtt gct aag   1507
Val Leu Ala Ile Ile Leu Pro Val Ala Val Tyr Ile Gly Val Ala Lys
    455                 460                 465

gtg tgt att cgc aag gtg gag aag gat ctt ccg gag atc ttc gac aag   1555
Val Cys Ile Arg Lys Val Glu Lys Asp Leu Pro Glu Ile Phe Asp Lys
470                 475                 480                 485

gtg aaa act cac gtg aaa tagaaaaatg cggggt                        1589
Val Lys Thr His Val Lys
                490
```

<210> 2128
<211> 491
<212> PRT
<213> Corynebacterium glutamicum

<400> 2128

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Met Gly Leu Phe Gly Phe Gly Ile Phe Leu Ala Leu Gly Leu Gly Gln
  1               5                  10                  15

Asp His Met Gly Ile Leu Ala Gly Val Val Ser Val Gly Met Val Ala
             20                  25                  30

Tyr Cys Ile Ala Ala Phe Met Trp Pro Ser Gly Glu Gly Gln Leu Asp
         35                  40                  45

Pro Thr Ala Phe Ser Thr Met Pro Leu Ser Ala Lys Gln Leu Leu Pro
     50                  55                  60

Gly Phe Ala Ile Gly Thr Leu Leu Gln Ser Arg Gly Ile Ile Ala Val
 65                  70                  75                  80

Ile Cys Thr Val Ala Thr Ser Ile Ile Ala Ala Val Phe Leu Pro Val
                 85                  90                  95

Gly Ser Trp Pro Met Ile Val Phe Met Met Ala Val Ser Leu Val Thr
            100                 105                 110

Thr Leu Leu Leu Gly Glu Leu Leu Gly Ala Leu Thr Ser Gly Ser Ser
```

```
        115                 120                 125

Ser Arg Val Ser Asn Asp Arg Arg Thr Val Leu Thr Ser Val Val Phe
    130                 135                 140

Met Val Phe Val Val Gly Tyr Asn Met Leu Ile Gly Ala Asp Gly Met
145                 150                 155                 160

Ser Arg Ile Asp Ala Ile Gly Ala Tyr Thr Lys Trp Thr Pro Phe Gly
                165                 170                 175

Ala Gly Ala Gly Ala Ile Glu Ala Phe Ala Val Gly Leu Trp Gly Glu
            180                 185                 190

Ala Gly Leu Leu Thr Leu Leu Ala Phe Val Tyr Val Ala Ala Gly Phe
        195                 200                 205

Trp Leu Trp Ser Gln Leu Ile Asn Arg Ala Leu Thr Ala Pro Leu Asp
    210                 215                 220

Gln Gly Gly Gln Gly Gln Ser Ala Lys Asp Ser Ala Gly Glu Gly Lys
225                 230                 235                 240

Lys Val Leu Phe Leu Pro Gly Ile Pro Trp Ser Val Gly Gly Ala Ile
                245                 250                 255

Phe Ser Arg Ser Leu Arg Tyr Met Phe Arg Asp Ser Arg Leu Leu Gly
            260                 265                 270

Ser Met Ile Val Phe Pro Leu Leu Gly Val Leu Phe Ile Phe Gln Ser
        275                 280                 285

Phe Thr Val Glu Phe Phe Met Ile Tyr Val Gly Leu Ile Met Met Ala
    290                 295                 300

Val Phe Ala Gly Ser Val Ala Thr Asn Asp Phe Gly Tyr Asp Gly Pro
305                 310                 315                 320

Ser Leu Trp Leu Asn Ile Val Ala Gly Val Lys Ala Arg Thr Leu Leu
                325                 330                 335

Met Pro Arg His Trp Ala Ser Met Leu Pro Gly Ser Val Ser Ile Val
            340                 345                 350

Val Phe Met Ile Ile Thr Ile Val Leu Ala Glu Asn Lys Thr Thr Ala
        355                 360                 365

Val Leu Ile Cys Phe Ile Gly Leu Gly Ile Phe Ile Ser Ser Ala Ala
    370                 375                 380

Val Ala Leu Leu Val Thr Thr Phe Asn Pro Tyr Pro Thr Ser Lys Pro
385                 390                 395                 400

Gly Thr Ser Pro Trp Gly Asp Arg Ser Gly Tyr Ser Gly Ala Ala Phe
                405                 410                 415

Val Gly Ala Phe Ala Ala Leu Leu Leu Gly Trp Ile Pro Thr Ile Pro
            420                 425                 430

Thr Ile Ala Leu Gly Ile Phe Gly Leu Val Thr Asp Gln Met Trp Met
        435                 440                 445
```

```
Ile Ile Leu Ala Glu Val Leu Ala Ile Ile Leu Pro Val Ala Val Tyr
    450                 455                 460

Ile Gly Val Ala Lys Val Cys Ile Arg Lys Val Glu Lys Asp Leu Pro
465                 470                 475                 480

Glu Ile Phe Asp Lys Val Lys Thr His Val Lys
                485                 490


<210> 2129
<211> 1221
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1198)
<223> RXA01186

<400> 2129
ttgctcatac agccattgaa ctcgtagaat caccgttccg ccacccaaat cagcccaata 60

agttcaacaa ttacataaca tctgaaagaa tagggacatt atg gct aca cct gta   115
                                        Met Ala Thr Pro Val
                                          1               5

cca ctg gtt ttt aac gca cct aag cgt ggc atg ccc cca acc cac ttt   163
Pro Leu Val Phe Asn Ala Pro Lys Arg Gly Met Pro Pro Thr His Phe
                10                  15                  20

gcg gat ctt aat gat gag gct cgc att gag gct ctt aaa gag ctc ggc   211
Ala Asp Leu Asn Asp Glu Ala Arg Ile Glu Ala Leu Lys Glu Leu Gly
            25                  30                  35

ttg ccc aaa ttc cga ctc aat cag atc gct cga cac tac tat ggt cgc   259
Leu Pro Lys Phe Arg Leu Asn Gln Ile Ala Arg His Tyr Tyr Gly Arg
        40                  45                  50

ctc gag gct gac cca ctc act atg acg gac ctg cct gaa ggt gct cgt   307
Leu Glu Ala Asp Pro Leu Thr Met Thr Asp Leu Pro Glu Gly Ala Arg
    55                  60                  65

caa gaa gtc aag gat gct ctt ttt cca acg ttg atg tct cct ctg cgc   355
Gln Glu Val Lys Asp Ala Leu Phe Pro Thr Leu Met Ser Pro Leu Arg
70                  75                  80                  85

gtc gtc gaa acc gat gac gat aca act cag aag acg tta tgg aag ctc   403
Val Val Glu Thr Asp Asp Asp Thr Thr Gln Lys Thr Leu Trp Lys Leu
                90                  95                  100

cat gat ggc act ttg ctt gag tct gtt ctc atg cgc tat tca gat cgc   451
His Asp Gly Thr Leu Leu Glu Ser Val Leu Met Arg Tyr Ser Asp Arg
            105                 110                 115

tcc acg ctg tgt att tct tcg cag gct ggt tgc ggc atg gcg tgc cca   499
Ser Thr Leu Cys Ile Ser Ser Gln Ala Gly Cys Gly Met Ala Cys Pro
        120                 125                 130

ttc tgt gca act ggt cag ggc ggt ttg gac cgt aac ctt tca atc ggt   547
```

```
Phe Cys Ala Thr Gly Gln Gly Gly Leu Asp Arg Asn Leu Ser Ile Gly
    135                 140                 145

gag atc gtg gat cag gtt cgt aat gct gct gca acg atg cag tca gag   595
Glu Ile Val Asp Gln Val Arg Asn Ala Ala Ala Thr Met Gln Ser Glu
150                 155                 160                 165

ggc ggt cgt ctg tcc aac att gtg ttc atg gga atg ggc gag cct ctc   643
Gly Gly Arg Leu Ser Asn Ile Val Phe Met Gly Met Gly Glu Pro Leu
                170                 175                 180

gct aac tac aag cgc gtg gtg tcg gct gtt cgt cag atc acg cag cca   691
Ala Asn Tyr Lys Arg Val Val Ser Ala Val Arg Gln Ile Thr Gln Pro
            185                 190                 195

agc cct gcg ggc ttc ggc att tcc cag cgc agt gtg act gtc tcc acc   739
Ser Pro Ala Gly Phe Gly Ile Ser Gln Arg Ser Val Thr Val Ser Thr
        200                 205                 210

gtg ggc ctc gct cca gct atc agg aag ctt gcc gac gaa gag atg tcc   787
Val Gly Leu Ala Pro Ala Ile Arg Lys Leu Ala Asp Glu Glu Met Ser
    215                 220                 225

gta act ttg gca gtt tcc ttg cac act cca gac gat gag ttg cgt gac   835
Val Thr Leu Ala Val Ser Leu His Thr Pro Asp Asp Glu Leu Arg Asp
230                 235                 240                 245

act ctc gtg cca gtc aac aat cgt tgg cct gtc gct gag gta ctg gac   883
Thr Leu Val Pro Val Asn Asn Arg Trp Pro Val Ala Glu Val Leu Asp
                250                 255                 260

gct gct cgt tac tac gca gat aag tct ggc cgt cgc gtc tcc atc gag   931
Ala Ala Arg Tyr Tyr Ala Asp Lys Ser Gly Arg Arg Val Ser Ile Glu
            265                 270                 275

tat gcg ctc att cgc gat gtg aat gac cag gat tgg cgc gca gat atg   979
Tyr Ala Leu Ile Arg Asp Val Asn Asp Gln Asp Trp Arg Ala Asp Met
        280                 285                 290

ctg ggc gag aag ctg cat aag gct ttg ggc tcc cgt gtg cac gtc aac   1027
Leu Gly Glu Lys Leu His Lys Ala Leu Gly Ser Arg Val His Val Asn
    295                 300                 305

ttg att cca ttg aac cca act cct ggt tct aag tgg gat gct gca cca   1075
Leu Ile Pro Leu Asn Pro Thr Pro Gly Ser Lys Trp Asp Ala Ala Pro
310                 315                 320                 325

aag gct cgt cag gat gag ttt gtg cgt cgt gtg atc gcc aag ggt gtt   1123
Lys Ala Arg Gln Asp Glu Phe Val Arg Arg Val Ile Ala Lys Gly Val
                330                 335                 340

cca tgc act gtg cgt gat acc aag gga caa gaa atc gct gcg gct tgt   1171
Pro Cys Thr Val Arg Asp Thr Lys Gly Gln Glu Ile Ala Ala Ala Cys
            345                 350                 355

gga cag ctt gct gcg gag gaa tct gct taagccctca aagctcaaaa         1218
Gly Gln Leu Ala Ala Glu Glu Ser Ala
        360                 365

gcc                                                              1221
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<210> 2130
<211> 366
<212> PRT
<213> Corynebacterium glutamicum

<400> 2130

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Met Ala Thr Pro Val Pro Leu Val Phe Asn Ala Pro Lys Arg Gly Met
 1               5                  10                  15

Pro Pro Thr His Phe Ala Asp Leu Asn Asp Glu Ala Arg Ile Glu Ala
            20                  25                  30

Leu Lys Glu Leu Gly Leu Pro Lys Phe Arg Leu Asn Gln Ile Ala Arg
        35                  40                  45

His Tyr Tyr Gly Arg Leu Glu Ala Asp Pro Leu Thr Met Thr Asp Leu
    50                  55                  60

Pro Glu Gly Ala Arg Gln Glu Val Lys Asp Ala Leu Phe Pro Thr Leu
65                  70                  75                  80

Met Ser Pro Leu Arg Val Val Glu Thr Asp Asp Asp Thr Thr Gln Lys
                85                  90                  95

Thr Leu Trp Lys Leu His Asp Gly Thr Leu Leu Glu Ser Val Leu Met
            100                 105                 110

Arg Tyr Ser Asp Arg Ser Thr Leu Cys Ile Ser Ser Gln Ala Gly Cys
        115                 120                 125

Gly Met Ala Cys Pro Phe Cys Ala Thr Gly Gln Gly Gly Leu Asp Arg
    130                 135                 140

Asn Leu Ser Ile Gly Glu Ile Val Asp Gln Val Arg Asn Ala Ala Ala
145                 150                 155                 160

Thr Met Gln Ser Glu Gly Gly Arg Leu Ser Asn Ile Val Phe Met Gly
                165                 170                 175

Met Gly Glu Pro Leu Ala Asn Tyr Lys Arg Val Val Ser Ala Val Arg
            180                 185                 190

Gln Ile Thr Gln Pro Ser Pro Ala Gly Phe Gly Ile Ser Gln Arg Ser
        195                 200                 205

Val Thr Val Ser Thr Val Gly Leu Ala Pro Ala Ile Arg Lys Leu Ala
    210                 215                 220

Asp Glu Glu Met Ser Val Thr Leu Ala Val Ser Leu His Thr Pro Asp
225                 230                 235                 240

Asp Glu Leu Arg Asp Thr Leu Val Pro Val Asn Asn Arg Trp Pro Val
                245                 250                 255

Ala Glu Val Leu Asp Ala Ala Arg Tyr Tyr Ala Asp Lys Ser Gly Arg
            260                 265                 270

Arg Val Ser Ile Glu Tyr Ala Leu Ile Arg Asp Val Asn Asp Gln Asp
        275                 280                 285
```

```
Trp Arg Ala Asp Met Leu Gly Glu Lys Leu His Lys Ala Leu Gly Ser
    290                 295                 300

Arg Val His Val Asn Leu Ile Pro Leu Asn Pro Thr Pro Gly Ser Lys
305                 310                 315                 320

Trp Asp Ala Ala Pro Lys Ala Arg Gln Asp Glu Phe Val Arg Arg Val
                325                 330                 335

Ile Ala Lys Gly Val Pro Cys Thr Val Arg Asp Thr Lys Gly Gln Glu
            340                 345                 350

Ile Ala Ala Ala Cys Gly Gln Leu Ala Ala Glu Glu Ser Ala
        355                 360                 365
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<210> 2131
<211> 1221
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1198)
<223> RXA01186

<400> 2131

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ttgctcatac agccattgaa ctcgtagaat caccgttccg ccacccaaat cagcccaata 60

agttcaacaa ttacataaca tctgaaagaa tagggacatt atg gct aca cct gta   115
                                        Met Ala Thr Pro Val
                                          1               5

cca ctg gtt ttt aac gca cct aag cgt ggc atg ccc cca acc cac ttt   163
Pro Leu Val Phe Asn Ala Pro Lys Arg Gly Met Pro Pro Thr His Phe
                10                  15                  20

gcg gat ctt aat gat gag gct cgc att gag gct ctt aaa gag ctc ggc   211
Ala Asp Leu Asn Asp Glu Ala Arg Ile Glu Ala Leu Lys Glu Leu Gly
            25                  30                  35

ttg ccc aaa ttc cga ctc aat cag atc gct cga cac tac tat ggt cgc   259
Leu Pro Lys Phe Arg Leu Asn Gln Ile Ala Arg His Tyr Tyr Gly Arg
        40                  45                  50

ctc gag gct gac cca ctc act atg acg gac ctg cct gaa ggt gct cgt   307
Leu Glu Ala Asp Pro Leu Thr Met Thr Asp Leu Pro Glu Gly Ala Arg
    55                  60                  65

caa gaa gtc aag gat gct ctt ttt cca acg ttg atg tct cct ctg cgc   355
Gln Glu Val Lys Asp Ala Leu Phe Pro Thr Leu Met Ser Pro Leu Arg
70                  75                  80                  85

gtc gtc gaa acc gat gac gat aca act cag aag acg tta tgg aag ctc   403
Val Val Glu Thr Asp Asp Asp Thr Thr Gln Lys Thr Leu Trp Lys Leu
                90                  95                  100

cat gat ggc act ttg ctt gag tct gtt ctc atg cgc tat tca gat cgc   451
His Asp Gly Thr Leu Leu Glu Ser Val Leu Met Arg Tyr Ser Asp Arg
            105                 110                 115
```

```
tcc acg ctg tgt att tct tcg cag gct ggt tgc ggc atg gcg tgc cca   499
Ser Thr Leu Cys Ile Ser Ser Gln Ala Gly Cys Gly Met Ala Cys Pro
        120                 125                 130

ttc tgt gca act ggt cag ggc ggt ttg gac cgt aac ctt tca atc ggt   547
Phe Cys Ala Thr Gly Gln Gly Gly Leu Asp Arg Asn Leu Ser Ile Gly
    135                 140                 145

gag atc gtg gat cag gtt cgt aat gct gct gca acg atg cag tca gag   595
Glu Ile Val Asp Gln Val Arg Asn Ala Ala Ala Thr Met Gln Ser Glu
150                 155                 160                 165

ggc ggt cgt ctg tcc aac att gtg ttc atg gga atg ggc gag cct ctc   643
Gly Gly Arg Leu Ser Asn Ile Val Phe Met Gly Met Gly Glu Pro Leu
                170                 175                 180

gct aac tac aag cgc gtg gtg tcg gct gtt cgt cag atc acg cag cca   691
Ala Asn Tyr Lys Arg Val Val Ser Ala Val Arg Gln Ile Thr Gln Pro
            185                 190                 195

agc cct gcg ggc ttc ggc att tcc cag cgc agt gtg act gtc tcc acc   739
Ser Pro Ala Gly Phe Gly Ile Ser Gln Arg Ser Val Thr Val Ser Thr
        200                 205                 210

gtg ggc ctc gct cca gct atc agg aag ctt gcc gac gaa gag atg tcc   787
Val Gly Leu Ala Pro Ala Ile Arg Lys Leu Ala Asp Glu Glu Met Ser
    215                 220                 225

gta act ttg gca gtt tcc ttg cac act cca gac gat gag ttg cgt gac   835
Val Thr Leu Ala Val Ser Leu His Thr Pro Asp Asp Glu Leu Arg Asp
230                 235                 240                 245

act ctc gtg cca gtc aac aat cgt tgg cct gtc gct gag gta ctg gac   883
Thr Leu Val Pro Val Asn Asn Arg Trp Pro Val Ala Glu Val Leu Asp
                250                 255                 260

gct gct cgt tac tac gca gat aag tct ggc cgt cgc gtc tcc atc gag   931
Ala Ala Arg Tyr Tyr Ala Asp Lys Ser Gly Arg Arg Val Ser Ile Glu
            265                 270                 275

tat gcg ctc att cgc gat gtg aat gac cag gat tgg cgc gca gat atg   979
Tyr Ala Leu Ile Arg Asp Val Asn Asp Gln Asp Trp Arg Ala Asp Met
        280                 285                 290

ctg ggc gag aag ctg cat aag gct ttg ggc tcc cgt gtg cac gtc aac  1027
Leu Gly Glu Lys Leu His Lys Ala Leu Gly Ser Arg Val His Val Asn
    295                 300                 305

ttg att cca ttg aac cca act cct ggt tct aag tgg gat gct gca cca  1075
Leu Ile Pro Leu Asn Pro Thr Pro Gly Ser Lys Trp Asp Ala Ala Pro
310                 315                 320                 325

aag gct cgt cag gat gag ttt gtg cgt cgt gtg atc gcc aag ggt gtt  1123
Lys Ala Arg Gln Asp Glu Phe Val Arg Arg Val Ile Ala Lys Gly Val
                330                 335                 340

cca tgc act gtg cgt gat acc aag gga caa gaa atc gct gcg gct tgt  1171
Pro Cys Thr Val Arg Asp Thr Lys Gly Gln Glu Ile Ala Ala Ala Cys
            345                 350                 355

gga cag ctt gct gcg gag gaa tct gct taagccctca aagctcaaaa        1218
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Gly Gln Leu Ala Ala Glu Glu Ser Ala
360 365

gcc 1221

<210> 2132
<211> 366
<212> PRT
<213> Corynebacterium glutamicum

<400> 2132
Met Ala Thr Pro Val Pro Leu Val Phe Asn Ala Pro Lys Arg Gly Met
1 5 10 15

Pro Pro Thr His Phe Ala Asp Leu Asn Asp Glu Ala Arg Ile Glu Ala
20 25 30

Leu Lys Glu Leu Gly Leu Pro Lys Phe Arg Leu Asn Gln Ile Ala Arg
35 40 45

His Tyr Tyr Gly Arg Leu Glu Ala Asp Pro Leu Thr Met Thr Asp Leu
50 55 60

Pro Glu Gly Ala Arg Gln Glu Val Lys Asp Ala Leu Phe Pro Thr Leu
65 70 75 80

Met Ser Pro Leu Arg Val Val Glu Thr Asp Asp Asp Thr Thr Gln Lys
85 90 95

Thr Leu Trp Lys Leu His Asp Gly Thr Leu Leu Glu Ser Val Leu Met
100 105 110

Arg Tyr Ser Asp Arg Ser Thr Leu Cys Ile Ser Ser Gln Ala Gly Cys
115 120 125

Gly Met Ala Cys Pro Phe Cys Ala Thr Gly Gln Gly Gly Leu Asp Arg
130 135 140

Asn Leu Ser Ile Gly Glu Ile Val Asp Gln Val Arg Asn Ala Ala Ala
145 150 155 160

Thr Met Gln Ser Glu Gly Gly Arg Leu Ser Asn Ile Val Phe Met Gly
165 170 175

Met Gly Glu Pro Leu Ala Asn Tyr Lys Arg Val Val Ser Ala Val Arg
180 185 190

Gln Ile Thr Gln Pro Ser Pro Ala Gly Phe Gly Ile Ser Gln Arg Ser
195 200 205

Val Thr Val Ser Thr Val Gly Leu Ala Pro Ala Ile Arg Lys Leu Ala
210 215 220

Asp Glu Glu Met Ser Val Thr Leu Ala Val Ser Leu His Thr Pro Asp
225 230 235 240

Asp Glu Leu Arg Asp Thr Leu Val Pro Val Asn Asn Arg Trp Pro Val
245 250 255

Ala Glu Val Leu Asp Ala Ala Arg Tyr Tyr Ala Asp Lys Ser Gly Arg

260 265 270

Arg Val Ser Ile Glu Tyr Ala Leu Ile Arg Asp Val Asn Asp Gln Asp
275 280 285

Trp Arg Ala Asp Met Leu Gly Glu Lys Leu His Lys Ala Leu Gly Ser
290 295 300

Arg Val His Val Asn Leu Ile Pro Leu Asn Pro Thr Pro Gly Ser Lys
305 310 315 320

Trp Asp Ala Ala Pro Lys Ala Arg Gln Asp Glu Phe Val Arg Arg Val
325 330 335

Ile Ala Lys Gly Val Pro Cys Thr Val Arg Asp Thr Lys Gly Gln Glu
340 345 350

Ile Ala Ala Ala Cys Gly Gln Leu Ala Ala Glu Glu Ser Ala
355 360 365

<210> 2133
<211> 573
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(559)
<223> RXA01187

<400> 2133
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gtgattctac gagttcaatg gctgtatgag caacagacct gtg gat cca ttt gag 115
Val Asp Pro Phe Glu
1 5

acc aac cca aac gac ctt ccc acc ggt tta gac cca gca tac gaa ggt 163
Thr Asn Pro Asn Asp Leu Pro Thr Gly Leu Asp Pro Ala Tyr Glu Gly
10 15 20

aac agt gag tta aac ccg ctt gga gga aaa aat att ccc gac gag cct 211
Asn Ser Glu Leu Asn Pro Leu Gly Gly Lys Asn Ile Pro Asp Glu Pro
25 30 35

gag gtg act gca aac aca cct gca gtt caa gaa gaa cct gct tac tcg 259
Glu Val Thr Ala Asn Thr Pro Ala Val Gln Glu Glu Pro Ala Tyr Ser
40 45 50

gag cca gaa act gcc gtt gag tcg aag cgt cag gcg aag cag aac aca 307
Glu Pro Glu Thr Ala Val Glu Ser Lys Arg Gln Ala Lys Gln Asn Thr
55 60 65

aag aag tcc gaa cct gtt gtg gct cca aaa caa aca ctt gcc ggt ggc 355
Lys Lys Ser Glu Pro Val Val Ala Pro Lys Gln Thr Leu Ala Gly Gly
70 75 80 85

acg tgg gta gct ctc atc gta ggc gca ctt ttg cta atc cta ctg ttg 403
Thr Trp Val Ala Leu Ile Val Gly Ala Leu Leu Leu Ile Leu Leu Leu
90 95 100

```
gtc ttc atc atg cag aac caa acc acc gta gag ctt aac ctt ttt gcg   451
Val Phe Ile Met Gln Asn Gln Thr Thr Val Glu Leu Asn Leu Phe Ala
            105                 110                 115

tgg acc ttc caa ttc cca gcc gga atc ggt ttc cta cta gca gcc att   499
Trp Thr Phe Gln Phe Pro Ala Gly Ile Gly Phe Leu Leu Ala Ala Ile
        120                 125                 130

acc ggt gca ttg att atg gcg ctt ggt ggt ggc gtg cgc atg ttt gag   547
Thr Gly Ala Leu Ile Met Ala Leu Gly Gly Gly Val Arg Met Phe Glu
    135                 140                 145

tac cgt cgc agt taagaaaaat ccgt                                   573
Tyr Arg Arg Ser
150
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<210> 2134
<211> 153
<212> PRT
<213> Corynebacterium glutamicum

<400> 2134

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Val Asp Pro Phe Glu Thr Asn Pro Asn Asp Leu Pro Thr Gly Leu Asp
  1               5                  10                  15

Pro Ala Tyr Glu Gly Asn Ser Glu Leu Asn Pro Leu Gly Gly Lys Asn
             20                  25                  30

Ile Pro Asp Glu Pro Glu Val Thr Ala Asn Thr Pro Ala Val Gln Glu
         35                  40                  45

Glu Pro Ala Tyr Ser Glu Pro Glu Thr Ala Val Glu Ser Lys Arg Gln
     50                  55                  60

Ala Lys Gln Asn Thr Lys Lys Ser Glu Pro Val Val Ala Pro Lys Gln
 65                  70                  75                  80

Thr Leu Ala Gly Gly Thr Trp Val Ala Leu Ile Val Gly Ala Leu Leu
                 85                  90                  95

Leu Ile Leu Leu Leu Val Phe Ile Met Gln Asn Gln Thr Thr Val Glu
            100                 105                 110

Leu Asn Leu Phe Ala Trp Thr Phe Gln Phe Pro Ala Gly Ile Gly Phe
        115                 120                 125

Leu Leu Ala Ala Ile Thr Gly Ala Leu Ile Met Ala Leu Gly Gly Gly
    130                 135                 140

Val Arg Met Phe Glu Tyr Arg Arg Ser
145                 150
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<210> 2135
<211> 570
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(547)
<223> RXA01195

<400> 2135
ggtttcgcgc caggcgacat tgtgagtagg atcgtctaaa atcgttttct tatcgcagga 60

aggactcaaa aaggccgtgg aatatttgac ctggggtttg gtg att gtt gca gtg 115
Val Ile Val Ala Val
1 5

tcg gca gtt ctt ctt gct gcc tgg cgg ttt ttc acc tta cgt tct cgg 163
Ser Ala Val Leu Leu Ala Ala Trp Arg Phe Phe Thr Leu Arg Ser Arg
10 15 20

gga acc act gtg att ctg cgt gag ttg cca caa agc ggt gtg cat ggc 211
Gly Thr Thr Val Ile Leu Arg Glu Leu Pro Gln Ser Gly Val His Gly
25 30 35

tgg cgc cat gga tca ttt cgc tac aac ggc aac gac ttg gag tac ttc 259
Trp Arg His Gly Ser Phe Arg Tyr Asn Gly Asn Asp Leu Glu Tyr Phe
40 45 50

aag ctg cgc tct ttg tct ccc atg gct gac ctt att ttg aac cgc ctt 307
Lys Leu Arg Ser Leu Ser Pro Met Ala Asp Leu Ile Leu Asn Arg Leu
55 60 65

tca gta act ttg ctt gat cgt aga gat cca gct gct gat gag gcg gtt 355
Ser Val Thr Leu Leu Asp Arg Arg Asp Pro Ala Ala Asp Glu Ala Val
70 75 80 85

ttt atg tct caa ggc tta aaa att ctg cac att aaa tcc aaa aat gat 403
Phe Met Ser Gln Gly Leu Lys Ile Leu His Ile Lys Ser Lys Asn Asp
90 95 100

cag att gaa tta gct ttg gac gcc cac ggg gag atg gcg ttt act gcc 451
Gln Ile Glu Leu Ala Leu Asp Ala His Gly Glu Met Ala Phe Thr Ala
105 110 115

tgg ttg gaa gca gca cca gat gcg cgg gcg gag cat tca ttg aat cca 499
Trp Leu Glu Ala Ala Pro Asp Ala Arg Ala Glu His Ser Leu Asn Pro
120 125 130

cgt gat ttc aac cgc ttt cga gcc agc aaa gac acc cgc aaa aac cgc 547
Arg Asp Phe Asn Arg Phe Arg Ala Ser Lys Asp Thr Arg Lys Asn Arg
135 140 145

taagtagacg tcattgttat ggt 570

<210> 2136
<211> 149
<212> PRT
<213> Corynebacterium glutamicum

<400> 2136
Val Ile Val Ala Val Ser Ala Val Leu Leu Ala Ala Trp Arg Phe Phe
1 5 10 15

Thr Leu Arg Ser Arg Gly Thr Thr Val Ile Leu Arg Glu Leu Pro Gln
20 25 30

```
Ser Gly Val His Gly Trp Arg His Gly Ser Phe Arg Tyr Asn Gly Asn
         35                  40                  45

Asp Leu Glu Tyr Phe Lys Leu Arg Ser Leu Ser Pro Met Ala Asp Leu
     50                  55                  60

Ile Leu Asn Arg Leu Ser Val Thr Leu Leu Asp Arg Arg Asp Pro Ala
 65                  70                  75                  80

Ala Asp Glu Ala Val Phe Met Ser Gln Gly Leu Lys Ile Leu His Ile
                 85                  90                  95

Lys Ser Lys Asn Asp Gln Ile Glu Leu Ala Leu Asp Ala His Gly Glu
            100                 105                 110

Met Ala Phe Thr Ala Trp Leu Glu Ala Ala Pro Asp Ala Arg Ala Glu
        115                 120                 125

His Ser Leu Asn Pro Arg Asp Phe Asn Arg Phe Arg Ala Ser Lys Asp
    130                 135                 140

Thr Arg Lys Asn Arg
145
```

US 20050153417 A1 20050714

<210> 2137
<211> 813
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(790)
<223> RXA01196

<400> 2137

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gggcggagca ttcattgaat ccacgtgatt tcaaccgctt tcgagccagc aaagacaccc 60

gcaaaaaccg ctaagtagac gtcattgtta tggtgggtgc atg cgt tta gtc atc   115
                                            Met Arg Leu Val Ile
                                              1               5

gcc cgt tgc tca gtt gat tat gtt ggc cgt ttg gaa gct cat ctt ccg   163
Ala Arg Cys Ser Val Asp Tyr Val Gly Arg Leu Glu Ala His Leu Pro
                 10                  15                  20

tcc gcc gat cgc ctt ttg atg gtt aag gcg gat ggt tct gta tcc atc   211
Ser Ala Asp Arg Leu Leu Met Val Lys Ala Asp Gly Ser Val Ser Ile
             25                  30                  35

cat gcc gat gac cgt gcc tat aag cca ctg aac tgg atg aca cct cca   259
His Ala Asp Asp Arg Ala Tyr Lys Pro Leu Asn Trp Met Thr Pro Pro
         40                  45                  50

tgt tct tta gtt gaa act ccc atc act gat gaa gat ggt gaa gca aca   307
Cys Ser Leu Val Glu Thr Pro Ile Thr Asp Glu Asp Gly Glu Ala Thr
     55                  60                  65

ggg gaa agc ctg tgg gtg gtg gaa aac aaa aag ggc gag cag ctt cga   355
Gly Glu Ser Leu Trp Val Val Glu Asn Lys Lys Gly Glu Gln Leu Arg
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```
 70                  75                  80                  85

att act gtg gaa gaa att cat tcg gaa caa aac ttc gat cta ggc caa   403
Ile Thr Val Glu Glu Ile His Ser Glu Gln Asn Phe Asp Leu Gly Gln
                 90                  95                 100

gac cca ggt ttg gtg aaa gac gga gtg gaa gat cat ctc caa gag ctt   451
Asp Pro Gly Leu Val Lys Asp Gly Val Glu Asp His Leu Gln Glu Leu
            105                 110                 115

ctt gca gag cac atc act acg ttg ggt gat ggg tac aca ttg att cgt   499
Leu Ala Glu His Ile Thr Thr Leu Gly Asp Gly Tyr Thr Leu Ile Arg
        120                 125                 130

cgg gag tat cca aca gct att ggg cct gtc gat att ttg tgt cgc aac   547
Arg Glu Tyr Pro Thr Ala Ile Gly Pro Val Asp Ile Leu Cys Arg Asn
    135                 140                 145

tct gac ggc gag act gtc gct gtg gag atc aag cgt cgt ggt ggc atc   595
Ser Asp Gly Glu Thr Val Ala Val Glu Ile Lys Arg Arg Gly Gly Ile
150                 155                 160                 165

gac ggc gtt gag cag ttg acc agg tat ttg gaa ttg ctc aac cgt gat   643
Asp Gly Val Glu Gln Leu Thr Arg Tyr Leu Glu Leu Leu Asn Arg Asp
                170                 175                 180

gaa ttg ctc aag cct gtt cat gga gtg ttt gca gcc cag gag att aag   691
Glu Leu Leu Lys Pro Val His Gly Val Phe Ala Ala Gln Glu Ile Lys
            185                 190                 195

cct cag gca aag act ctc gcg gag gat cgt ggc atc aag tgc gtg acg   739
Pro Gln Ala Lys Thr Leu Ala Glu Asp Arg Gly Ile Lys Cys Val Thr
        200                 205                 210

ttg gat tat caa gcg ctt cgt ggc att gag tcc aat gag ctg aca ttg   787
Leu Asp Tyr Gln Ala Leu Arg Gly Ile Glu Ser Asn Glu Leu Thr Leu
    215                 220                 225

ttc taagaacatg ggccgaaaaa ata                                    813
Phe
230
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<210> 2138
<211> 230
<212> PRT
<213> Corynebacterium glutamicum

<400> 2138

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Met Arg Leu Val Ile Ala Arg Cys Ser Val Asp Tyr Val Gly Arg Leu
  1               5                  10                  15

Glu Ala His Leu Pro Ser Ala Asp Arg Leu Leu Met Val Lys Ala Asp
             20                  25                  30

Gly Ser Val Ser Ile His Ala Asp Asp Arg Ala Tyr Lys Pro Leu Asn
         35                  40                  45

Trp Met Thr Pro Pro Cys Ser Leu Val Glu Thr Pro Ile Thr Asp Glu
     50                  55                  60
```

```
Asp Gly Glu Ala Thr Gly Glu Ser Leu Trp Val Val Glu Asn Lys Lys
 65                  70                  75                  80

Gly Glu Gln Leu Arg Ile Thr Val Glu Glu Ile His Ser Glu Gln Asn
                85                  90                  95

Phe Asp Leu Gly Gln Asp Pro Gly Leu Val Lys Asp Gly Val Glu Asp
            100                 105                 110

His Leu Gln Glu Leu Leu Ala Glu His Ile Thr Thr Leu Gly Asp Gly
        115                 120                 125

Tyr Thr Leu Ile Arg Arg Glu Tyr Pro Thr Ala Ile Gly Pro Val Asp
    130                 135                 140

Ile Leu Cys Arg Asn Ser Asp Gly Glu Thr Val Ala Val Glu Ile Lys
145                 150                 155                 160

Arg Arg Gly Gly Ile Asp Gly Val Glu Gln Leu Thr Arg Tyr Leu Glu
                165                 170                 175

Leu Leu Asn Arg Asp Glu Leu Leu Lys Pro Val His Gly Val Phe Ala
            180                 185                 190

Ala Gln Glu Ile Lys Pro Gln Ala Lys Thr Leu Ala Glu Asp Arg Gly
        195                 200                 205

Ile Lys Cys Val Thr Leu Asp Tyr Gln Ala Leu Arg Gly Ile Glu Ser
    210                 215                 220

Asn Glu Leu Thr Leu Phe
225                 230


<210> 2139
<211> 576
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(553)
<223> RXA01197

<400> 2139
agcaacaatc atatctgcca ccctaccttg gggttggcat gtgatgacta gcttgcccaa 60

tcctcaatat tcccccacct gctatgccta aaattaagcc atg tct acc gaa cag   115
                                              Met Ser Thr Glu Gln
                                                1               5

tct ttg aat atc ccc cac gaa tac gtc atc tgc ctc gat cat gtt ggc   163
Ser Leu Asn Ile Pro His Glu Tyr Val Ile Cys Leu Asp His Val Gly
                10                  15                  20

atc gcc gtc cct gac ctc gag gaa gcc atc gaa ttt tac cgt tcc gca   211
Ile Ala Val Pro Asp Leu Glu Glu Ala Ile Glu Phe Tyr Arg Ser Ala
            25                  30                  35

ttc ggc tgg gta aac cac cac caa gaa atc aat gag gaa caa ggc att   259
Phe Gly Trp Val Asn His His Gln Glu Ile Asn Glu Glu Gln Gly Ile
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```
         40                  45                  50

tca gag gcc atg atc ggc ccc aaa gac att aaa agc aca gaa ggc atg   307
Ser Glu Ala Met Ile Gly Pro Lys Asp Ile Lys Ser Thr Glu Gly Met
     55                  60                  65

att cag ctc atc gcg ccg ctc aac gag gac tcc aca atc gcc aaa ttc   355
Ile Gln Leu Ile Ala Pro Leu Asn Glu Asp Ser Thr Ile Ala Lys Phe
 70                  75                  80                  85

ctc gaa aag aaa ggt ccc ggc atc cag caa atg tgc ctg cgc acc aac   403
Leu Glu Lys Lys Gly Pro Gly Ile Gln Gln Met Cys Leu Arg Thr Asn
                 90                  95                 100

aac atc gat gcg ctc tcc gag cac ctg cgc cgc caa ggc gtg cgc ctg   451
Asn Ile Asp Ala Leu Ser Glu His Leu Arg Arg Gln Gly Val Arg Leu
            105                 110                 115

ctc tac ccc gaa ccc aaa aac ggc acc ggc ggt gcc cgc atc aac ttc   499
Leu Tyr Pro Glu Pro Lys Asn Gly Thr Gly Gly Ala Arg Ile Asn Phe
        120                 125                 130

ctg cac ccc aaa gac gcg ggc ggc gtg ctg ctc gag atc acg cag cct   547
Leu His Pro Lys Asp Ala Gly Gly Val Leu Leu Glu Ile Thr Gln Pro
    135                 140                 145

caa agc taattgctta tcgacgctcc cag                                576
Gln Ser
150
```

Sequence Listing.ST25.txt 2010-12-29 09:39 20,648,448

<210> 2140
<211> 151
<212> PRT
<213> Corynebacterium glutamicum

<400> 2140

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  1               5                  10                  15

Leu Asp His Val Gly Ile Ala Val Pro Asp Leu Glu Glu Ala Ile Glu
            20                  25                  30

Phe Tyr Arg Ser Ala Phe Gly Trp Val Asn His His Gln Glu Ile Asn
        35                  40                  45

Glu Glu Gln Gly Ile Ser Glu Ala Met Ile Gly Pro Lys Asp Ile Lys
    50                  55                  60

Ser Thr Glu Gly Met Ile Gln Leu Ile Ala Pro Leu Asn Glu Asp Ser
65                  70                  75                  80

Thr Ile Ala Lys Phe Leu Glu Lys Lys Gly Pro Gly Ile Gln Gln Met
                85                  90                  95

Cys Leu Arg Thr Asn Asn Ile Asp Ala Leu Ser Glu His Leu Arg Arg
            100                 105                 110

Gln Gly Val Arg Leu Leu Tyr Pro Glu Pro Lys Asn Gly Thr Gly Gly
        115                 120                 125
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Ala Arg Ile Asn Phe Leu His Pro Lys Asp Ala Gly Gly Val Leu Leu
    130                 135                 140

Glu Ile Thr Gln Pro Gln Ser
145                 150


<210> 2141
<211> 426
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(403)
<223> RXA01198

<400> 2141
ttcggtagac atggcttaat tttaggcata gcaggtgggg gaatattgag gattgggcaa 60

gctagtcatc acatgccaac cccaaggtag ggtggcagat atg att gtt gct ttt   115
                                            Met Ile Val Ala Phe
                                              1               5

tct gta gcc ccg act gtt act gat aat cca gat gct gag atg gcc gat   163
Ser Val Ala Pro Thr Val Thr Asp Asn Pro Asp Ala Glu Met Ala Asp
                 10                  15                  20

gcg gtc acg gag gcg att cga atc gtc cgc gca tcg ggt ctg cct aat   211
Ala Val Thr Glu Ala Ile Arg Ile Val Arg Ala Ser Gly Leu Pro Asn
             25                  30                  35

gaa act aac gcg atg ttc acg ctc att gag ggg gag tgg gat gag gtg   259
Glu Thr Asn Ala Met Phe Thr Leu Ile Glu Gly Glu Trp Asp Glu Val
         40                  45                  50

atg gcg gtg att aag gag gcc act gag gcg atc tct agg gta tct ccg   307
Met Ala Val Ile Lys Glu Ala Thr Glu Ala Ile Ser Arg Val Ser Pro
     55                  60                  65

cgt aca tcg ttg gta att aag gct gat att cgt ccg gga cac act ggc   355
Arg Thr Ser Leu Val Ile Lys Ala Asp Ile Arg Pro Gly His Thr Gly
 70                  75                  80                  85

caa ttg acg agg aag gtg gag gcg gtg gag gaa cgc cta gct agg gat   403
Gln Leu Thr Arg Lys Val Glu Ala Val Glu Glu Arg Leu Ala Arg Asp
                 90                  95                 100

tagctttgta cttaaacttg ttg                                        426


<210> 2142
<211> 101
<212> PRT
<213> Corynebacterium glutamicum

<400> 2142
Met Ile Val Ala Phe Ser Val Ala Pro Thr Val Thr Asp Asn Pro Asp
  1               5                  10                  15

Ala Glu Met Ala Asp Ala Val Thr Glu Ala Ile Arg Ile Val Arg Ala
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            20                  25                  30

Ser Gly Leu Pro Asn Glu Thr Asn Ala Met Phe Thr Leu Ile Glu Gly
        35                  40                  45

Glu Trp Asp Glu Val Met Ala Val Ile Lys Glu Ala Thr Glu Ala Ile
    50                  55                  60

Ser Arg Val Ser Pro Arg Thr Ser Leu Val Ile Lys Ala Asp Ile Arg
65                  70                  75                  80

Pro Gly His Thr Gly Gln Leu Thr Arg Lys Val Glu Ala Val Glu Glu
                85                  90                  95

Arg Leu Ala Arg Asp
            100
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<210> 2143
<211> 771
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(748)
<223> RXA01207

<400> 2143

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cttcatgatc tcaccggcag agcgcgtttt gttacagcgc gtaaactgtg actttgaaaa 60

atttttgaac aatccgtaca ccaacttcag gagaaaaaca gtg agc aga atc tat   115
                                              Val Ser Arg Ile Tyr
                                                1               5

gac tgt gcc gac caa gac tcc cgt gca gca ggc cta aag gcg gct gtc   163
Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val
                10                  15                  20

gat gca gtc aaa gcc ggt cag ctc gtt gtc ctt ccc acg gat acc ctt   211
Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu Pro Thr Asp Thr Leu
            25                  30                  35

tat gga ctc ggc tgc gac gct ttc aac aac gag gca gta gcc aac ctt   259
Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu
        40                  45                  50

ctg gcc acc aaa cac cgt ggc ccc gat atg ccc gtt cca gtg ctc gtc   307
Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val
    55                  60                  65

ggc agc tgg gac acc att caa gga ctt gtg cac tcc tat tct gcg cag   355
Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln
70                  75                  80                  85

gca aaa gcg ctt gtg gag gcg ttc tgg cct ggt gga ctg tcc atc atc   403
Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly Gly Leu Ser Ile Ile
                90                  95                  100

gtt ccg cag gca cca agc ctt ccg tgg aac ctt ggc gat acc cgt ggc   451
Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly
```

```
            105                 110                 115

acc gta atg ctg cgc atg cca ctg cac cca gtt gcc att gaa ttg ctg   499
Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu
        120                 125                 130

cgc caa acc gga cca atg gct gtc tcc tcc gcc aac atc tcc gga cat   547
Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His
    135                 140                 145

act cct cca acc acc gtg ctg gag gct cgt cag cag ctc aac caa aat   595
Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln Gln Leu Asn Gln Asn
150                 155                 160                 165

gtc gct gtc tac ctc gat ggt ggc gaa tgc gcg ctg gcc acc cct tca   643
Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala Leu Ala Thr Pro Ser
                170                 175                 180

acc atc gtg gat att tca ggc ccc gca cca aag att ttg cgt gag ggt   691
Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly
            185                 190                 195

gcc atc agc gca gaa cgc gtt ggc gaa gta ctt gga gtg tcg gca gaa   739
Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu Gly Val Ser Ala Glu
        200                 205                 210

agc ctg cgc taaatgggag tcggtttcgc ggg                            771
Ser Leu Arg
    215
```

Confidential - Subject to Protective Order

<210> 2144
<211> 216
<212> PRT
<213> Corynebacterium glutamicum

<400> 2144

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Val Ser Arg Ile Tyr Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly
  1               5                  10                  15

Leu Lys Ala Ala Val Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu
             20                  25                  30

Pro Thr Asp Thr Leu Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu
         35                  40                  45

Ala Val Ala Asn Leu Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro
     50                  55                  60

Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His
 65                  70                  75                  80

Ser Tyr Ser Ala Gln Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly
                 85                  90                  95

Gly Leu Ser Ile Ile Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu
            100                 105                 110

Gly Asp Thr Arg Gly Thr Val Met Leu Arg Met Pro Leu His Pro Val
        115                 120                 125
```

```
Ala Ile Glu Leu Leu Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala
    130                 135                 140

Asn Ile Ser Gly His Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln
145                 150                 155                 160

Gln Leu Asn Gln Asn Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala
                165                 170                 175

Leu Ala Thr Pro Ser Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys
            180                 185                 190

Ile Leu Arg Glu Gly Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu
        195                 200                 205

Gly Val Ser Ala Glu Ser Leu Arg
    210                 215


<210> 2145
<211> 1350
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1327)
<223> RXA01213

<400> 2145
aactctggca acaacatgcg ccttcactcc ctcaaacaaa ttttcataaa caccccacat 60

catatcaacc aaacggtgta gttcttctaa gctttcaccc atg aca aat ccc aca   115
                                            Met Thr Asn Pro Thr
                                              1               5

gag gag cgc aac gca cgc cgc ctc att tgg gcc aac ggc ctg caa aac   163
Glu Glu Arg Asn Ala Arg Arg Leu Ile Trp Ala Asn Gly Leu Gln Asn
                  10                  15                  20

atc ggc gat caa atc gtt gcc gcc aaa aca gtc ctg ccc tgg ttg ctg   211
Ile Gly Asp Gln Ile Val Ala Ala Lys Thr Val Leu Pro Trp Leu Leu
              25                  30                  35

caa gcc gct ggc gcg ccg ggc ttt ttg ctg gcg ctt ctg gtt cca atc   259
Gln Ala Ala Gly Ala Pro Gly Phe Leu Leu Ala Leu Leu Val Pro Ile
          40                  45                  50

cgc gaa gcc gga tcg atg ctg ccg caa gct gcc att act ggc tgg gtg   307
Arg Glu Ala Gly Ser Met Leu Pro Gln Ala Ala Ile Thr Gly Trp Val
      55                  60                  65

ctg agg cag acg tcg aga agc aaa gtc tgg gtg att ggc tcg aac ggc   355
Leu Arg Gln Thr Ser Arg Ser Lys Val Trp Val Ile Gly Ser Asn Gly
  70                  75                  80                  85

cag ttc gtc tcg gcg ctg ggt atc ggc gtg gct gcg ctg ttt ttg cgt   403
Gln Phe Val Ser Ala Leu Gly Ile Gly Val Ala Ala Leu Phe Leu Arg
                  90                  95                 100

ggg tgg gcg ctg ggc atc acg gtg atc gtg ctg ctt gcg gcg ctg tcg   451
```

```
Gly Trp Ala Leu Gly Ile Thr Val Ile Val Leu Leu Ala Ala Leu Ser
            105                 110                 115

ctg ttt cga tcg atg tgt tcg att gca tcg aag gat gtt cag ggc aag   499
Leu Phe Arg Ser Met Cys Ser Ile Ala Ser Lys Asp Val Gln Gly Lys
        120                 125                 130

gtg att tcc aag ggc aag cgt ggg ctg gta acg ggc cgc gcg acg gtg   547
Val Ile Ser Lys Gly Lys Arg Gly Leu Val Thr Gly Arg Ala Thr Val
    135                 140                 145

att ggc ggt gtg atg ggc ctg gtt gca ggc ctg gcg atc gct att ttc   595
Ile Gly Gly Val Met Gly Leu Val Ala Gly Leu Ala Ile Ala Ile Phe
150                 155                 160                 165

ttg ggc tcg cat tcc ccg acg agg gtg ctg gcc gca gtg gtg atc gcg   643
Leu Gly Ser His Ser Pro Thr Arg Val Leu Ala Ala Val Val Ile Ala
                170                 175                 180

agc tcg ttt agc tgg ctg ttt gcc tcc att gtt ttc gcg cgc atc gaa   691
Ser Ser Phe Ser Trp Leu Phe Ala Ser Ile Val Phe Ala Arg Ile Glu
            185                 190                 195

tac gcg aag cca gcg act cca aaa aac gcg cct tcc gca aac ccg tgg   739
Tyr Ala Lys Pro Ala Thr Pro Lys Asn Ala Pro Ser Ala Asn Pro Trp
        200                 205                 210

gtg cgt cgc tgc atc gcc gca tta aaa gat gat aaa gct ttt cga cgt   787
Val Arg Arg Cys Ile Ala Ala Leu Lys Asp Asp Lys Ala Phe Arg Arg
    215                 220                 225

ttc gtt ctg gtt cgc tca atg atg ctg gtg aca gca ctc tcc acg gct   835
Phe Val Leu Val Arg Ser Met Met Leu Val Thr Ala Leu Ser Thr Ala
230                 235                 240                 245

ttc atc gtc gca ctc gcc gct gaa tcc gga aac agc atc gac tcc ttg   883
Phe Ile Val Ala Leu Ala Ala Glu Ser Gly Asn Ser Ile Asp Ser Leu
                250                 255                 260

gga ttc ttc ctc atc gcc tcc ggc ttg gcg tcc atg gtt ggt ggc cga   931
Gly Phe Phe Leu Ile Ala Ser Gly Leu Ala Ser Met Val Gly Gly Arg
            265                 270                 275

atc tct gga atc tgg tcg gat cat tcc tcc aaa aac gtc atg gcg ggc   979
Ile Ser Gly Ile Trp Ser Asp His Ser Ser Lys Asn Val Met Ala Gly
        280                 285                 290

ggt gcc cta ttc ggt tcc atc gtg tta atc ctc gtg gtg ctc agc tcc   1027
Gly Ala Leu Phe Gly Ser Ile Val Leu Ile Leu Val Val Leu Ser Ser
    295                 300                 305

gcg ttt gca ccc gcg cag atc aac acg ctg gtg ttc ccg ttg agt ttc   1075
Ala Phe Ala Pro Ala Gln Ile Asn Thr Leu Val Phe Pro Leu Ser Phe
310                 315                 320                 325

ttc ctc atc acc ttg gcc cac acc gcc atc cgc gtg gcc cgc aaa act   1123
Phe Leu Ile Thr Leu Ala His Thr Ala Ile Arg Val Ala Arg Lys Thr
                330                 335                 340

tat gta atg gac atg gct gaa ggt gat cag cgc acc cgc tat gtt gcc   1171
Tyr Val Met Asp Met Ala Glu Gly Asp Gln Arg Thr Arg Tyr Val Ala
```

```
            345                 350                 355

gac gcc aac aca cta atg ggt gta gtt ttg ctc att gtt ggc gca tta   1219
Asp Ala Asn Thr Leu Met Gly Val Val Leu Leu Ile Val Gly Ala Leu
        360                 365                 370

tct ggc ttc att gca att ttc gga aac gaa gcc gca ctg ctc ttc ttg   1267
Ser Gly Phe Ile Ala Ile Phe Gly Asn Glu Ala Ala Leu Leu Phe Leu
    375                 380                 385

gcg gca att ggc ctg ctt gga acc att agc gcc cgt ggc ctc aag gaa   1315
Ala Ala Ile Gly Leu Leu Gly Thr Ile Ser Ala Arg Gly Leu Lys Glu
390                 395                 400                 405

gta tcc gcc gga tagttttaca acttttccac cca                         1350
Val Ser Ala Gly
```

<210> 2146
<211> 409
<212> PRT
<213> Corynebacterium glutamicum

<400> 2146

```
Met Thr Asn Pro Thr Glu Glu Arg Asn Ala Arg Arg Leu Ile Trp Ala
  1               5                  10                  15

Asn Gly Leu Gln Asn Ile Gly Asp Gln Ile Val Ala Ala Lys Thr Val
             20                  25                  30

Leu Pro Trp Leu Leu Gln Ala Ala Gly Ala Pro Gly Phe Leu Leu Ala
         35                  40                  45

Leu Leu Val Pro Ile Arg Glu Ala Gly Ser Met Leu Pro Gln Ala Ala
     50                  55                  60

Ile Thr Gly Trp Val Leu Arg Gln Thr Ser Arg Ser Lys Val Trp Val
 65                  70                  75                  80

Ile Gly Ser Asn Gly Gln Phe Val Ser Ala Leu Gly Ile Gly Val Ala
                 85                  90                  95

Ala Leu Phe Leu Arg Gly Trp Ala Leu Gly Ile Thr Val Ile Val Leu
            100                 105                 110

Leu Ala Ala Leu Ser Leu Phe Arg Ser Met Cys Ser Ile Ala Ser Lys
        115                 120                 125

Asp Val Gln Gly Lys Val Ile Ser Lys Gly Lys Arg Gly Leu Val Thr
    130                 135                 140

Gly Arg Ala Thr Val Ile Gly Gly Val Met Gly Leu Val Ala Gly Leu
145                 150                 155                 160

Ala Ile Ala Ile Phe Leu Gly Ser His Ser Pro Thr Arg Val Leu Ala
                165                 170                 175

Ala Val Val Ile Ala Ser Ser Phe Ser Trp Leu Phe Ala Ser Ile Val
            180                 185                 190
```

Phe Ala Arg Ile Glu Tyr Ala Lys Pro Ala Thr Pro Lys Asn Ala Pro
195 200 205

Ser Ala Asn Pro Trp Val Arg Arg Cys Ile Ala Ala Leu Lys Asp Asp
210 215 220

Lys Ala Phe Arg Arg Phe Val Leu Val Arg Ser Met Met Leu Val Thr
225 230 235 240

Ala Leu Ser Thr Ala Phe Ile Val Ala Leu Ala Ala Glu Ser Gly Asn
245 250 255

Ser Ile Asp Ser Leu Gly Phe Phe Leu Ile Ala Ser Gly Leu Ala Ser
260 265 270

Met Val Gly Gly Arg Ile Ser Gly Ile Trp Ser Asp His Ser Ser Lys
275 280 285

Asn Val Met Ala Gly Gly Ala Leu Phe Gly Ser Ile Val Leu Ile Leu
290 295 300

Val Val Leu Ser Ser Ala Phe Ala Pro Ala Gln Ile Asn Thr Leu Val
305 310 315 320

Phe Pro Leu Ser Phe Phe Leu Ile Thr Leu Ala His Thr Ala Ile Arg
325 330 335

Val Ala Arg Lys Thr Tyr Val Met Asp Met Ala Glu Gly Asp Gln Arg
340 345 350

Thr Arg Tyr Val Ala Asp Ala Asn Thr Leu Met Gly Val Val Leu Leu
355 360 365

Ile Val Gly Ala Leu Ser Gly Phe Ile Ala Ile Phe Gly Asn Glu Ala
370 375 380

Ala Leu Leu Phe Leu Ala Ala Ile Gly Leu Leu Gly Thr Ile Ser Ala
385 390 395 400

Arg Gly Leu Lys Glu Val Ser Ala Gly
405

<210> 2147
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(529)
<223> RXA01218

<400> 2147
ctaaatatgc tagcacgatg gccaaaccta atccaaaaac cggcagtata ctgattgggg 60

tcacattagc caaaaggcac tttgaggaag tggaactcct atg gca cga ctt cag 115
Met Ala Arg Leu Gln
1 5

cac gac atg att ttc atc aac cta cca gta tct gac ctt gca gca tct 163

```
His Asp Met Ile Phe Ile Asn Leu Pro Val Ser Asp Leu Ala Ala Ser
                10                  15                  20

aag cgt ttt tat gca ggt ctt ggc ttc aaa gaa aac acc gtc ttc agt   211
Lys Arg Phe Tyr Ala Gly Leu Gly Phe Lys Glu Asn Thr Val Phe Ser
            25                  30                  35

gat gag cac act gca tct ttt gag gtc agt gac gcc atc gtg gtg atg   259
Asp Glu His Thr Ala Ser Phe Glu Val Ser Asp Ala Ile Val Val Met
        40                  45                  50

ctt ctg gaa acc gcg cgc ttc agt gat ttc act aag cgc ccc atc gtg   307
Leu Leu Glu Thr Ala Arg Phe Ser Asp Phe Thr Lys Arg Pro Ile Val
    55                  60                  65

gag aag aac ggc tcc cgc gaa gtg ctc aac tgc ctg tct gta tgt tcc   355
Glu Lys Asn Gly Ser Arg Glu Val Leu Asn Cys Leu Ser Val Cys Ser
70                  75                  80                  85

acc gag gat gcg gat gag ttc gtg cgt cgc gcc cag gaa ttc gga ggc   403
Thr Glu Asp Ala Asp Glu Phe Val Arg Arg Ala Gln Glu Phe Gly Gly
                90                  95                  100

acg atc acc cgt gag ctt gca gcg gaa ggc ccc atg tac ggc gga gct   451
Thr Ile Thr Arg Glu Leu Ala Ala Glu Gly Pro Met Tyr Gly Gly Ala
            105                 110                 115

ttt gat gat cca gat gga cac ggt tgg gag ctg atg tac ttc gat cca   499
Phe Asp Asp Pro Asp Gly His Gly Trp Glu Leu Met Tyr Phe Asp Pro
        120                 125                 130

gag gca ctc gct cag atg atg cct gag ggc taaatattct tcagggcttc     549
Glu Ala Leu Ala Gln Met Met Pro Glu Gly
    135                 140

tcg                                                               552


<210> 2148
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 2148
Met Ala Arg Leu Gln His Asp Met Ile Phe Ile Asn Leu Pro Val Ser
  1               5                  10                  15

Asp Leu Ala Ala Ser Lys Arg Phe Tyr Ala Gly Leu Gly Phe Lys Glu
            20                  25                  30

Asn Thr Val Phe Ser Asp Glu His Thr Ala Ser Phe Glu Val Ser Asp
        35                  40                  45

Ala Ile Val Val Met Leu Leu Glu Thr Ala Arg Phe Ser Asp Phe Thr
    50                  55                  60

Lys Arg Pro Ile Val Glu Lys Asn Gly Ser Arg Glu Val Leu Asn Cys
65                  70                  75                  80

Leu Ser Val Cys Ser Thr Glu Asp Ala Asp Glu Phe Val Arg Arg Ala
                85                  90                  95
```

```
Gln Glu Phe Gly Gly Thr Ile Thr Arg Glu Leu Ala Ala Glu Gly Pro
            100                 105                 110

Met Tyr Gly Gly Ala Phe Asp Asp Pro Asp Gly His Gly Trp Glu Leu
        115                 120                 125

Met Tyr Phe Asp Pro Glu Ala Leu Ala Gln Met Met Pro Glu Gly
    130                 135                 140


<210> 2149
<211> 507
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(484)
<223> RXA01234

<400> 2149
agaaacaata gccagaccca gaagagcaga ctggagagct tcgaggattt agtgctcctg 60

tgcatttatt cgggtcactt caacgttgaa aagcatagga atg tgg aag ttc atg   115
                                            Met Trp Lys Phe Met
                                              1               5

aag act caa tac gta tgt acc act tat ttc atc gct gca ccc gag gat   163
Lys Thr Gln Tyr Val Cys Thr Thr Tyr Phe Ile Ala Ala Pro Glu Asp
                10                  15                  20

gaa gac gag gcg tac caa act tat cgc agc cga atg aac tct ttg gca   211
Glu Asp Glu Ala Tyr Gln Thr Tyr Arg Ser Arg Met Asn Ser Leu Ala
            25                  30                  35

gca ttg aac ggc gct gac gta gtt tca gtg gca gat ggc cta cgg atg   259
Ala Leu Asn Gly Ala Asp Val Val Ser Val Ala Asp Gly Leu Arg Met
        40                  45                  50

gaa gta gac cag gat att tgg gga agc ctt gct gag cag tat cag att   307
Glu Val Asp Gln Asp Ile Trp Gly Ser Leu Ala Glu Gln Tyr Gln Ile
    55                  60                  65

gag caa gaa ggc ctg tat ccc act ggt cac aac ttg tac ttt gtt gtc   355
Glu Gln Glu Gly Leu Tyr Pro Thr Gly His Asn Leu Tyr Phe Val Val
70                  75                  80                  85

acc gtg gtg aac cta gat gat tca gat gag gtt tat gac cga aca atg   403
Thr Val Val Asn Leu Asp Asp Ser Asp Glu Val Tyr Asp Arg Thr Met
                90                  95                  100

gag cat ctg att atg gat gac cct tat gtg cga gtg gat cgt ttc cca   451
Glu His Leu Ile Met Asp Asp Pro Tyr Val Arg Val Asp Arg Phe Pro
            105                 110                 115

agc act gtc cat gcc agc acc cag atc atg ttg tagaaaaaga aaaagcacca 504
Ser Thr Val His Ala Ser Thr Gln Ile Met Leu
        120                 125

ccc                                                               507
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<210> 2150
<211> 128
<212> PRT
<213> Corynebacterium glutamicum

<400> 2150
Met Trp Lys Phe Met Lys Thr Gln Tyr Val Cys Thr Thr Tyr Phe Ile
1 5 10 15

Ala Ala Pro Glu Asp Glu Asp Glu Ala Tyr Gln Thr Tyr Arg Ser Arg
20 25 30

Met Asn Ser Leu Ala Ala Leu Asn Gly Ala Asp Val Val Ser Val Ala
35 40 45

Asp Gly Leu Arg Met Glu Val Asp Gln Asp Ile Trp Gly Ser Leu Ala
50 55 60

Glu Gln Tyr Gln Ile Glu Gln Glu Gly Leu Tyr Pro Thr Gly His Asn
65 70 75 80

Leu Tyr Phe Val Val Thr Val Val Asn Leu Asp Asp Ser Asp Glu Val
85 90 95

Tyr Asp Arg Thr Met Glu His Leu Ile Met Asp Asp Pro Tyr Val Arg
100 105 110

Val Asp Arg Phe Pro Ser Thr Val His Ala Ser Thr Gln Ile Met Leu
115 120 125

<210> 2151
<211> 564
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(541)
<223> RXA01237

<400> 2151
aaaccaaaaa tcacgacgca ttaagtaaca gagacttaaa ttaagaactc cgaacaacaa 60

cttcggattg tttcattttt gaggatgaaa gagcttttca atg aac gta cag ttt 115
Met Asn Val Gln Phe
1 5

gaa tca gac atg gcc gtc caa cca gga aac acc atg gaa gct acc gtc 163
Glu Ser Asp Met Ala Val Gln Pro Gly Asn Thr Met Glu Ala Thr Val
10 15 20

acc gac att cgt gat gcc aag cgt aaa aca acc cag ctt gat tca gta 211
Thr Asp Ile Arg Asp Ala Lys Arg Lys Thr Thr Gln Leu Asp Ser Val
25 30 35

```
acg ccg ttt aag aag aat tgc ccg agc cgc acc ttg ctc gac acc atc   259
Thr Pro Phe Lys Lys Asn Cys Pro Ser Arg Thr Leu Leu Asp Thr Ile
         40                  45                  50

agt gac aag tgg gcg gtg ctg atc ctg ctc agc atg gaa aat ggt cca   307
Ser Asp Lys Trp Ala Val Leu Ile Leu Leu Ser Met Glu Asn Gly Pro
     55                  60                  65

cag cgc aat ggt gaa atc aaa gat cag gtc caa gga att acc cca aag   355
Gln Arg Asn Gly Glu Ile Lys Asp Gln Val Gln Gly Ile Thr Pro Lys
 70                  75                  80                  85

atg ctc acc cag cgt ctt gga gtg ttg gtg gaa gac gga ctg gtc act   403
Met Leu Thr Gln Arg Leu Gly Val Leu Val Glu Asp Gly Leu Val Thr
                 90                  95                 100

cgc acc tcc cac gca gtt gtg ccg cct cgt gtg gat tat cag ctc acc   451
Arg Thr Ser His Ala Val Val Pro Pro Arg Val Asp Tyr Gln Leu Thr
            105                 110                 115

gat ctg ggt gct tct gtc att gag cct tgc cgt gcg atg tat tcc tgg   499
Asp Leu Gly Ala Ser Val Ile Glu Pro Cys Arg Ala Met Tyr Ser Trp
        120                 125                 130

gca gtg gag aac att aag caa gtg gag gcc tac cgc tca gca           541
Ala Val Glu Asn Ile Lys Gln Val Glu Ala Tyr Arg Ser Ala
    135                 140                 145

taagaacact tggcaaacct cac                                        564


<210> 2152
<211> 147
<212> PRT
<213> Corynebacterium glutamicum

<400> 2152
Met Asn Val Gln Phe Glu Ser Asp Met Ala Val Gln Pro Gly Asn Thr
  1               5                  10                  15

Met Glu Ala Thr Val Thr Asp Ile Arg Asp Ala Lys Arg Lys Thr Thr
             20                  25                  30

Gln Leu Asp Ser Val Thr Pro Phe Lys Lys Asn Cys Pro Ser Arg Thr
         35                  40                  45

Leu Leu Asp Thr Ile Ser Asp Lys Trp Ala Val Leu Ile Leu Leu Ser
     50                  55                  60

Met Glu Asn Gly Pro Gln Arg Asn Gly Glu Ile Lys Asp Gln Val Gln
 65                  70                  75                  80

Gly Ile Thr Pro Lys Met Leu Thr Gln Arg Leu Gly Val Leu Val Glu
                 85                  90                  95

Asp Gly Leu Val Thr Arg Thr Ser His Ala Val Val Pro Pro Arg Val
            100                 105                 110

Asp Tyr Gln Leu Thr Asp Leu Gly Ala Ser Val Ile Glu Pro Cys Arg
        115                 120                 125
```

```
Ala Met Tyr Ser Trp Ala Val Glu Asn Ile Lys Gln Val Glu Ala Tyr
    130                 135                 140

Arg Ser Ala
145
```

<210> 2153
<211> 1437
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1414)
<223> RXA01267

<400> 2153

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tgctagtttt aaagaggcgt tgaggggtag tatcgcgtaa gtttattagt ggttagcgta 60

gatttttcga attgaagatg tttctgaaag gtatttagat atg tat gca gaa att   115
                                            Met Tyr Ala Glu Ile
                                              1               5

aat ggc ggt ttt att cca gag ggc acc gtg cgg gta agc ggc gca aaa   163
Asn Gly Gly Phe Ile Pro Glu Gly Thr Val Arg Val Ser Gly Ala Lys
                10                  15                  20

aac tct gct act aga ctt ctc gcg gcg gca ctg cta acc gat gag gtg   211
Asn Ser Ala Thr Arg Leu Leu Ala Ala Ala Leu Leu Thr Asp Glu Val
            25                  30                  35

gtg cat ctt ggt aat ttc cca acc aag ctt gtg gat gtt gaa cat aaa   259
Val His Leu Gly Asn Phe Pro Thr Lys Leu Val Asp Val Glu His Lys
        40                  45                  50

att cgc ttt att gaa gag ctt ggc gga aaa gtg cat gtc gac cat gat   307
Ile Arg Phe Ile Glu Glu Leu Gly Gly Lys Val His Val Asp His Asp
    55                  60                  65

gag caa att tta gta gtt gat gct aag gat ctt gca gcg cga gaa atg   355
Glu Gln Ile Leu Val Val Asp Ala Lys Asp Leu Ala Ala Arg Glu Met
70                  75                  80                  85

act act gat gaa ctg aat att ccg att cga act act tat ctc cta gca   403
Thr Thr Asp Glu Leu Asn Ile Pro Ile Arg Thr Thr Tyr Leu Leu Ala
                90                  95                  100

gca gcg cag att ggg cgt ggg gaa att gct cga gtt cct ttt cct ggg   451
Ala Ala Gln Ile Gly Arg Gly Glu Ile Ala Arg Val Pro Phe Pro Gly
            105                 110                 115

ggg tgt gct att gga gga ggt cct gct ggc gga cga gga tat gat ctt   499
Gly Cys Ala Ile Gly Gly Gly Pro Ala Gly Gly Arg Gly Tyr Asp Leu
        120                 125                 130

cat ctt atg gtc tgg gaa cag cta ggt tgt aaa att ctt gaa aaa gat   547
His Leu Met Val Trp Glu Gln Leu Gly Cys Lys Ile Leu Glu Lys Asp
    135                 140                 145

gat cac att gaa gta act gca ccc cag ggc ttt atc ggg gga gtt att   595
```

```
Asp His Ile Glu Val Thr Ala Pro Gln Gly Phe Ile Gly Gly Val Ile
150                 155                 160                 165

gac ttt cct att tct act gtg gga ggc act gaa aac gcg tta cta tgc   643
Asp Phe Pro Ile Ser Thr Val Gly Gly Thr Glu Asn Ala Leu Leu Cys
                170                 175                 180

gca agt att gct tca ggg gat act aaa att gcc aat gct tat att acc   691
Ala Ser Ile Ala Ser Gly Asp Thr Lys Ile Ala Asn Ala Tyr Ile Thr
            185                 190                 195

cct gag ata act gat ctt att gaa ctt ctg cga cgt atg ggt gcg gag   739
Pro Glu Ile Thr Asp Leu Ile Glu Leu Leu Arg Arg Met Gly Ala Glu
        200                 205                 210

atc act gtc tac ggt acc agc cgt att cat gta aag ggt cga gca ggt   787
Ile Thr Val Tyr Gly Thr Ser Arg Ile His Val Lys Gly Arg Ala Gly
    215                 220                 225

ctt ttg cag ggc gca tat atg gac gta atg ccg gat cgt att gag gca   835
Leu Leu Gln Gly Ala Tyr Met Asp Val Met Pro Asp Arg Ile Glu Ala
230                 235                 240                 245

ttg acg tgg atc gtg tat gga att att tca ggc gga agg att acc gtc   883
Leu Thr Trp Ile Val Tyr Gly Ile Ile Ser Gly Gly Arg Ile Thr Val
                250                 255                 260

gaa ggt gtt cca ttt agc tcg atg gaa gtt cct ttt atc cac ctt gag   931
Glu Gly Val Pro Phe Ser Ser Met Glu Val Pro Phe Ile His Leu Glu
            265                 270                 275

aag gct gga gtg gat ctt ttc cgt aat tca agt tcc gta tat att aca   979
Lys Ala Gly Val Asp Leu Phe Arg Asn Ser Ser Ser Val Tyr Ile Thr
        280                 285                 290

cca gaa tgc ttg cct tca ggc tca gtt cag cca ttt gag cta gcg tgt   1027
Pro Glu Cys Leu Pro Ser Gly Ser Val Gln Pro Phe Glu Leu Ala Cys
    295                 300                 305

gga act cac ccc gga gta att tcg gac atg cag gca ctt ttt gtt ctt   1075
Gly Thr His Pro Gly Val Ile Ser Asp Met Gln Ala Leu Phe Val Leu
310                 315                 320                 325

tta gga tta aaa ggt gca gga act tca cgc gtc tat gac tat cga tac   1123
Leu Gly Leu Lys Gly Ala Gly Thr Ser Arg Val Tyr Asp Tyr Arg Tyr
                330                 335                 340

cca gaa aga att gca ttt gtt gag gaa ttg aca aat cta gtt tcg ggc   1171
Pro Glu Arg Ile Ala Phe Val Glu Glu Leu Thr Asn Leu Val Ser Gly
            345                 350                 355

gac aaa tta agt gca gag gct ggc aag atc act atc cag gga gat gct   1219
Asp Lys Leu Ser Ala Glu Ala Gly Lys Ile Thr Ile Gln Gly Asp Ala
        360                 365                 370

act ttc cgg cca gga tat gcg aac tca act gat cta cgt ggt tct atg   1267
Thr Phe Arg Pro Gly Tyr Ala Asn Ser Thr Asp Leu Arg Gly Ser Met
    375                 380                 385

gct gtt gtt tta gcg gcg ctt tgc gct gat gga aag tcc acg att aat   1315
Ala Val Val Leu Ala Ala Leu Cys Ala Asp Gly Lys Ser Thr Ile Asn
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390                 395                 400                 405

aac gtc cat atg gcg tta cgt ggg tac aac gag ttg gat aaa aaa ctt   1363
Asn Val His Met Ala Leu Arg Gly Tyr Asn Glu Leu Asp Lys Lys Leu
            410                 415                 420

cgt tta ctt ggt gcg gat tta act atc aga gaa ggc gaa gtt cct tca   1411
Arg Leu Leu Gly Ala Asp Leu Thr Ile Arg Glu Gly Glu Val Pro Ser
        425                 430                 435

cct taagaacgaa agttttacat tga                                    1437
Pro
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<210> 2154
<211> 438
<212> PRT
<213> Corynebacterium glutamicum

<400> 2154

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Met Tyr Ala Glu Ile Asn Gly Gly Phe Ile Pro Glu Gly Thr Val Arg
  1               5                  10                  15

Val Ser Gly Ala Lys Asn Ser Ala Thr Arg Leu Leu Ala Ala Ala Leu
             20                  25                  30

Leu Thr Asp Glu Val Val His Leu Gly Asn Phe Pro Thr Lys Leu Val
         35                  40                  45

Asp Val Glu His Lys Ile Arg Phe Ile Glu Glu Leu Gly Gly Lys Val
     50                  55                  60

His Val Asp His Asp Glu Gln Ile Leu Val Val Asp Ala Lys Asp Leu
 65                  70                  75                  80

Ala Ala Arg Glu Met Thr Thr Asp Glu Leu Asn Ile Pro Ile Arg Thr
                 85                  90                  95

Thr Tyr Leu Leu Ala Ala Ala Gln Ile Gly Arg Gly Glu Ile Ala Arg
            100                 105                 110

Val Pro Phe Pro Gly Gly Cys Ala Ile Gly Gly Gly Pro Ala Gly Gly
        115                 120                 125

Arg Gly Tyr Asp Leu His Leu Met Val Trp Glu Gln Leu Gly Cys Lys
    130                 135                 140

Ile Leu Glu Lys Asp Asp His Ile Glu Val Thr Ala Pro Gln Gly Phe
145                 150                 155                 160

Ile Gly Gly Val Ile Asp Phe Pro Ile Ser Thr Val Gly Gly Thr Glu
                165                 170                 175

Asn Ala Leu Leu Cys Ala Ser Ile Ala Ser Gly Asp Thr Lys Ile Ala
            180                 185                 190

Asn Ala Tyr Ile Thr Pro Glu Ile Thr Asp Leu Ile Glu Leu Leu Arg
        195                 200                 205

Arg Met Gly Ala Glu Ile Thr Val Tyr Gly Thr Ser Arg Ile His Val
```

```
    210                 215                 220

Lys Gly Arg Ala Gly Leu Leu Gln Gly Ala Tyr Met Asp Val Met Pro
225                 230                 235                 240

Asp Arg Ile Glu Ala Leu Thr Trp Ile Val Tyr Gly Ile Ile Ser Gly
                245                 250                 255

Gly Arg Ile Thr Val Glu Gly Val Pro Phe Ser Ser Met Glu Val Pro
            260                 265                 270

Phe Ile His Leu Glu Lys Ala Gly Val Asp Leu Phe Arg Asn Ser Ser
        275                 280                 285

Ser Val Tyr Ile Thr Pro Glu Cys Leu Pro Ser Gly Ser Val Gln Pro
    290                 295                 300

Phe Glu Leu Ala Cys Gly Thr His Pro Gly Val Ile Ser Asp Met Gln
305                 310                 315                 320

Ala Leu Phe Val Leu Leu Gly Leu Lys Gly Ala Gly Thr Ser Arg Val
                325                 330                 335

Tyr Asp Tyr Arg Tyr Pro Glu Arg Ile Ala Phe Val Glu Glu Leu Thr
            340                 345                 350

Asn Leu Val Ser Gly Asp Lys Leu Ser Ala Glu Ala Gly Lys Ile Thr
        355                 360                 365

Ile Gln Gly Asp Ala Thr Phe Arg Pro Gly Tyr Ala Asn Ser Thr Asp
    370                 375                 380

Leu Arg Gly Ser Met Ala Val Val Leu Ala Ala Leu Cys Ala Asp Gly
385                 390                 395                 400

Lys Ser Thr Ile Asn Asn Val His Met Ala Leu Arg Gly Tyr Asn Glu
                405                 410                 415

Leu Asp Lys Lys Leu Arg Leu Leu Gly Ala Asp Leu Thr Ile Arg Glu
            420                 425                 430

Gly Glu Val Pro Ser Pro
        435


<210> 2155
<211> 963
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(940)
<223> RXA01268

<400> 2155
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gctgatagtt ggaactccga aagcttcatt gctgggagtc gtg gca gca cga att   115
                                               Val Ala Ala Arg Ile
                                                 1               5
```

```
gct cga gtg cca cga att gtc tat gtg gca cat ggg ctg cgc tct gaa   163
Ala Arg Val Pro Arg Ile Val Tyr Val Ala His Gly Leu Arg Ser Glu
                10                  15                  20

act gtt tta ggc tta aaa aag aag att cta gtg ttt ttg gaa tat ttg   211
Thr Val Leu Gly Leu Lys Lys Lys Ile Leu Val Phe Leu Glu Tyr Leu
            25                  30                  35

acc cag ttg ttt gca cat caa act ttg gct gta agt cat tct ctg aag   259
Thr Gln Leu Phe Ala His Gln Thr Leu Ala Val Ser His Ser Leu Lys
        40                  45                  50

aaa gca att gaa gat gcg cac cct cgt ttt aaa gga aga gtg caa gtc   307
Lys Ala Ile Glu Asp Ala His Pro Arg Phe Lys Gly Arg Val Gln Val
    55                  60                  65

tta ggt tat ggc agt atg aat gga gtt gag ctt gat cgc ttt aga gtt   355
Leu Gly Tyr Gly Ser Met Asn Gly Val Glu Leu Asp Arg Phe Arg Val
70                  75                  80                  85

cca tcc ctt gaa gag aaa tta tct gct cgt aat gct tta aac ctg cct   403
Pro Ser Leu Glu Glu Lys Leu Ser Ala Arg Asn Ala Leu Asn Leu Pro
                90                  95                  100

agt aaa tct gtc att gtt ggt ttt gtc ggc aga ata aat aaa gat aag   451
Ser Lys Ser Val Ile Val Gly Phe Val Gly Arg Ile Asn Lys Asp Lys
            105                 110                 115

gga gga gat ctt ctc gct gct ctt aca aaa cat gag gct ttt acc cga   499
Gly Gly Asp Leu Leu Ala Ala Leu Thr Lys His Glu Ala Phe Thr Arg
        120                 125                 130

ttg cga ctg cat ctc tta att att ggt gaa ttg gaa gac gat gac ttg   547
Leu Arg Leu His Leu Leu Ile Ile Gly Glu Leu Glu Asp Asp Asp Leu
    135                 140                 145

cga gaa gca ttc att aaa tta gtt aat gaa ggg cag gtt acg att aca   595
Arg Glu Ala Phe Ile Lys Leu Val Asn Glu Gly Gln Val Thr Ile Thr
150                 155                 160                 165

gga tgg att gat ttc cct gaa gaa cca tta gct gca gtt gat gtt ttg   643
Gly Trp Ile Asp Phe Pro Glu Glu Pro Leu Ala Ala Val Asp Val Leu
                170                 175                 180

ctt cac cca act cag cga gaa ggt tta ggt atg tct ttg ctg gaa gct   691
Leu His Pro Thr Gln Arg Glu Gly Leu Gly Met Ser Leu Leu Glu Ala
            185                 190                 195

cag gct atg gga gtg cct gta ttg acg aat gct gtg act gga aca gtt   739
Gln Ala Met Gly Val Pro Val Leu Thr Asn Ala Val Thr Gly Thr Val
        200                 205                 210

gat gca gta aca agt gga gaa ggt ggc ttt ttt gcc gat gac gat tct   787
Asp Ala Val Thr Ser Gly Glu Gly Gly Phe Phe Ala Asp Asp Asp Ser
    215                 220                 225

gtt gag tcc tgg gtt tct aag att gat tta tta gtt tcc gat cct aag   835
Val Glu Ser Trp Val Ser Lys Ile Asp Leu Leu Val Ser Asp Pro Lys
230                 235                 240                 245
```

```
tta aga gac cgg atg gga cgt gct ggt cgc cag ttt gtg tca gct cgt   883
Leu Arg Asp Arg Met Gly Arg Ala Gly Arg Gln Phe Val Ser Ala Arg
                250                 255                 260

ttc aat cgt gat gat gtc gca gct cgt ttc agt cat ttc gtg gaa caa   931
Phe Asn Arg Asp Asp Val Ala Ala Arg Phe Ser His Phe Val Glu Gln
            265                 270                 275

ttc aaa aaa tagggctcat tcaatttcaa tat                            963
Phe Lys Lys
        280
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<210> 2156
<211> 280
<212> PRT
<213> Corynebacterium glutamicum

<400> 2156

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Val Ala Ala Arg Ile Ala Arg Val Pro Arg Ile Val Tyr Val Ala His
  1               5                  10                  15

Gly Leu Arg Ser Glu Thr Val Leu Gly Leu Lys Lys Lys Ile Leu Val
             20                  25                  30

Phe Leu Glu Tyr Leu Thr Gln Leu Phe Ala His Gln Thr Leu Ala Val
         35                  40                  45

Ser His Ser Leu Lys Lys Ala Ile Glu Asp Ala His Pro Arg Phe Lys
     50                  55                  60

Gly Arg Val Gln Val Leu Gly Tyr Gly Ser Met Asn Gly Val Glu Leu
 65                  70                  75                  80

Asp Arg Phe Arg Val Pro Ser Leu Glu Glu Lys Leu Ser Ala Arg Asn
                 85                  90                  95

Ala Leu Asn Leu Pro Ser Lys Ser Val Ile Val Gly Phe Val Gly Arg
            100                 105                 110

Ile Asn Lys Asp Lys Gly Gly Asp Leu Leu Ala Ala Leu Thr Lys His
        115                 120                 125

Glu Ala Phe Thr Arg Leu Arg Leu His Leu Leu Ile Ile Gly Glu Leu
    130                 135                 140

Glu Asp Asp Asp Leu Arg Glu Ala Phe Ile Lys Leu Val Asn Glu Gly
145                 150                 155                 160

Gln Val Thr Ile Thr Gly Trp Ile Asp Phe Pro Glu Glu Pro Leu Ala
                165                 170                 175

Ala Val Asp Val Leu Leu His Pro Thr Gln Arg Glu Gly Leu Gly Met
            180                 185                 190

Ser Leu Leu Glu Ala Gln Ala Met Gly Val Pro Val Leu Thr Asn Ala
        195                 200                 205

Val Thr Gly Thr Val Asp Ala Val Thr Ser Gly Glu Gly Gly Phe Phe
    210                 215                 220
```

```
Ala Asp Asp Asp Ser Val Glu Ser Trp Val Ser Lys Ile Asp Leu Leu
225                 230                 235                 240

Val Ser Asp Pro Lys Leu Arg Asp Arg Met Gly Arg Ala Gly Arg Gln
                245                 250                 255

Phe Val Ser Ala Arg Phe Asn Arg Asp Asp Val Ala Ala Arg Phe Ser
            260                 265                 270

His Phe Val Glu Gln Phe Lys Lys
        275                 280


<210> 2157
<211> 1935
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1912)
<223> RXA01271

<400> 2157
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ttggcgaaac ccaatttatt tcaaaagatg gtggacaaac atg gca ata agc att   115
                                            Met Ala Ile Ser Ile
                                              1               5

ggt aaa gca gga cag aac tta aaa ggg tca gtg cct atc gga aaa gtc   163
Gly Lys Ala Gly Gln Asn Leu Lys Gly Ser Val Pro Ile Gly Lys Val
                10                  15                  20

ctt ttt ctc att gat gcc ctt gcc tgg att tct gca cta ttt atc ggt   211
Leu Phe Leu Ile Asp Ala Leu Ala Trp Ile Ser Ala Leu Phe Ile Gly
            25                  30                  35

gtg gtt ttg cgg tat gaa ttc aat ctg agt tct atc aac tgg agt gcg   259
Val Val Leu Arg Tyr Glu Phe Asn Leu Ser Ser Ile Asn Trp Ser Ala
        40                  45                  50

ttt gca tgg ttc ggg ctt gct gca gtt att ttg cag ttt gtt ctc gga   307
Phe Ala Trp Phe Gly Leu Ala Ala Val Ile Leu Gln Phe Val Leu Gly
    55                  60                  65

ctt tct ctc cat ctt tac cgc aag gga tta cgt cac ctt ttc ggt agc   355
Leu Ser Leu His Leu Tyr Arg Lys Gly Leu Arg His Leu Phe Gly Ser
70                  75                  80                  85

ttc gaa gat aca cta aac gtt tct atc tcg gtc att gtt gtc ggt gtt   403
Phe Glu Asp Thr Leu Asn Val Ser Ile Ser Val Ile Val Val Gly Val
                90                  95                  100

gtc ctt tgg atc gcc tca cta ttt gtt ggt cag cgt tgg aaa atc tca   451
Val Leu Trp Ile Ala Ser Leu Phe Val Gly Gln Arg Trp Lys Ile Ser
            105                 110                 115

cgc ggt gtc atg ctg cta gtt atc ccg ctt gct ctc gta ttc gta ttg   499
Arg Gly Val Met Leu Leu Val Ile Pro Leu Ala Leu Val Phe Val Leu
        120                 125                 130
```

```
gca gtg cgt tat ctc gcg cgt atg cga gtt gag cgt ttt cgt cgt ccg   547
Ala Val Arg Tyr Leu Ala Arg Met Arg Val Glu Arg Phe Arg Arg Pro
    135                 140                 145

gct gcg gat tcc aca cca gca ttg att ctt ggt ggt gga tac atc ggt   595
Ala Ala Asp Ser Thr Pro Ala Leu Ile Leu Gly Gly Gly Tyr Ile Gly
150                 155                 160                 165

acc aac ctg atc cag tgg atg atg tcc gat cct aag tcg cct ttc cgc   643
Thr Asn Leu Ile Gln Trp Met Met Ser Asp Pro Lys Ser Pro Phe Arg
                170                 175                 180

cca gtc ggc gtt att gat gat aac cct gaa tta gca tgc caa cgc gta   691
Pro Val Gly Val Ile Asp Asp Asn Pro Glu Leu Ala Cys Gln Arg Val
            185                 190                 195

cgt ggt gtg ccg gtt ctt ggc aag ttt gat gat atc gcc caa gtt gca   739
Arg Gly Val Pro Val Leu Gly Lys Phe Asp Asp Ile Ala Gln Val Ala
        200                 205                 210

tca gac act ggc gca gaa ctt ctt atc gtt gct att ggt gat gcc gac   787
Ser Asp Thr Gly Ala Glu Leu Leu Ile Val Ala Ile Gly Asp Ala Asp
    215                 220                 225

tct gca ctt tta agg cgt gtc caa gat acc gct aat aaa aat ggt ctt   835
Ser Ala Leu Leu Arg Arg Val Gln Asp Thr Ala Asn Lys Asn Gly Leu
230                 235                 240                 245

tca gta aag gta atg ccg gct att gac cgc gtc gtt tct aag ggc gtt   883
Ser Val Lys Val Met Pro Ala Ile Asp Arg Val Val Ser Lys Gly Val
                250                 255                 260

cgt gga aac gat ttg cgt gat ctc tct att gaa gat ttg ctt gga cgt   931
Arg Gly Asn Asp Leu Arg Asp Leu Ser Ile Glu Asp Leu Leu Gly Arg
            265                 270                 275

caa cct gtt gaa acc aat gtt tca gaa att act ggc tat cta aca ggt   979
Gln Pro Val Glu Thr Asn Val Ser Glu Ile Thr Gly Tyr Leu Thr Gly
        280                 285                 290

aag cgt gtt ctt gtt acc ggt gca ggt ggg tca att ggt tcc cag cta   1027
Lys Arg Val Leu Val Thr Gly Ala Gly Gly Ser Ile Gly Ser Gln Leu
    295                 300                 305

tgt acg gaa att gcc aaa tac gga cct gct gag ctt atg atg ctt gat   1075
Cys Thr Glu Ile Ala Lys Tyr Gly Pro Ala Glu Leu Met Met Leu Asp
310                 315                 320                 325

cgc gat gag act ggt ttg cag cag gtt ctg att aac gtt gct ggt aac   1123
Arg Asp Glu Thr Gly Leu Gln Gln Val Leu Ile Asn Val Ala Gly Asn
                330                 335                 340

ggt ttg ttg gat acg gat gct gtg gtt ctt gcg gat atc cgc gaa gca   1171
Gly Leu Leu Asp Thr Asp Ala Val Val Leu Ala Asp Ile Arg Glu Ala
            345                 350                 355

gac gcg atg aaa gag att ttt ctc aag cgt aaa cca gaa gtt gtc ttc   1219
Asp Ala Met Lys Glu Ile Phe Leu Lys Arg Lys Pro Glu Val Val Phe
        360                 365                 370
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cat gca gca gca tta aag cac ttg cca atg ctg gag cag tat cca gat   1267
His Ala Ala Ala Leu Lys His Leu Pro Met Leu Glu Gln Tyr Pro Asp
    375                 380                 385

gag ggc tgg aaa aca aac gtt cta gga act ctt aac gtt ctt gct gcc   1315
Glu Gly Trp Lys Thr Asn Val Leu Gly Thr Leu Asn Val Leu Ala Ala
390                 395                 400                 405

gca gaa gct gtt ggt gtt gag act ttc gtc aat att tcc acc gat aag   1363
Ala Glu Ala Val Gly Val Glu Thr Phe Val Asn Ile Ser Thr Asp Lys
                410                 415                 420

gca gct aat cca acc agc gtc tta ggg cac tca aag cga gtc gct gaa   1411
Ala Ala Asn Pro Thr Ser Val Leu Gly His Ser Lys Arg Val Ala Glu
            425                 430                 435

aag ctg act gcc tgg tat gga cag aat tcc acc agc aag tac cta tcg   1459
Lys Leu Thr Ala Trp Tyr Gly Gln Asn Ser Thr Ser Lys Tyr Leu Ser
        440                 445                 450

gtt cga ttt gga aac gtc att ggt agc cgt gga tcg atg ctc ccg act   1507
Val Arg Phe Gly Asn Val Ile Gly Ser Arg Gly Ser Met Leu Pro Thr
    455                 460                 465

ttc acc agg cta atc atg gaa gat aaa ccg cta aca gtg acg cac ccg   1555
Phe Thr Arg Leu Ile Met Glu Asp Lys Pro Leu Thr Val Thr His Pro
470                 475                 480                 485

gat gtc act agg ttc ttc atg aca att cct gaa gct tgc caa ttg gtc   1603
Asp Val Thr Arg Phe Phe Met Thr Ile Pro Glu Ala Cys Gln Leu Val
                490                 495                 500

ctg caa gcc ggt ggt att gga cgt tcc ggc gag gtt ctc atc ctt gac   1651
Leu Gln Ala Gly Gly Ile Gly Arg Ser Gly Glu Val Leu Ile Leu Asp
            505                 510                 515

atg ggt gag cct gta agc atc ctt gaa att gca cag cgc atg atc gca   1699
Met Gly Glu Pro Val Ser Ile Leu Glu Ile Ala Gln Arg Met Ile Ala
        520                 525                 530

atg tcc ggt aaa gat att gac atc gtg ttc acc ggc ctt cgc gag ggc   1747
Met Ser Gly Lys Asp Ile Asp Ile Val Phe Thr Gly Leu Arg Glu Gly
    535                 540                 545

gaa aag atg cac gaa gag ctg gtt ggt gat ggt gaa acc gaa gat cgt   1795
Glu Lys Met His Glu Glu Leu Val Gly Asp Gly Glu Thr Glu Asp Arg
550                 555                 560                 565

cca ttc cac tca aag att tcg cat gca cat gca gaa agc ctc gct cct   1843
Pro Phe His Ser Lys Ile Ser His Ala His Ala Glu Ser Leu Ala Pro
                570                 575                 580

aat aat ctc gat aga gat cga ttt atg caa cgt gct gga aaa cta gct   1891
Asn Asn Leu Asp Arg Asp Arg Phe Met Gln Arg Ala Gly Lys Leu Ala
            585                 590                 595

tca aca gat tcg gag atc atc taaatgacta atgaacgaat ttt             1935
Ser Thr Asp Ser Glu Ile Ile
        600
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<210> 2158
<211> 604
<212> PRT
<213> Corynebacterium glutamicum

<400> 2158
Met Ala Ile Ser Ile Gly Lys Ala Gly Gln Asn Leu Lys Gly Ser Val
1 5 10 15

Pro Ile Gly Lys Val Leu Phe Leu Ile Asp Ala Leu Ala Trp Ile Ser
20 25 30

Ala Leu Phe Ile Gly Val Val Leu Arg Tyr Glu Phe Asn Leu Ser Ser
35 40 45

Ile Asn Trp Ser Ala Phe Ala Trp Phe Gly Leu Ala Ala Val Ile Leu
50 55 60

Gln Phe Val Leu Gly Leu Ser Leu His Leu Tyr Arg Lys Gly Leu Arg
65 70 75 80

His Leu Phe Gly Ser Phe Glu Asp Thr Leu Asn Val Ser Ile Ser Val
85 90 95

Ile Val Val Gly Val Val Leu Trp Ile Ala Ser Leu Phe Val Gly Gln
100 105 110

Arg Trp Lys Ile Ser Arg Gly Val Met Leu Leu Val Ile Pro Leu Ala
115 120 125

Leu Val Phe Val Leu Ala Val Arg Tyr Leu Ala Arg Met Arg Val Glu
130 135 140

Arg Phe Arg Arg Pro Ala Ala Asp Ser Thr Pro Ala Leu Ile Leu Gly
145 150 155 160

Gly Gly Tyr Ile Gly Thr Asn Leu Ile Gln Trp Met Met Ser Asp Pro
165 170 175

Lys Ser Pro Phe Arg Pro Val Gly Val Ile Asp Asp Asn Pro Glu Leu
180 185 190

Ala Cys Gln Arg Val Arg Gly Val Pro Val Leu Gly Lys Phe Asp Asp
195 200 205

Ile Ala Gln Val Ala Ser Asp Thr Gly Ala Glu Leu Leu Ile Val Ala
210 215 220

Ile Gly Asp Ala Asp Ser Ala Leu Leu Arg Arg Val Gln Asp Thr Ala
225 230 235 240

Asn Lys Asn Gly Leu Ser Val Lys Val Met Pro Ala Ile Asp Arg Val
245 250 255

Val Ser Lys Gly Val Arg Gly Asn Asp Leu Arg Asp Leu Ser Ile Glu
260 265 270

Asp Leu Leu Gly Arg Gln Pro Val Glu Thr Asn Val Ser Glu Ile Thr
275 280 285

Gly Tyr Leu Thr Gly Lys Arg Val Leu Val Thr Gly Ala Gly Gly Ser

290 295 300

Ile Gly Ser Gln Leu Cys Thr Glu Ile Ala Lys Tyr Gly Pro Ala Glu
305 310 315 320

Leu Met Met Leu Asp Arg Asp Glu Thr Gly Leu Gln Gln Val Leu Ile
325 330 335

Asn Val Ala Gly Asn Gly Leu Leu Asp Thr Asp Ala Val Val Leu Ala
340 345 350

Asp Ile Arg Glu Ala Asp Ala Met Lys Glu Ile Phe Leu Lys Arg Lys
355 360 365

Pro Glu Val Val Phe His Ala Ala Ala Leu Lys His Leu Pro Met Leu
370 375 380

Glu Gln Tyr Pro Asp Glu Gly Trp Lys Thr Asn Val Leu Gly Thr Leu
385 390 395 400

Asn Val Leu Ala Ala Ala Glu Ala Val Gly Val Glu Thr Phe Val Asn
405 410 415

Ile Ser Thr Asp Lys Ala Ala Asn Pro Thr Ser Val Leu Gly His Ser
420 425 430

Lys Arg Val Ala Glu Lys Leu Thr Ala Trp Tyr Gly Gln Asn Ser Thr
435 440 445

Ser Lys Tyr Leu Ser Val Arg Phe Gly Asn Val Ile Gly Ser Arg Gly
450 455 460

Ser Met Leu Pro Thr Phe Thr Arg Leu Ile Met Glu Asp Lys Pro Leu
465 470 475 480

Thr Val Thr His Pro Asp Val Thr Arg Phe Phe Met Thr Ile Pro Glu
485 490 495

Ala Cys Gln Leu Val Leu Gln Ala Gly Gly Ile Gly Arg Ser Gly Glu
500 505 510

Val Leu Ile Leu Asp Met Gly Glu Pro Val Ser Ile Leu Glu Ile Ala
515 520 525

Gln Arg Met Ile Ala Met Ser Gly Lys Asp Ile Asp Ile Val Phe Thr
530 535 540

Gly Leu Arg Glu Gly Glu Lys Met His Glu Glu Leu Val Gly Asp Gly
545 550 555 560

Glu Thr Glu Asp Arg Pro Phe His Ser Lys Ile Ser His Ala His Ala
565 570 575

Glu Ser Leu Ala Pro Asn Asn Leu Asp Arg Asp Arg Phe Met Gln Arg
580 585 590

Ala Gly Lys Leu Ala Ser Thr Asp Ser Glu Ile Ile
595 600

<210> 2159

<211> 1557
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1534)
<223> RXA01273

<400> 2159
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tctattggtt aaaaattgat ctgcaagagg actgcaaaat atg gaa tta agg gaa 115
Met Glu Leu Arg Glu
1 5

tac gcg aca atc ctg atg aag aat tgg gtg ttg atc gtt atc gca tcc 163
Tyr Ala Thr Ile Leu Met Lys Asn Trp Val Leu Ile Val Ile Ala Ser
10 15 20

att ctt gga att gca gcg ggc gct ggt ttt tcc ctt cta gct aca ccg 211
Ile Leu Gly Ile Ala Ala Gly Ala Gly Phe Ser Leu Leu Ala Thr Pro
25 30 35

gag tat cag tca cgt act cag ttg tat gta tcg gtg cgg tcg ggg gct 259
Glu Tyr Gln Ser Arg Thr Gln Leu Tyr Val Ser Val Arg Ser Gly Ala
40 45 50

ggg aca acc tct gac atg gtt cag ggt gct aac ttt tcg cgt cag att 307
Gly Thr Thr Ser Asp Met Val Gln Gly Ala Asn Phe Ser Arg Gln Ile
55 60 65

gtg aat agt tat gtt gat gtc att aag acg ggt gtt gtt cta gag ccg 355
Val Asn Ser Tyr Val Asp Val Ile Lys Thr Gly Val Val Leu Glu Pro
70 75 80 85

gtt gtt gat gag ctt ggt ctg gag ttg acg gct aac cag ttg agt tct 403
Val Val Asp Glu Leu Gly Leu Glu Leu Thr Ala Asn Gln Leu Ser Ser
90 95 100

cat atc agt gcg gct tct cct gct gat act gcg ttg atc aac atc act 451
His Ile Ser Ala Ala Ser Pro Ala Asp Thr Ala Leu Ile Asn Ile Thr
105 110 115

gct tct agt cct tct cct cag cag gcg gct gag atc gcc aat gca gtg 499
Ala Ser Ser Pro Ser Pro Gln Gln Ala Ala Glu Ile Ala Asn Ala Val
120 125 130

ggg gag agt ttc aag aat gtg att cag act gaa ttg gaa cca gac tcc 547
Gly Glu Ser Phe Lys Asn Val Ile Gln Thr Glu Leu Glu Pro Asp Ser
135 140 145

ggc gat ggc atg agc ccg att aac ctg act act act cag gtg gct ctg 595
Gly Asp Gly Met Ser Pro Ile Asn Leu Thr Thr Thr Gln Val Ala Leu
150 155 160 165

gaa cca tct tct ccg gtc agt cct aat gtg atg atg aat atc ctc ctc 643
Glu Pro Ser Ser Pro Val Ser Pro Asn Val Met Met Asn Ile Leu Leu
170 175 180

ggc cta ctt gta ggt ctt gca ata ggt gtt ggt att gca gtg ctt cgc 691

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Gly Leu Leu Val Gly Leu Ala Ile Gly Val Gly Ile Ala Val Leu Arg
            185                 190                 195

gcg gct ttg gat act cgt att cat tcc ttg cgc gat att gaa gag gtt   739
Ala Ala Leu Asp Thr Arg Ile His Ser Leu Arg Asp Ile Glu Glu Val
        200                 205                 210

act gat aag cca ctt ttg ggc gga atc att gcg gat tct gaa gtt gag   787
Thr Asp Lys Pro Leu Leu Gly Gly Ile Ile Ala Asp Ser Glu Val Glu
    215                 220                 225

aag cac ccg ttg atc att aag cac aag ccg cat agt cct att gcg gag   835
Lys His Pro Leu Ile Ile Lys His Lys Pro His Ser Pro Ile Ala Glu
230                 235                 240                 245

tcc ttt cgt gcg tta cgt act aac ctg cag ttc ctt aac gtc ggc ggc   883
Ser Phe Arg Ala Leu Arg Thr Asn Leu Gln Phe Leu Asn Val Gly Gly
                250                 255                 260

tca tct tca gta ttt gtt atc tcc tct gct aat cct ggt gag ggt aag   931
Ser Ser Ser Val Phe Val Ile Ser Ser Ala Asn Pro Gly Glu Gly Lys
            265                 270                 275

tca acc act tct gta aac cta gct ttg gcg ctt gca gag gcc ggc tcc   979
Ser Thr Thr Ser Val Asn Leu Ala Leu Ala Leu Ala Glu Ala Gly Ser
        280                 285                 290

cgt gta gcg ctg atc gaa gct gat ctt cgc ttg cca cga gtg agc aag   1027
Arg Val Ala Leu Ile Glu Ala Asp Leu Arg Leu Pro Arg Val Ser Lys
    295                 300                 305

tac ctc gga gtt gag ggc aac gca ggt ctg act gac att ctc att ggc   1075
Tyr Leu Gly Val Glu Gly Asn Ala Gly Leu Thr Asp Ile Leu Ile Gly
310                 315                 320                 325

aag gcc gag gtt aat gat gtg ttg cag cgt tgg ggt agg act cag ttg   1123
Lys Ala Glu Val Asn Asp Val Leu Gln Arg Trp Gly Arg Thr Gln Leu
                330                 335                 340

tac tat ctc ccg gca ggg cgc att ccg ccg aac ccg agt gag ttg ctt   1171
Tyr Tyr Leu Pro Ala Gly Arg Ile Pro Pro Asn Pro Ser Glu Leu Leu
            345                 350                 355

ggt tca gct gag atg gac aag gtc att gcg gag ctt gag gaa agc ttt   1219
Gly Ser Ala Glu Met Asp Lys Val Ile Ala Glu Leu Glu Glu Ser Phe
        360                 365                 370

gat tat gtg atc atc gat gcc cct ccg gcg ttg gcg gtt acc gat gct   1267
Asp Tyr Val Ile Ile Asp Ala Pro Pro Ala Leu Ala Val Thr Asp Ala
    375                 380                 385

gca gtt att ggt cat ggc aag gct ggc atc ctg att gcg gtc tcc gca   1315
Ala Val Ile Gly His Gly Lys Ala Gly Ile Leu Ile Ala Val Ser Ala
390                 395                 400                 405

ggt tct aca aag aag cct gag ttg gaa gct acg ctg tcc acg ctt gag   1363
Gly Ser Thr Lys Lys Pro Glu Leu Glu Ala Thr Leu Ser Thr Leu Glu
                410                 415                 420

aat gcg gat gcc aat gtt gtt ggc gtt gtc gct acg atg ctc ccg cct   1411
Asn Ala Asp Ala Asn Val Val Gly Val Val Ala Thr Met Leu Pro Pro
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            425                 430                 435

aag tct gtg gct ggt tat ggc tac gga aat tac ggc tac ggc gac acc   1459
Lys Ser Val Ala Gly Tyr Gly Tyr Gly Asn Tyr Gly Tyr Gly Asp Thr
        440                 445                 450

tcc aaa atc aat gcc cct aag ccc gac aac acc gaa cta acc acc acc   1507
Ser Lys Ile Asn Ala Pro Lys Pro Asp Asn Thr Glu Leu Thr Thr Thr
    455                 460                 465

gat gct tcc aag gcc aac aat gag caa tagcttcact attctcactg         1554
Asp Ala Ser Lys Ala Asn Asn Glu Gln
470                 475

tct                                                               1557


<210> 2160
<211> 478
<212> PRT
<213> Corynebacterium glutamicum

<400> 2160
Met Glu Leu Arg Glu Tyr Ala Thr Ile Leu Met Lys Asn Trp Val Leu
  1               5                  10                  15

Ile Val Ile Ala Ser Ile Leu Gly Ile Ala Ala Gly Ala Gly Phe Ser
             20                  25                  30

Leu Leu Ala Thr Pro Glu Tyr Gln Ser Arg Thr Gln Leu Tyr Val Ser
         35                  40                  45

Val Arg Ser Gly Ala Gly Thr Thr Ser Asp Met Val Gln Gly Ala Asn
     50                  55                  60

Phe Ser Arg Gln Ile Val Asn Ser Tyr Val Asp Val Ile Lys Thr Gly
 65                  70                  75                  80

Val Val Leu Glu Pro Val Val Asp Glu Leu Gly Leu Glu Leu Thr Ala
                 85                  90                  95

Asn Gln Leu Ser Ser His Ile Ser Ala Ala Ser Pro Ala Asp Thr Ala
            100                 105                 110

Leu Ile Asn Ile Thr Ala Ser Ser Pro Ser Pro Gln Gln Ala Ala Glu
        115                 120                 125

Ile Ala Asn Ala Val Gly Glu Ser Phe Lys Asn Val Ile Gln Thr Glu
    130                 135                 140

Leu Glu Pro Asp Ser Gly Asp Gly Met Ser Pro Ile Asn Leu Thr Thr
145                 150                 155                 160

Thr Gln Val Ala Leu Glu Pro Ser Ser Pro Val Ser Pro Asn Val Met
                165                 170                 175

Met Asn Ile Leu Leu Gly Leu Leu Val Gly Leu Ala Ile Gly Val Gly
            180                 185                 190

Ile Ala Val Leu Arg Ala Ala Leu Asp Thr Arg Ile His Ser Leu Arg
        195                 200                 205
```

```
Asp Ile Glu Glu Val Thr Asp Lys Pro Leu Leu Gly Gly Ile Ile Ala
    210                 215                 220

Asp Ser Glu Val Glu Lys His Pro Leu Ile Ile Lys His Lys Pro His
225                 230                 235                 240

Ser Pro Ile Ala Glu Ser Phe Arg Ala Leu Arg Thr Asn Leu Gln Phe
                245                 250                 255

Leu Asn Val Gly Gly Ser Ser Ser Val Phe Val Ile Ser Ser Ala Asn
            260                 265                 270

Pro Gly Glu Gly Lys Ser Thr Thr Ser Val Asn Leu Ala Leu Ala Leu
        275                 280                 285

Ala Glu Ala Gly Ser Arg Val Ala Leu Ile Glu Ala Asp Leu Arg Leu
    290                 295                 300

Pro Arg Val Ser Lys Tyr Leu Gly Val Glu Gly Asn Ala Gly Leu Thr
305                 310                 315                 320

Asp Ile Leu Ile Gly Lys Ala Glu Val Asn Asp Val Leu Gln Arg Trp
                325                 330                 335

Gly Arg Thr Gln Leu Tyr Tyr Leu Pro Ala Gly Arg Ile Pro Pro Asn
            340                 345                 350

Pro Ser Glu Leu Leu Gly Ser Ala Glu Met Asp Lys Val Ile Ala Glu
        355                 360                 365

Leu Glu Glu Ser Phe Asp Tyr Val Ile Ile Asp Ala Pro Pro Ala Leu
    370                 375                 380

Ala Val Thr Asp Ala Ala Val Ile Gly His Gly Lys Ala Gly Ile Leu
385                 390                 395                 400

Ile Ala Val Ser Ala Gly Ser Thr Lys Lys Pro Glu Leu Glu Ala Thr
                405                 410                 415

Leu Ser Thr Leu Glu Asn Ala Asp Ala Asn Val Val Gly Val Val Ala
            420                 425                 430

Thr Met Leu Pro Pro Lys Ser Val Ala Gly Tyr Gly Tyr Gly Asn Tyr
        435                 440                 445

Gly Tyr Gly Asp Thr Ser Lys Ile Asn Ala Pro Lys Pro Asp Asn Thr
    450                 455                 460

Glu Leu Thr Thr Thr Asp Ala Ser Lys Ala Asn Asn Glu Gln
465                 470                 475


<210> 2161
<211> 903
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(880)
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<223> RXA01282

<400> 2161

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caggatgggt cggaacgttc gcgtcgtttg cggtgtggtt ctgggtcatt tggtgggcag 60

cggtaggaaa tacaaaaagc ccactctaag atggcagggt atg gat gag ctg ctc   115
                                            Met Asp Glu Leu Leu
                                              1               5

aaa cag gaa gtc aag gat ttc ctc acc acc agg cgt gca cgg att acg   163
Lys Gln Glu Val Lys Asp Phe Leu Thr Thr Arg Arg Ala Arg Ile Thr
                 10                  15                  20

ccg gcc gct gcg gga cta gaa acg cag ccg tgg agt gat cgt cgg gtg   211
Pro Ala Ala Ala Gly Leu Glu Thr Gln Pro Trp Ser Asp Arg Arg Val
             25                  30                  35

ccg ggg ctt cgg cgg gaa gaa gtc gcg gat ctg gcg ggc att tct ttg   259
Pro Gly Leu Arg Arg Glu Glu Val Ala Asp Leu Ala Gly Ile Ser Leu
         40                  45                  50

gag tat tac atc cgg ttt gag cgc gga aat ctc aag ggt gca tcg cct   307
Glu Tyr Tyr Ile Arg Phe Glu Arg Gly Asn Leu Lys Gly Ala Ser Pro
     55                  60                  65

gaa ata ttg caa tcg ttg gct aag gct ctc caa ctg agc cca att gag   355
Glu Ile Leu Gln Ser Leu Ala Lys Ala Leu Gln Leu Ser Pro Ile Glu
 70                  75                  80                  85

cgc gaa cac ctt cac aat ttg gct tat cgc gcc gac cat ccg cgc aac   403
Arg Glu His Leu His Asn Leu Ala Tyr Arg Ala Asp His Pro Arg Asn
                 90                  95                 100

cta cct agt gca gag acc cca acg gca ccc ctc cag gac atc gtt gat   451
Leu Pro Ser Ala Glu Thr Pro Thr Ala Pro Leu Gln Asp Ile Val Asp
            105                 110                 115

gcg gtc aca gat aaa ccg gcg tgg atc cgc aac gag cag atg gat att   499
Ala Val Thr Asp Lys Pro Ala Trp Ile Arg Asn Glu Gln Met Asp Ile
        120                 125                 130

ttg gct aca aat cgg ctc tgc gcg gaa ctt tac gcc ccg att ttc aag   547
Leu Ala Thr Asn Arg Leu Cys Ala Glu Leu Tyr Ala Pro Ile Phe Lys
    135                 140                 145

gat ctg ccc gat cgg ccc aac act gcg cgg cat tgc ttt atc ggc gca   595
Asp Leu Pro Asp Arg Pro Asn Thr Ala Arg His Cys Phe Ile Gly Ala
150                 155                 160                 165

aca gcc tcc gag ttc tgg gtg gac cgg gat cag ttc agt gcg gag ttc   643
Thr Ala Ser Glu Phe Trp Val Asp Arg Asp Gln Phe Ser Ala Glu Phe
                170                 175                 180

gct gcc aaa cta cgc ctc gag tac gcc cgg cgc ccc agc gtg cca ggt   691
Ala Ala Lys Leu Arg Leu Glu Tyr Ala Arg Arg Pro Ser Val Pro Gly
            185                 190                 195

tta aag gag ctt atc gac gag ctc cat cag aaa agt tct gtt ttc cgc   739
Leu Lys Glu Leu Ile Asp Glu Leu His Gln Lys Ser Ser Val Phe Arg
        200                 205                 210
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gat aat tgg gcg tct gct gat gtt ttg tca ttc ggc tct ggc atc aaa   787
Asp Asn Trp Ala Ser Ala Asp Val Leu Ser Phe Gly Ser Gly Ile Lys
    215                 220                 225

cgt ttc agg cac cca aca ctg ggg gag cgg gtc tat gaa tac gag acg   835
Arg Phe Arg His Pro Thr Leu Gly Glu Arg Val Tyr Glu Tyr Glu Thr
230                 235                 240                 245

ttt aat ctc aat agt gca ccg ggg tat gtg ttg agc att tac ttt       880
Phe Asn Leu Asn Ser Ala Pro Gly Tyr Val Leu Ser Ile Tyr Phe
                250                 255                 260

taggtggtgg aggggcgcgt cga                                        903


<210> 2162
<211> 260
<212> PRT
<213> Corynebacterium glutamicum

<400> 2162
Met Asp Glu Leu Leu Lys Gln Glu Val Lys Asp Phe Leu Thr Thr Arg
  1               5                  10                  15

Arg Ala Arg Ile Thr Pro Ala Ala Ala Gly Leu Glu Thr Gln Pro Trp
             20                  25                  30

Ser Asp Arg Arg Val Pro Gly Leu Arg Arg Glu Glu Val Ala Asp Leu
         35                  40                  45

Ala Gly Ile Ser Leu Glu Tyr Tyr Ile Arg Phe Glu Arg Gly Asn Leu
     50                  55                  60

Lys Gly Ala Ser Pro Glu Ile Leu Gln Ser Leu Ala Lys Ala Leu Gln
 65                  70                  75                  80

Leu Ser Pro Ile Glu Arg Glu His Leu His Asn Leu Ala Tyr Arg Ala
                 85                  90                  95

Asp His Pro Arg Asn Leu Pro Ser Ala Glu Thr Pro Thr Ala Pro Leu
            100                 105                 110

Gln Asp Ile Val Asp Ala Val Thr Asp Lys Pro Ala Trp Ile Arg Asn
        115                 120                 125

Glu Gln Met Asp Ile Leu Ala Thr Asn Arg Leu Cys Ala Glu Leu Tyr
    130                 135                 140

Ala Pro Ile Phe Lys Asp Leu Pro Asp Arg Pro Asn Thr Ala Arg His
145                 150                 155                 160

Cys Phe Ile Gly Ala Thr Ala Ser Glu Phe Trp Val Asp Arg Asp Gln
                165                 170                 175

Phe Ser Ala Glu Phe Ala Ala Lys Leu Arg Leu Glu Tyr Ala Arg Arg
            180                 185                 190

Pro Ser Val Pro Gly Leu Lys Glu Leu Ile Asp Glu Leu His Gln Lys
        195                 200                 205

Ser Ser Val Phe Arg Asp Asn Trp Ala Ser Ala Asp Val Leu Ser Phe
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    210                 215                 220

Gly Ser Gly Ile Lys Arg Phe Arg His Pro Thr Leu Gly Glu Arg Val
225                 230                 235                 240

Tyr Glu Tyr Glu Thr Phe Asn Leu Asn Ser Ala Pro Gly Tyr Val Leu
                245                 250                 255

Ser Ile Tyr Phe
            260


<210> 2163
<211> 789
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(766)
<223> RXA01294

<400> 2163
atgaagggat accgctcctt ttcgggggta cagcactcca gcaagactca ttcggctcag 60

ttagagttca ccacaacgac tcaaaaaaga aagtggcagc atg tct acg att cct   115
                                            Met Ser Thr Ile Pro
                                              1               5

gat gtt ttc acc agt gaa gtg ttc cct gaa atc agt ggc acc aaa gaa   163
Asp Val Phe Thr Ser Glu Val Phe Pro Glu Ile Ser Gly Thr Lys Glu
                10                  15                  20

ttc cgt ggc ctg act tat atg ttc ttt gat caa ttc act ttg ccc acc   211
Phe Arg Gly Leu Thr Tyr Met Phe Phe Asp Gln Phe Thr Leu Pro Thr
            25                  30                  35

gca gaa cag ctt gag caa gct aaa gca gct ggc tgg tca ctg atc acc   259
Ala Glu Gln Leu Glu Gln Ala Lys Ala Ala Gly Trp Ser Leu Ile Thr
        40                  45                  50

tgg gga tgg tgg aat agc gac acc gat ctt gag gat gtc gaa ttg gaa   307
Trp Gly Trp Trp Asn Ser Asp Thr Asp Leu Glu Asp Val Glu Leu Glu
    55                  60                  65

gac atc act aat gaa ggc gac agc cta cca aaa ctc acg gat gaa ttc   355
Asp Ile Thr Asn Glu Gly Asp Ser Leu Pro Lys Leu Thr Asp Glu Phe
70                  75                  80                  85

gct gtg tct tca ctg agc acc ttc gat cta aat tcc caa ggt ctg ccc   403
Ala Val Ser Ser Leu Ser Thr Phe Asp Leu Asn Ser Gln Gly Leu Pro
                90                  95                  100

aat gat gat cgt gag ccg caa cca att gaa gaa gcc gac tca cta gat   451
Asn Asp Asp Arg Glu Pro Gln Pro Ile Glu Glu Ala Asp Ser Leu Asp
            105                 110                 115

gac atc ttc tcc gag gaa gag ggc tgg ggt cta atg gca atc aat tgc   499
Asp Ile Phe Ser Glu Glu Glu Gly Trp Gly Leu Met Ala Ile Asn Cys
        120                 125                 130
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ccg aat tgg caa gtc cca gca gcg tgt gaa tgg ctc ggc tgc atg aat   547
Pro Asn Trp Gln Val Pro Ala Ala Cys Glu Trp Leu Gly Cys Met Asn
    135                 140                 145

gtt ggt gaa cca ttt gaa atg tca cac gta ctt agg gtg tgg cag aac   595
Val Gly Glu Pro Phe Glu Met Ser His Val Leu Arg Val Trp Gln Asn
150                 155                 160                 165

agt tgg ggc gtc gag gcc ctg gct ttt ggt ggt gaa gaa gac gac gcg   643
Ser Trp Gly Val Glu Ala Leu Ala Phe Gly Gly Glu Glu Asp Asp Ala
                170                 175                 180

gat ctg ctg ctt cga gtc cct gaa gaa agc gaa gag cta ctg aag gct   691
Asp Leu Leu Leu Arg Val Pro Glu Glu Ser Glu Glu Leu Leu Lys Ala
            185                 190                 195

ctc gca gtc gct tct gac caa gtc act acc tac aag cat gaa gat ctg   739
Leu Ala Val Ala Ser Asp Gln Val Thr Thr Tyr Lys His Glu Asp Leu
        200                 205                 210

gga ttc tta gct agt ctt tgg ttt gac taactacaat caatgtcatg         786
Gly Phe Leu Ala Ser Leu Trp Phe Asp
    215                 220

acc                                                              789


<210> 2164
<211> 222
<212> PRT
<213> Corynebacterium glutamicum

<400> 2164
Met Ser Thr Ile Pro Asp Val Phe Thr Ser Glu Val Phe Pro Glu Ile
  1               5                  10                  15

Ser Gly Thr Lys Glu Phe Arg Gly Leu Thr Tyr Met Phe Phe Asp Gln
             20                  25                  30

Phe Thr Leu Pro Thr Ala Glu Gln Leu Glu Gln Ala Lys Ala Ala Gly
         35                  40                  45

Trp Ser Leu Ile Thr Trp Gly Trp Trp Asn Ser Asp Thr Asp Leu Glu
     50                  55                  60

Asp Val Glu Leu Glu Asp Ile Thr Asn Glu Gly Asp Ser Leu Pro Lys
 65                  70                  75                  80

Leu Thr Asp Glu Phe Ala Val Ser Ser Leu Ser Thr Phe Asp Leu Asn
                 85                  90                  95

Ser Gln Gly Leu Pro Asn Asp Asp Arg Glu Pro Gln Pro Ile Glu Glu
            100                 105                 110

Ala Asp Ser Leu Asp Asp Ile Phe Ser Glu Glu Glu Gly Trp Gly Leu
        115                 120                 125

Met Ala Ile Asn Cys Pro Asn Trp Gln Val Pro Ala Ala Cys Glu Trp
    130                 135                 140

Leu Gly Cys Met Asn Val Gly Glu Pro Phe Glu Met Ser His Val Leu
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145                 150                 155                 160

Arg Val Trp Gln Asn Ser Trp Gly Val Glu Ala Leu Ala Phe Gly Gly
                165                 170                 175

Glu Glu Asp Asp Ala Asp Leu Leu Leu Arg Val Pro Glu Glu Ser Glu
            180                 185                 190

Glu Leu Leu Lys Ala Leu Ala Val Ala Ser Asp Gln Val Thr Thr Tyr
        195                 200                 205

Lys His Glu Asp Leu Gly Phe Leu Ala Ser Leu Trp Phe Asp
    210                 215                 220


<210> 2165
<211> 1098
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1075)
<223> RXA01295

<400> 2165
tttctggtgt taccctcggg taattgtaaa aaattcattg attaaaaacg atcagccaat 60

tggcatgctc agactccttg tgaagaaagt gacagtttcg atg acc gaa aat ctt   115
                                              Met Thr Glu Asn Leu
                                                1               5

gat aat gcg ttg cta tcc atg cgg atg aaa cct gta caa atg gcg ctt   163
Asp Asn Ala Leu Leu Ser Met Arg Met Lys Pro Val Gln Met Ala Leu
                10                  15                  20

atg aca ctg ggc tac aac cat gac atg gcg gtg acc gat tcc ggt atg   211
Met Thr Leu Gly Tyr Asn His Asp Met Ala Val Thr Asp Ser Gly Met
            25                  30                  35

gaa ctt ata gtg cgc cgc cca ggg ctg acc gtg aac ttc aac ttg gat   259
Glu Leu Ile Val Arg Arg Pro Gly Leu Thr Val Asn Phe Asn Leu Asp
        40                  45                  50

tcg gtc acc ttg tgc atc gtc gct gat ttc atg tgg cat ggc tgt gtc   307
Ser Val Thr Leu Cys Ile Val Ala Asp Phe Met Trp His Gly Cys Val
    55                  60                  65

cct gca aag aaa cag gca gag tac ctg cgg gcc gct aat gaa ttc aac   355
Pro Ala Lys Lys Gln Ala Glu Tyr Leu Arg Ala Ala Asn Glu Phe Asn
70                  75                  80                  85

agg cca acc cgt gat ctg cag gtg gtt tta gat gaa gct gat tca aag   403
Arg Pro Thr Arg Asp Leu Gln Val Val Leu Asp Glu Ala Asp Ser Lys
                90                  95                  100

aac atg act gtg cga ggt cgt gaa ttc ttc ttc tca agc gtc ggc gca   451
Asn Met Thr Val Arg Gly Arg Glu Phe Phe Phe Ser Ser Val Gly Ala
            105                 110                 115

acg tgg gaa cag tcg gca gag ttc gtg cac tac tgc atg aat gat gtg   499
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Thr Trp Glu Gln Ser Ala Glu Phe Val His Tyr Cys Met Asn Asp Val
        120                 125                 130

gca acg act ttc gtg tct tgg tgc gaa caa atc tgg ccg aag ttt tcc   547
Ala Thr Thr Phe Val Ser Trp Cys Glu Gln Ile Trp Pro Lys Phe Ser
    135                 140                 145

cct gaa cgc gta gag ttc aac gca act cct cca gat gtg gat ttc gag   595
Pro Glu Arg Val Glu Phe Asn Ala Thr Pro Pro Asp Val Asp Phe Glu
150                 155                 160                 165

ttc tct gaa gat caa ctc aaa gaa ggc aat ccc ttc ggg ctg att gac   643
Phe Ser Glu Asp Gln Leu Lys Glu Gly Asn Pro Phe Gly Leu Ile Asp
                170                 175                 180

gaa ccc acc ccg ctg gtt tct ttg gat cgt atc tac caa caa tac gaa   691
Glu Pro Thr Pro Leu Val Ser Leu Asp Arg Ile Tyr Gln Gln Tyr Glu
            185                 190                 195

tta atg ggt gcg gat caa ctc aag atg ggg gag gac ttc gtt gag tat   739
Leu Met Gly Ala Asp Gln Leu Lys Met Gly Glu Asp Phe Val Glu Tyr
        200                 205                 210

ctg cat atg ggt caa cgt gtc agt gca tgg ttg acc gat ggc aac aac   787
Leu His Met Gly Gln Arg Val Ser Ala Trp Leu Thr Asp Gly Asn Asn
    215                 220                 225

ggc agc gat cga aaa acc cta gcg gtg tct tcc ggt aca ggt gtg aaa   835
Gly Ser Asp Arg Lys Thr Leu Ala Val Ser Ser Gly Thr Gly Val Lys
230                 235                 240                 245

atc aaa aac aag aag caa ctt cag gaa ctt ctt gga ctg tgc aac ctg   883
Ile Lys Asn Lys Lys Gln Leu Gln Glu Leu Leu Gly Leu Cys Asn Leu
                250                 255                 260

tac tcg aaa gaa cat gta ctg gtc aca gta ttt gcg gaa gag atc gaa   931
Tyr Ser Lys Glu His Val Leu Val Thr Val Phe Ala Glu Glu Ile Glu
            265                 270                 275

aac ggc gca agg tgg ggt att ttc gcc gaa gca cgc atc gat cta ccg   979
Asn Gly Ala Arg Trp Gly Ile Phe Ala Glu Ala Arg Ile Asp Leu Pro
        280                 285                 290

gca ggg tta aac gat cat cag ttg tgg gta ttc ctc gcc aac tcc agc   1027
Ala Gly Leu Asn Asp His Gln Leu Trp Val Phe Leu Ala Asn Ser Ser
    295                 300                 305

aaa tgg act gca gag gtg tgc ctg acc gtg gca cac cga ctg cag aac   1075
Lys Trp Thr Ala Glu Val Cys Leu Thr Val Ala His Arg Leu Gln Asn
310                 315                 320                 325

taaaggcaga acttaagcgt tca                                        1098


<210> 2166
<211> 325
<212> PRT
<213> Corynebacterium glutamicum

<400> 2166
Met Thr Glu Asn Leu Asp Asn Ala Leu Leu Ser Met Arg Met Lys Pro
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  1               5                  10                  15

Val Gln Met Ala Leu Met Thr Leu Gly Tyr Asn His Asp Met Ala Val
            20                  25                  30

Thr Asp Ser Gly Met Glu Leu Ile Val Arg Arg Pro Gly Leu Thr Val
        35                  40                  45

Asn Phe Asn Leu Asp Ser Val Thr Leu Cys Ile Val Ala Asp Phe Met
    50                  55                  60

Trp His Gly Cys Val Pro Ala Lys Lys Gln Ala Glu Tyr Leu Arg Ala
65                  70                  75                  80

Ala Asn Glu Phe Asn Arg Pro Thr Arg Asp Leu Gln Val Val Leu Asp
                85                  90                  95

Glu Ala Asp Ser Lys Asn Met Thr Val Arg Gly Arg Glu Phe Phe Phe
            100                 105                 110

Ser Ser Val Gly Ala Thr Trp Glu Gln Ser Ala Glu Phe Val His Tyr
        115                 120                 125

Cys Met Asn Asp Val Ala Thr Thr Phe Val Ser Trp Cys Glu Gln Ile
    130                 135                 140

Trp Pro Lys Phe Ser Pro Glu Arg Val Glu Phe Asn Ala Thr Pro Pro
145                 150                 155                 160

Asp Val Asp Phe Glu Phe Ser Glu Asp Gln Leu Lys Glu Gly Asn Pro
                165                 170                 175

Phe Gly Leu Ile Asp Glu Pro Thr Pro Leu Val Ser Leu Asp Arg Ile
            180                 185                 190

Tyr Gln Gln Tyr Glu Leu Met Gly Ala Asp Gln Leu Lys Met Gly Glu
        195                 200                 205

Asp Phe Val Glu Tyr Leu His Met Gly Gln Arg Val Ser Ala Trp Leu
    210                 215                 220

Thr Asp Gly Asn Asn Gly Ser Asp Arg Lys Thr Leu Ala Val Ser Ser
225                 230                 235                 240

Gly Thr Gly Val Lys Ile Lys Asn Lys Lys Gln Leu Gln Glu Leu Leu
                245                 250                 255

Gly Leu Cys Asn Leu Tyr Ser Lys Glu His Val Leu Val Thr Val Phe
            260                 265                 270

Ala Glu Glu Ile Glu Asn Gly Ala Arg Trp Gly Ile Phe Ala Glu Ala
        275                 280                 285

Arg Ile Asp Leu Pro Ala Gly Leu Asn Asp His Gln Leu Trp Val Phe
    290                 295                 300

Leu Ala Asn Ser Ser Lys Trp Thr Ala Glu Val Cys Leu Thr Val Ala
305                 310                 315                 320

His Arg Leu Gln Asn
                325
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<210> 2167
<211> 609
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(586)
<223> RXA01304

<400> 2167
atgcaggtaa acgaatttgt gcttatatca acattcgtga ttcggcaaaa ttaattaaac 60

tgaaaaaggg gattaattac ccccacttga ggagaaattg atg ccc gca cag aac 115
Met Pro Ala Gln Asn
1 5

aaa aac ctc cca gga tcc gtc atc gtt gtg tct gat cgg att aaa tcg 163
Lys Asn Leu Pro Gly Ser Val Ile Val Val Ser Asp Arg Ile Lys Ser
10 15 20

gga gaa aga att gat aaa gca gga ccc gta gca gta gac ctt ctt cag 211
Gly Glu Arg Ile Asp Lys Ala Gly Pro Val Ala Val Asp Leu Leu Gln
25 30 35

gaa tca ggc gtg gag att tcc aca ttc acc gtc gtg gag gag ggc ttt 259
Glu Ser Gly Val Glu Ile Ser Thr Phe Thr Val Val Glu Glu Gly Phe
40 45 50

gaa cct gtc cat caa gaa ttg gtt aag gcg ttg gcg cgc cgg gat cgc 307
Glu Pro Val His Gln Glu Leu Val Lys Ala Leu Ala Arg Arg Asp Arg
55 60 65

gtc atc atc acc atc ggc gga acg ggc gtg ggg cct aga aat cgg acg 355
Val Ile Ile Thr Ile Gly Gly Thr Gly Val Gly Pro Arg Asn Arg Thr
70 75 80 85

ccg gag gcc aca gaa ccg cac atc gat acg cta ctg ccg ggt ctg atg 403
Pro Glu Ala Thr Glu Pro His Ile Asp Thr Leu Leu Pro Gly Leu Met
90 95 100

acg cag att ttg ttc tct gga ctg tcc aat acc gcg cag gcg ggg tta 451
Thr Gln Ile Leu Phe Ser Gly Leu Ser Asn Thr Ala Gln Ala Gly Leu
105 110 115

tct cgg ggg ctg gtg ggc ttg agt gct cgc gat tcc acg gcc gcg ctc 499
Ser Arg Gly Leu Val Gly Leu Ser Ala Arg Asp Ser Thr Ala Ala Leu
120 125 130

atc gtc aac gcg ccg agt tct tcc ggg ggc gtg cgc gac gcg ctc ggg 547
Ile Val Asn Ala Pro Ser Ser Ser Gly Gly Val Arg Asp Ala Leu Gly
135 140 145

gtg gtc tgc ccg ctt ttc ggt tcc att ttt gag cgt ctt taaaagattt 596
Val Val Cys Pro Leu Phe Gly Ser Ile Phe Glu Arg Leu
150 155 160

ttgcttatcg acg 609

<210> 2168
<211> 162
<212> PRT
<213> Corynebacterium glutamicum

<400> 2168
Met Pro Ala Gln Asn Lys Asn Leu Pro Gly Ser Val Ile Val Val Ser
1 5 10 15

Asp Arg Ile Lys Ser Gly Glu Arg Ile Asp Lys Ala Gly Pro Val Ala
20 25 30

Val Asp Leu Leu Gln Glu Ser Gly Val Glu Ile Ser Thr Phe Thr Val
35 40 45

Val Glu Glu Gly Phe Glu Pro Val His Gln Glu Leu Val Lys Ala Leu
50 55 60

Ala Arg Arg Asp Arg Val Ile Ile Thr Ile Gly Gly Thr Gly Val Gly
65 70 75 80

Pro Arg Asn Arg Thr Pro Glu Ala Thr Glu Pro His Ile Asp Thr Leu
85 90 95

Leu Pro Gly Leu Met Thr Gln Ile Leu Phe Ser Gly Leu Ser Asn Thr
100 105 110

Ala Gln Ala Gly Leu Ser Arg Gly Leu Val Gly Leu Ser Ala Arg Asp
115 120 125

Ser Thr Ala Ala Leu Ile Val Asn Ala Pro Ser Ser Ser Gly Gly Val
130 135 140

Arg Asp Ala Leu Gly Val Val Cys Pro Leu Phe Gly Ser Ile Phe Glu
145 150 155 160

Arg Leu

<210> 2169
<211> 450
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(427)
<223> RXA01310

<400> 2169
aaggaacgtg cgcgtgcagc tttccgaggc aaagacgact agtctttaat ccaagtaagt 60

accggttcag acagttaaac cagaaagacg agtgaacacc atg tcc tcc gcg aaa 115
Met Ser Ser Ala Lys
1 5

aag aaa ccc gca ccg gag cgt atg cac tac atc aag ggc tat gta cct 163
Lys Lys Pro Ala Pro Glu Arg Met His Tyr Ile Lys Gly Tyr Val Pro
10 15 20

```
gtg gcg tat agc tct cca cac tca tcc ctc gag cgc agc gca acc tgg   211
Val Ala Tyr Ser Ser Pro His Ser Ser Leu Glu Arg Ser Ala Thr Trp
             25                  30                  35

ttg ggc atg gga ttc ctc ctc act gct ctg gca ggc gtt ggc gca gtc   259
Leu Gly Met Gly Phe Leu Leu Thr Ala Leu Ala Gly Val Gly Ala Val
         40                  45                  50

ctc ttc gca gtc ggc gca aac agc gtt ggc cag cag cag gaa cac tgg   307
Leu Phe Ala Val Gly Ala Asn Ser Val Gly Gln Gln Gln Glu His Trp
     55                  60                  65

gtc ctc tac agc atc atc ggt gtt gta ttc gcc gtt gtc tgc aca gtt   355
Val Leu Tyr Ser Ile Ile Gly Val Val Phe Ala Val Val Cys Thr Val
 70                  75                  80                  85

ttg ggc acc gtc ctg atc atc aag ggc cga gca cct tac aac cgt tac   403
Leu Gly Thr Val Leu Ile Ile Lys Gly Arg Ala Pro Tyr Asn Arg Tyr
                 90                  95                 100

gtc aag gaa acc ggc cgt acg cag tagtttctgt atgcaggttc ttt         450
Val Lys Glu Thr Gly Arg Thr Gln
            105
```

Sequence Listing

<210> 2170
<211> 109
<212> PRT
<213> Corynebacterium glutamicum

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<400> 2170
Met Ser Ser Ala Lys Lys Lys Pro Ala Pro Glu Arg Met His Tyr Ile
  1               5                  10                  15

Lys Gly Tyr Val Pro Val Ala Tyr Ser Ser Pro His Ser Ser Leu Glu
             20                  25                  30

Arg Ser Ala Thr Trp Leu Gly Met Gly Phe Leu Leu Thr Ala Leu Ala
         35                  40                  45

Gly Val Gly Ala Val Leu Phe Ala Val Gly Ala Asn Ser Val Gly Gln
     50                  55                  60

Gln Gln Glu His Trp Val Leu Tyr Ser Ile Ile Gly Val Val Phe Ala
 65                  70                  75                  80

Val Val Cys Thr Val Leu Gly Thr Val Leu Ile Ile Lys Gly Arg Ala
                 85                  90                  95

Pro Tyr Asn Arg Tyr Val Lys Glu Thr Gly Arg Thr Gln
            100                 105
```

<210> 2171
<211> 968
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (1)..(945)
<223> RXA01313

<400> 2171

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gcc cta cgc ctc att tca cag ctg ctt gca cca tct gcg gcg ttg aat   48
Ala Leu Arg Leu Ile Ser Gln Leu Leu Ala Pro Ser Ala Ala Leu Asn
  1               5                  10                  15

ttt aag tcc gag cgc aat gcc gtc gac gtg gca aaa cac atg ctc gcc   96
Phe Lys Ser Glu Arg Asn Ala Val Asp Val Ala Lys His Met Leu Ala
             20                  25                  30

agc cag gcc caa caa cgc ggt tcc gca ctc gtt gcg cta gac acc cgc   144
Ser Gln Ala Gln Gln Arg Gly Ser Ala Leu Val Ala Leu Asp Thr Arg
         35                  40                  45

tcg gaa aac gcc gac gcc gcc acg gca tta aga aag tca ctg ctc atc   192
Ser Glu Asn Ala Asp Ala Ala Thr Ala Leu Arg Lys Ser Leu Leu Ile
     50                  55                  60

cgc agc tgg acg cag cgc ggc acc cac caa ata ctt gcc gcc gaa gac   240
Arg Ser Trp Thr Gln Arg Gly Thr His Gln Ile Leu Ala Ala Glu Asp
 65                  70                  75                  80

gtc cgc tgg atg acg cta cta tgc tcc cca cgc atc ctg gct gct tca   288
Val Arg Trp Met Thr Leu Leu Cys Ser Pro Arg Ile Leu Ala Ala Ser
                 85                  90                  95

gcc aag cgc cgc tcc agc ctt tcg ctt gat agc gcc gca gtc cag cgc   336
Ala Lys Arg Arg Ser Ser Leu Ser Leu Asp Ser Ala Ala Val Gln Arg
            100                 105                 110

gcc cgc gac gca cta aca acc gcc gcc gaa aaa tcc ccc gta tcc aga   384
Ala Arg Asp Ala Leu Thr Thr Ala Ala Glu Lys Ser Pro Val Ser Arg
        115                 120                 125

acc cag gcc tac gaa att ttc cga tcc gta gac gtt gac ccc ggc gag   432
Thr Gln Ala Tyr Glu Ile Phe Arg Ser Val Asp Val Asp Pro Gly Glu
    130                 135                 140

cac aga ggc caa cat tta ctc cgg cat ttc ggt ggc gaa ggt gac atc   480
His Arg Gly Gln His Leu Leu Arg His Phe Gly Gly Glu Gly Asp Ile
145                 150                 155                 160

gta caa ggc ccg ccc atc gga acg gaa gat tcc ttt gtg ctt ctc gat   528
Val Gln Gly Pro Pro Ile Gly Thr Glu Asp Ser Phe Val Leu Leu Asp
                165                 170                 175

tcc atc tgc ccc ctt tcc cta gca ctt aac ggc gac gaa gcg ctc aca   576
Ser Ile Cys Pro Leu Ser Leu Ala Leu Asn Gly Asp Glu Ala Leu Thr
            180                 185                 190

gag atg acc cgt cgc tac ttc cac tcc cgt ggt gct gcc act gtg aaa   624
Glu Met Thr Arg Arg Tyr Phe His Ser Arg Gly Ala Ala Thr Val Lys
        195                 200                 205

gat ctg gtg tgg tgg acc gga ctg act gtg cgt gat gta aag aaa ggc   672
Asp Leu Val Trp Trp Thr Gly Leu Thr Val Arg Asp Val Lys Lys Gly
    210                 215                 220

atc gct gcc gtg tct tcg gat gga ctg att cac tct gtt gaa ggc ccg   720
```

```
Ile Ala Ala Val Ser Ser Asp Gly Leu Ile His Ser Val Glu Gly Pro
225                 230                 235                 240

aat ggt gaa gaa atg tgg atc cct acc tgg gca gat gat gtc aca gac   768
Asn Gly Glu Glu Met Trp Ile Pro Thr Trp Ala Asp Asp Val Thr Asp
                245                 250                 255

gca gag gtt tct gat gca cta gcg ttg gaa cta acc ctc ccc gcc ttt   816
Ala Glu Val Ser Asp Ala Leu Ala Leu Glu Leu Thr Leu Pro Ala Phe
            260                 265                 270

gat gaa tac cta ctt tcc tac acc gac cgc agc cac gtc atg gat ccc   864
Asp Glu Tyr Leu Leu Ser Tyr Thr Asp Arg Ser His Val Met Asp Pro
        275                 280                 285

gag cac ctt ttc agc atc ggt ccc ggc aaa aac ggt gtg ttc aaa ccc   912
Glu His Leu Phe Ser Ile Gly Pro Gly Lys Asn Gly Val Phe Lys Pro
    290                 295                 300

ttc aaa gta gtt cag ggt gag gca ctg ccg gtt tagcccagca aaatcttcac 965
Phe Lys Val Val Gln Gly Glu Ala Leu Pro Val
305                 310                 315

ttg                                                               968


<210> 2172
<211> 315
<212> PRT
<213> Corynebacterium glutamicum

<400> 2172
Ala Leu Arg Leu Ile Ser Gln Leu Leu Ala Pro Ser Ala Ala Leu Asn
  1               5                  10                  15

Phe Lys Ser Glu Arg Asn Ala Val Asp Val Ala Lys His Met Leu Ala
             20                  25                  30

Ser Gln Ala Gln Gln Arg Gly Ser Ala Leu Val Ala Leu Asp Thr Arg
         35                  40                  45

Ser Glu Asn Ala Asp Ala Ala Thr Ala Leu Arg Lys Ser Leu Leu Ile
     50                  55                  60

Arg Ser Trp Thr Gln Arg Gly Thr His Gln Ile Leu Ala Ala Glu Asp
 65                  70                  75                  80

Val Arg Trp Met Thr Leu Leu Cys Ser Pro Arg Ile Leu Ala Ala Ser
                 85                  90                  95

Ala Lys Arg Arg Ser Ser Leu Ser Leu Asp Ser Ala Ala Val Gln Arg
            100                 105                 110

Ala Arg Asp Ala Leu Thr Thr Ala Ala Glu Lys Ser Pro Val Ser Arg
        115                 120                 125

Thr Gln Ala Tyr Glu Ile Phe Arg Ser Val Asp Val Asp Pro Gly Glu
    130                 135                 140

His Arg Gly Gln His Leu Leu Arg His Phe Gly Gly Glu Gly Asp Ile
145                 150                 155                 160
```

```
Val Gln Gly Pro Pro Ile Gly Thr Glu Asp Ser Phe Val Leu Leu Asp
                165                 170                 175

Ser Ile Cys Pro Leu Ser Leu Ala Leu Asn Gly Asp Glu Ala Leu Thr
            180                 185                 190

Glu Met Thr Arg Arg Tyr Phe His Ser Arg Gly Ala Ala Thr Val Lys
        195                 200                 205

Asp Leu Val Trp Trp Thr Gly Leu Thr Val Arg Asp Val Lys Lys Gly
    210                 215                 220

Ile Ala Ala Val Ser Ser Asp Gly Leu Ile His Ser Val Glu Gly Pro
225                 230                 235                 240

Asn Gly Glu Glu Met Trp Ile Pro Thr Trp Ala Asp Asp Val Thr Asp
                245                 250                 255

Ala Glu Val Ser Asp Ala Leu Ala Leu Glu Leu Thr Leu Pro Ala Phe
            260                 265                 270

Asp Glu Tyr Leu Leu Ser Tyr Thr Asp Arg Ser His Val Met Asp Pro
        275                 280                 285

Glu His Leu Phe Ser Ile Gly Pro Gly Lys Asn Gly Val Phe Lys Pro
    290                 295                 300

Phe Lys Val Val Gln Gly Glu Ala Leu Pro Val
305                 310                 315


<210> 2173
<211> 774
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(751)
<223> RXA01315

<400> 2173
catgtgcggt tgtgtcctaa gtcattgatg tcacctaacg cccctaagtt cactcggtgc 60

aatattgcac tgagtgcaag tttacactag gtttacttca gtg gat att gaa gag   115
                                              Val Asp Ile Glu Glu
                                                1               5

cag ccc tcg tta aga gaa atc aag cgc caa atg acc ctg gaa gcg ata   163
Gln Pro Ser Leu Arg Glu Ile Lys Arg Gln Met Thr Leu Glu Ala Ile
                10                  15                  20

gaa gat aac gca acc agg ctc att ctg gag cgt ggc ttc gac aat gtc   211
Glu Asp Asn Ala Thr Arg Leu Ile Leu Glu Arg Gly Phe Asp Asn Val
            25                  30                  35

aca atc gaa gac atc tgc gca gag gca ggg ata tcc aag cgc aca ttc   259
Thr Ile Glu Asp Ile Cys Ala Glu Ala Gly Ile Ser Lys Arg Thr Phe
        40                  45                  50
```

```
ttt aac tac gtg gag tcc aaa gag tct gtg gcc atc ggg cac aca gcc   307
Phe Asn Tyr Val Glu Ser Lys Glu Ser Val Ala Ile Gly His Thr Ala
     55                  60                  65

aag ctc cca acg gat gaa gaa cgt gaa gca ttc ctg gct acg cgt cat   355
Lys Leu Pro Thr Asp Glu Glu Arg Glu Ala Phe Leu Ala Thr Arg His
 70                  75                  80                  85

gaa aat att atc gat act gta ttt gac ctg gta atc aac ctc ttt ggc   403
Glu Asn Ile Ile Asp Thr Val Phe Asp Leu Val Ile Asn Leu Phe Gly
                 90                  95                 100

aac cac gac aac tcc aag tct gga gtt gca ggc gac att atg cgt cga   451
Asn His Asp Asn Ser Lys Ser Gly Val Ala Gly Asp Ile Met Arg Arg
            105                 110                 115

cgc aaa gag atc cgg gtg aag cat cca gaa ctg gca gtg caa cat ttc   499
Arg Lys Glu Ile Arg Val Lys His Pro Glu Leu Ala Val Gln His Phe
        120                 125                 130

gcc agg ttc cac caa gca cgc gaa ggg cta gaa cac cta att gtt gag   547
Ala Arg Phe His Gln Ala Arg Glu Gly Leu Glu His Leu Ile Val Glu
    135                 140                 145

tac ttc gaa aaa tgg cca ggc tcc caa cat cta gat gag cct gca gat   595
Tyr Phe Glu Lys Trp Pro Gly Ser Gln His Leu Asp Glu Pro Ala Asp
150                 155                 160                 165

cga gaa gca atc gcc ata gtt ggc ctg ctg atc tcg gtc atg ctt caa   643
Arg Glu Ala Ile Ala Ile Val Gly Leu Leu Ile Ser Val Met Leu Gln
                170                 175                 180

ggt tct cgt gaa tgg cac gac atg cca caa ggc acg caa gct gat ttc   691
Gly Ser Arg Glu Trp His Asp Met Pro Gln Gly Thr Gln Ala Asp Phe
            185                 190                 195

caa gcc tgc tgt cgc aaa gca att aaa aat act ttt ctt ctt aga ggt   739
Gln Ala Cys Cys Arg Lys Ala Ile Lys Asn Thr Phe Leu Leu Arg Gly
        200                 205                 210

gga ttt tca gaa tgacatcaca ggtcaagccg gac                        774
Gly Phe Ser Glu
    215
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<210> 2174
<211> 217
<212> PRT
<213> Corynebacterium glutamicum

<400> 2174

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Val Asp Ile Glu Glu Gln Pro Ser Leu Arg Glu Ile Lys Arg Gln Met
  1               5                  10                  15

Thr Leu Glu Ala Ile Glu Asp Asn Ala Thr Arg Leu Ile Leu Glu Arg
             20                  25                  30

Gly Phe Asp Asn Val Thr Ile Glu Asp Ile Cys Ala Glu Ala Gly Ile
         35                  40                  45

Ser Lys Arg Thr Phe Phe Asn Tyr Val Glu Ser Lys Glu Ser Val Ala
```

```
     50                  55                  60

Ile Gly His Thr Ala Lys Leu Pro Thr Asp Glu Glu Arg Glu Ala Phe
 65                  70                  75                  80

Leu Ala Thr Arg His Glu Asn Ile Ile Asp Thr Val Phe Asp Leu Val
                85                  90                  95

Ile Asn Leu Phe Gly Asn His Asp Asn Ser Lys Ser Gly Val Ala Gly
            100                 105                 110

Asp Ile Met Arg Arg Arg Lys Glu Ile Arg Val Lys His Pro Glu Leu
        115                 120                 125

Ala Val Gln His Phe Ala Arg Phe His Gln Ala Arg Glu Gly Leu Glu
    130                 135                 140

His Leu Ile Val Glu Tyr Phe Glu Lys Trp Pro Gly Ser Gln His Leu
145                 150                 155                 160

Asp Glu Pro Ala Asp Arg Glu Ala Ile Ala Ile Val Gly Leu Leu Ile
                165                 170                 175

Ser Val Met Leu Gln Gly Ser Arg Glu Trp His Asp Met Pro Gln Gly
            180                 185                 190

Thr Gln Ala Asp Phe Gln Ala Cys Cys Arg Lys Ala Ile Lys Asn Thr
        195                 200                 205

Phe Leu Leu Arg Gly Gly Phe Ser Glu
    210                 215


<210> 2175
<211> 426
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(403)
<223> RXA01316

<400> 2175
aaagcgcaag gctaagaagg attccccaga accaggcgat gacgatatca tcgatggaga 60

agtaattcct ccgcagaatt aaggaagtcg gtttcacccc atg gat att tcc atg   115
                                              Met Asp Ile Ser Met
                                                1               5

ctc aac gta ata acg agc tac acc att tgg gcc att ttt gcc atc atc   163
Leu Asn Val Ile Thr Ser Tyr Thr Ile Trp Ala Ile Phe Ala Ile Ile
                10                  15                  20

ggc atc tgc gga ttc gtt ggt gcc ttc ttg gca gcc acc acc aga gaa   211
Gly Ile Cys Gly Phe Val Gly Ala Phe Leu Ala Ala Thr Thr Arg Glu
            25                  30                  35

gat gcc ttt gag gtt gct gat cgc caa aag aaa atg gtg tgg gta gca   259
Asp Ala Phe Glu Val Ala Asp Arg Gln Lys Lys Met Val Trp Val Ala
        40                  45                  50
```

atc ctt atc gca tcc gga ttt gtc ctc acc gcg cta ggt cca tcg att 307
Ile Leu Ile Ala Ser Gly Phe Val Leu Thr Ala Leu Gly Pro Ser Ile
55 60 65

ccg atc ctg cca tgg gtc gcc atc atc atg atc ggc ctg tac tgg ttt 355
Pro Ile Leu Pro Trp Val Ala Ile Ile Met Ile Gly Leu Tyr Trp Phe
70 75 80 85

gat gtt cgc ccg caa atc aag agc atc ctt gaa ggt gcc ggc ggc tgg 403
Asp Val Arg Pro Gln Ile Lys Ser Ile Leu Glu Gly Ala Gly Gly Trp
90 95 100

taaaagctcc ctgaactgcg aaa 426

<210> 2176
<211> 101
<212> PRT
<213> Corynebacterium glutamicum

<400> 2176
Met Asp Ile Ser Met Leu Asn Val Ile Thr Ser Tyr Thr Ile Trp Ala
1 5 10 15

Ile Phe Ala Ile Ile Gly Ile Cys Gly Phe Val Gly Ala Phe Leu Ala
20 25 30

Ala Thr Thr Arg Glu Asp Ala Phe Glu Val Ala Asp Arg Gln Lys Lys
35 40 45

Met Val Trp Val Ala Ile Leu Ile Ala Ser Gly Phe Val Leu Thr Ala
50 55 60

Leu Gly Pro Ser Ile Pro Ile Leu Pro Trp Val Ala Ile Ile Met Ile
65 70 75 80

Gly Leu Tyr Trp Phe Asp Val Arg Pro Gln Ile Lys Ser Ile Leu Glu
85 90 95

Gly Ala Gly Gly Trp
100

<210> 2177
<211> 543
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(520)
<223> RXA01317

<400> 2177
atacatccgc cttaatggca caattgtagg tgcattagca ggactggcca tttacgctat 60

ttcccatatc ctcttcggag cttaactagg agtaaccatc atg tcc gat gca aaa 115
Met Ser Asp Ala Lys
1 5

```
gac gat tcc atc ttg tcc aag tgg agc aat gca gct tcc gag ctc agc   163
Asp Asp Ser Ile Leu Ser Lys Trp Ser Asn Ala Ala Ser Glu Leu Ser
                10                  15                  20

ggt gcc gtc agt gga gta gcg aag aag ctc cgt gaa gaa ctc tct gag   211
Gly Ala Val Ser Gly Val Ala Lys Lys Leu Arg Glu Glu Leu Ser Glu
            25                  30                  35

aag gaa acc ttc agc aag ctt aaa acc gaa gcc agc gaa gcc gtc gat   259
Lys Glu Thr Phe Ser Lys Leu Lys Thr Glu Ala Ser Glu Ala Val Asp
        40                  45                  50

caa gca aag tcc ggc tcc tac cta gat gcc ggt aag gaa ttc gcc cgc   307
Gln Ala Lys Ser Gly Ser Tyr Leu Asp Ala Gly Lys Glu Phe Ala Arg
    55                  60                  65

gac gcc gga tcc atc atc aaa gat gca gcc aaa acc gtc aaa ggt gcc   355
Asp Ala Gly Ser Ile Ile Lys Asp Ala Ala Lys Thr Val Lys Gly Ala
70                  75                  80                  85

gtc agt gat tcc gat aaa aac gac gtg aaa tcc gcc ttc ggt aac gcc   403
Val Ser Asp Ser Asp Lys Asn Asp Val Lys Ser Ala Phe Gly Asn Ala
                90                  95                  100

gtg gaa gct tcc cgc gac aag ttc gat gac acc ctc gaa aag cgc aag   451
Val Glu Ala Ser Arg Asp Lys Phe Asp Asp Thr Leu Glu Lys Arg Lys
            105                 110                 115

gct aag aag gat tcc cca gaa cca ggc gat gac gat atc atc gat gga   499
Ala Lys Lys Asp Ser Pro Glu Pro Gly Asp Asp Asp Ile Ile Asp Gly
        120                 125                 130

gaa gta att cct ccg cag aat taaggaagtc ggtttcaccc cat            543
Glu Val Ile Pro Pro Gln Asn
    135                 140
```

Application Filed with the Chinese Patent Office on 2007-12-28

<210> 2178
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

<400> 2178

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Met Ser Asp Ala Lys Asp Asp Ser Ile Leu Ser Lys Trp Ser Asn Ala
  1               5                  10                  15

Ala Ser Glu Leu Ser Gly Ala Val Ser Gly Val Ala Lys Lys Leu Arg
            20                  25                  30

Glu Glu Leu Ser Glu Lys Glu Thr Phe Ser Lys Leu Lys Thr Glu Ala
        35                  40                  45

Ser Glu Ala Val Asp Gln Ala Lys Ser Gly Ser Tyr Leu Asp Ala Gly
    50                  55                  60

Lys Glu Phe Ala Arg Asp Ala Gly Ser Ile Ile Lys Asp Ala Ala Lys
65                  70                  75                  80

Thr Val Lys Gly Ala Val Ser Asp Ser Asp Lys Asn Asp Val Lys Ser
                85                  90                  95
```

```
Ala Phe Gly Asn Ala Val Glu Ala Ser Arg Asp Lys Phe Asp Asp Thr
            100                 105                 110

Leu Glu Lys Arg Lys Ala Lys Lys Asp Ser Pro Glu Pro Gly Asp Asp
        115                 120                 125

Asp Ile Ile Asp Gly Glu Val Ile Pro Pro Gln Asn
    130                 135                 140


<210> 2179
<211> 1425
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1402)
<223> RXA01318

<400> 2179
ggacgcgttc cagagaaaag tgcaggcata acccctaaaa taccctgatc ttcccccgtg 60

tcctgccccc gtgtccaccc ctgcgtacat aataggacgc atg gga aaa cat gag   115
                                                Met Gly Lys His Glu
                                                  1               5

gtt gct cag cag acg gtt ccg ggt cct tcg ccg gaa atg gaa gcg cag   163
Val Ala Gln Gln Thr Val Pro Gly Pro Ser Pro Glu Met Glu Ala Gln
                10                  15                  20

cgg cgt aaa gag ttg cgc aag cac aag gcc att gcc act ggc ctg ttg   211
Arg Arg Lys Glu Leu Arg Lys His Lys Ala Ile Ala Thr Gly Leu Leu
            25                  30                  35

att ttt gct gcc gct gta tat ttt ctt tgc cgt ttc gtg gag acc cgt   259
Ile Phe Ala Ala Ala Val Tyr Phe Leu Cys Arg Phe Val Glu Thr Arg
        40                  45                  50

ccg ggt gaa act gca gcg tgg gta ggt ttt gtg cgc gct gcg gca gag   307
Pro Gly Glu Thr Ala Ala Trp Val Gly Phe Val Arg Ala Ala Ala Glu
    55                  60                  65

gcc gga atg att ggc ggg ttg gcc gac tgg ttc gcg gtc acc gcg ctg   355
Ala Gly Met Ile Gly Gly Leu Ala Asp Trp Phe Ala Val Thr Ala Leu
70                  75                  80                  85

ttc cgt cat cca ttg tgg ctg cct att ccg cac act gcg att atc ccg   403
Phe Arg His Pro Leu Trp Leu Pro Ile Pro His Thr Ala Ile Ile Pro
                90                  95                  100

cgc aag aaa gac cag tta ggt gag gcc tta agc ggg ttt gtg ggg gat   451
Arg Lys Lys Asp Gln Leu Gly Glu Ala Leu Ser Gly Phe Val Gly Asp
            105                 110                 115

aac ttc cta aat gcc cag ctc att acg gaa aaa gtc tct cag gcg cgg   499
Asn Phe Leu Asn Ala Gln Leu Ile Thr Glu Lys Val Ser Gln Ala Arg
        120                 125                 130

atc cca gag cgc gcc ggg gag tgg ctc gcc cag ccg gaa aac ggg gag   547
Ile Pro Glu Arg Ala Gly Glu Trp Leu Ala Gln Pro Glu Asn Gly Glu
```

```
    135                 140                 145

aaa gtt tcg cgc gaa gtc ggc aaa ttg acc gct aat att gtg cgc gca   595
Lys Val Ser Arg Glu Val Gly Lys Leu Thr Ala Asn Ile Val Arg Ala
150                 155                 160                 165

atc gat ccg tca gat gct gaa gcg gtg att aaa tct gcg gtg atc gac   643
Ile Asp Pro Ser Asp Ala Glu Ala Val Ile Lys Ser Ala Val Ile Asp
                170                 175                 180

aag ctt gcg gaa ccc acc tgg ggc cca cca gct ggg cgg ttg ctg gaa   691
Lys Leu Ala Glu Pro Thr Trp Gly Pro Pro Ala Gly Arg Leu Leu Glu
            185                 190                 195

caa ctc ctc gcc gaa ggc aaa gcc gaa cca gtt gtc cag gaa ctc gcg   739
Gln Leu Leu Ala Glu Gly Lys Ala Glu Pro Val Val Gln Glu Leu Ala
        200                 205                 210

cag tgg ctg cac aaa aag gcg ttg ggc tcc gag ccg ctg att gat cgc   787
Gln Trp Leu His Lys Lys Ala Leu Gly Ser Glu Pro Leu Ile Asp Arg
    215                 220                 225

ctg ctc aac gag cgc cgc ccg att tgg gcg ccg aaa ttc act gcg cag   835
Leu Leu Asn Glu Arg Arg Pro Ile Trp Ala Pro Lys Phe Thr Ala Gln
230                 235                 240                 245

ctg gtc agc ggc aaa gtc tat gac gag gtc ata aaa ttc act gaa gcc   883
Leu Val Ser Gly Lys Val Tyr Asp Glu Val Ile Lys Phe Thr Glu Ala
                250                 255                 260

gtc gct gcc gat cct aac cac gag gcc cgc aaa tcg ctg cgc cga ttc   931
Val Ala Ala Asp Pro Asn His Glu Ala Arg Lys Ser Leu Arg Arg Phe
            265                 270                 275

ctt aat aaa ttg gcg caa gac ctg cag cat gac cca ggc atg att att   979
Leu Asn Lys Leu Ala Gln Asp Leu Gln His Asp Pro Gly Met Ile Ile
        280                 285                 290

aaa gtt gaa gaa atc aaa cgc gac atc atg ggc tcc ggc gcc atc gcg  1027
Lys Val Glu Glu Ile Lys Arg Asp Ile Met Gly Ser Gly Ala Ile Ala
    295                 300                 305

caa gcc gcg cca acc atc tgg gcg tca gcc tcc gag tcg ctc att gaa  1075
Gln Ala Ala Pro Thr Ile Trp Ala Ser Ala Ser Glu Ser Leu Ile Glu
310                 315                 320                 325

tcc gca gaa gat gag tca tca att ctg cgt cgc aaa att gcc gaa gca  1123
Ser Ala Glu Asp Glu Ser Ser Ile Leu Arg Arg Lys Ile Ala Glu Ala
                330                 335                 340

gct acc agc tgg ggt caa aga ttg ctt gtc gac gac tcc ctc cgg cat  1171
Ala Thr Ser Trp Gly Gln Arg Leu Leu Val Asp Asp Ser Leu Arg His
            345                 350                 355

tca ctc gac acc cgg att acc ggc gcc gct gct ttc ctc gcc gac aat  1219
Ser Leu Asp Thr Arg Ile Thr Gly Ala Ala Ala Phe Leu Ala Asp Asn
        360                 365                 370

tac gcc ccc gaa gtc acc ggc att atc tcc gaa acc att gaa cga tgg  1267
Tyr Ala Pro Glu Val Thr Gly Ile Ile Ser Glu Thr Ile Glu Arg Trp
    375                 380                 385
```

```
gac gct gaa gaa gct tca gag aaa atc gaa ctc atg gtg ggc aaa gac   1315
Asp Ala Glu Glu Ala Ser Glu Lys Ile Glu Leu Met Val Gly Lys Asp
390                 395                 400                 405

ctc caa tac atc cgc ctt aat ggc aca att gta ggt gca tta gca gga   1363
Leu Gln Tyr Ile Arg Leu Asn Gly Thr Ile Val Gly Ala Leu Ala Gly
                410                 415                 420

ctg gcc att tac gct att tcc cat atc ctc ttc gga gct taactaggag    1412
Leu Ala Ile Tyr Ala Ile Ser His Ile Leu Phe Gly Ala
            425                 430

taaccatcat gtc                                                   1425


<210> 2180
<211> 434
<212> PRT
<213> Corynebacterium glutamicum

<400> 2180
Met Gly Lys His Glu Val Ala Gln Gln Thr Val Pro Gly Pro Ser Pro
  1               5                  10                  15

Glu Met Glu Ala Gln Arg Arg Lys Glu Leu Arg Lys His Lys Ala Ile
             20                  25                  30

Ala Thr Gly Leu Leu Ile Phe Ala Ala Ala Val Tyr Phe Leu Cys Arg
         35                  40                  45

Phe Val Glu Thr Arg Pro Gly Glu Thr Ala Ala Trp Val Gly Phe Val
     50                  55                  60

Arg Ala Ala Ala Glu Ala Gly Met Ile Gly Gly Leu Ala Asp Trp Phe
 65                  70                  75                  80

Ala Val Thr Ala Leu Phe Arg His Pro Leu Trp Leu Pro Ile Pro His
                 85                  90                  95

Thr Ala Ile Ile Pro Arg Lys Lys Asp Gln Leu Gly Glu Ala Leu Ser
            100                 105                 110

Gly Phe Val Gly Asp Asn Phe Leu Asn Ala Gln Leu Ile Thr Glu Lys
        115                 120                 125

Val Ser Gln Ala Arg Ile Pro Glu Arg Ala Gly Glu Trp Leu Ala Gln
    130                 135                 140

Pro Glu Asn Gly Glu Lys Val Ser Arg Glu Val Gly Lys Leu Thr Ala
145                 150                 155                 160

Asn Ile Val Arg Ala Ile Asp Pro Ser Asp Ala Glu Ala Val Ile Lys
                165                 170                 175

Ser Ala Val Ile Asp Lys Leu Ala Glu Pro Thr Trp Gly Pro Pro Ala
            180                 185                 190

Gly Arg Leu Leu Glu Gln Leu Leu Ala Glu Gly Lys Ala Glu Pro Val
        195                 200                 205
```

```
Val Gln Glu Leu Ala Gln Trp Leu His Lys Lys Ala Leu Gly Ser Glu
    210                 215                 220

Pro Leu Ile Asp Arg Leu Leu Asn Glu Arg Arg Pro Ile Trp Ala Pro
225                 230                 235                 240

Lys Phe Thr Ala Gln Leu Val Ser Gly Lys Val Tyr Asp Glu Val Ile
                245                 250                 255

Lys Phe Thr Glu Ala Val Ala Ala Asp Pro Asn His Glu Ala Arg Lys
            260                 265                 270

Ser Leu Arg Arg Phe Leu Asn Lys Leu Ala Gln Asp Leu Gln His Asp
        275                 280                 285

Pro Gly Met Ile Ile Lys Val Glu Glu Ile Lys Arg Asp Ile Met Gly
    290                 295                 300

Ser Gly Ala Ile Ala Gln Ala Ala Pro Thr Ile Trp Ala Ser Ala Ser
305                 310                 315                 320

Glu Ser Leu Ile Glu Ser Ala Glu Asp Glu Ser Ser Ile Leu Arg Arg
                325                 330                 335

Lys Ile Ala Glu Ala Ala Thr Ser Trp Gly Gln Arg Leu Leu Val Asp
            340                 345                 350

Asp Ser Leu Arg His Ser Leu Asp Thr Arg Ile Thr Gly Ala Ala Ala
        355                 360                 365

Phe Leu Ala Asp Asn Tyr Ala Pro Glu Val Thr Gly Ile Ile Ser Glu
    370                 375                 380

Thr Ile Glu Arg Trp Asp Ala Glu Glu Ala Ser Glu Lys Ile Glu Leu
385                 390                 395                 400

Met Val Gly Lys Asp Leu Gln Tyr Ile Arg Leu Asn Gly Thr Ile Val
                405                 410                 415

Gly Ala Leu Ala Gly Leu Ala Ile Tyr Ala Ile Ser His Ile Leu Phe
            420                 425                 430

Gly Ala
```

<210> 2181
<211> 579
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> RXA01330

<400> 2181
ccgtccgttt tcctggtggg tcggccccgc atccagccct agaaatatcg gagagctgct 60

cgttgaggcc caatgaaatg cctccgaaac agaaacaggc atg tgg aaa gac tta 115
Met Trp Lys Asp Leu

```
                                                    1               5

acc gaa ccg ctg ccc gaa gct tgc gct gag ggc tta gag atc cgg gtg   163
Thr Glu Pro Leu Pro Glu Ala Cys Ala Glu Gly Leu Glu Ile Arg Val
                10                  15                  20

gtt aaa tct ccc gaa gag ctg gca gat tac gct gca gtt ctt tct gcg   211
Val Lys Ser Pro Glu Glu Leu Ala Asp Tyr Ala Ala Val Leu Ser Ala
            25                  30                  35

aat tgg aat cca ccc gcc gaa act gtg cag cgt ttc tat acc gaa gca   259
Asn Trp Asn Pro Pro Ala Glu Thr Val Gln Arg Phe Tyr Thr Glu Ala
        40                  45                  50

gct gaa tac gca ctg aga aag aac tcg ccc gca ctt tat ctg gtg ggt   307
Ala Glu Tyr Ala Leu Arg Lys Asn Ser Pro Ala Leu Tyr Leu Val Gly
    55                  60                  65

tat gcg ggc aac cgc gca gtg tgt tct gcg gaa gca ttc ata cac gcg   355
Tyr Ala Gly Asn Arg Ala Val Cys Ser Ala Glu Ala Phe Ile His Ala
70                  75                  80                  85

agc gta gtt gga atc tac aat atc tcc acc ctt gag cac aaa cgc cgg   403
Ser Val Val Gly Ile Tyr Asn Ile Ser Thr Leu Glu His Lys Arg Arg
                90                  95                  100

cgt ggc tac ggc gga gcc atc acc tta gcc acg ttg cat acc gca cgt   451
Arg Gly Tyr Gly Gly Ala Ile Thr Leu Ala Thr Leu His Thr Ala Arg
            105                 110                 115

aac gca ggg tgt gac acc gcc gtg ttg caa gct tcc gaa gat ggt gag   499
Asn Ala Gly Cys Asp Thr Ala Val Leu Gln Ala Ser Glu Asp Gly Glu
        120                 125                 130

ccc gtt tat cgc aaa cta gga ttc acc gac tgc ggt cga ttt act gaa   547
Pro Val Tyr Arg Lys Leu Gly Phe Thr Asp Cys Gly Arg Phe Thr Glu
    135                 140                 145

tac tct ttg tgattagtta gggaccgtat gcg                            579
Tyr Ser Leu
150
```

<210> 2182
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 2182

```
Met Trp Lys Asp Leu Thr Glu Pro Leu Pro Glu Ala Cys Ala Glu Gly
  1               5                  10                  15

Leu Glu Ile Arg Val Val Lys Ser Pro Glu Glu Leu Ala Asp Tyr Ala
            20                  25                  30

Ala Val Leu Ser Ala Asn Trp Asn Pro Pro Ala Glu Thr Val Gln Arg
        35                  40                  45

Phe Tyr Thr Glu Ala Ala Glu Tyr Ala Leu Arg Lys Asn Ser Pro Ala
    50                  55                  60
```

```
Leu Tyr Leu Val Gly Tyr Ala Gly Asn Arg Ala Val Cys Ser Ala Glu
 65                  70                  75                  80

Ala Phe Ile His Ala Ser Val Val Gly Ile Tyr Asn Ile Ser Thr Leu
                85                  90                  95

Glu His Lys Arg Arg Arg Gly Tyr Gly Gly Ala Ile Thr Leu Ala Thr
            100                 105                 110

Leu His Thr Ala Arg Asn Ala Gly Cys Asp Thr Ala Val Leu Gln Ala
        115                 120                 125

Ser Glu Asp Gly Glu Pro Val Tyr Arg Lys Leu Gly Phe Thr Asp Cys
    130                 135                 140

Gly Arg Phe Thr Glu Tyr Ser Leu
145                 150


<210> 2183
<211> 1128
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1105)
<223> RXA01333

<400> 2183
cgccctttaa ggcccgtaaa gcactccaca acacttcacg gcaggccgta atttccctgt 60

gaggtacttt cttgcaagtt gtagcgcacc gccgatacca atg cct ggc ggg tgc   115
                                            Met Pro Gly Gly Cys
                                              1               5

tcc ggt aac atc gtc cgc atg ctg cct aaa tcc cgg att ttc tcc gca   163
Ser Gly Asn Ile Val Arg Met Leu Pro Lys Ser Arg Ile Phe Ser Ala
                10                  15                  20

atc ttg ctc gga att ggt gtg gca ctt gtg gtc tgg ggt ctg gtg gct   211
Ile Leu Leu Gly Ile Gly Val Ala Leu Val Val Trp Gly Leu Val Ala
            25                  30                  35

ccg cgc ttt gtg cac gct gat ggc cgt ttg cct ctt gat ttg gag gcg   259
Pro Arg Phe Val His Ala Asp Gly Arg Leu Pro Leu Asp Leu Glu Ala
        40                  45                  50

acg acg tac gtt ctc cat gac tct gac gct cag acc act att aat tct   307
Thr Thr Tyr Val Leu His Asp Ser Asp Ala Gln Thr Thr Ile Asn Ser
    55                  60                  65

gat ccg ttg gcc ggt gtg gtg act acg ccg gtg act cgt cag ttg cat   355
Asp Pro Leu Ala Gly Val Val Thr Thr Pro Val Thr Arg Gln Leu His
70                  75                  80                  85

ttt gag gtg atg gat cct gcg agt gct gat gat gcc act att cgt att   403
Phe Glu Val Met Asp Pro Ala Ser Ala Asp Asp Ala Thr Ile Arg Ile
                90                  95                  100

ggt gat tcg atg ttg cgt ggt aat cct gat act cag ggt ttt gag cag   451
```

```
Gly Asp Ser Met Leu Arg Gly Asn Pro Asp Thr Gln Gly Phe Glu Gln
            105                 110                 115

gaa cgg ctc ctg tca gcg act gtg tcg agt ttc cgc att gat cgc acc   499
Glu Arg Leu Leu Ser Ala Thr Val Ser Ser Phe Arg Ile Asp Arg Thr
        120                 125                 130

tct ggt gag gtt ttg tcc gat att gcg ctg act aat cag ttg gcg agc   547
Ser Gly Glu Val Leu Ser Asp Ile Ala Leu Thr Asn Gln Leu Ala Ser
    135                 140                 145

cct acg gtg cag tat tcg gtg gat ggc att tgg ttg aag ttc cca act   595
Pro Thr Val Gln Tyr Ser Val Asp Gly Ile Trp Leu Lys Phe Pro Thr
150                 155                 160                 165

gac gcg cag gag acc act tac aac gtg gtg gat ccg gtg ctg agg tct   643
Asp Ala Gln Glu Thr Thr Tyr Asn Val Val Asp Pro Val Leu Arg Ser
                170                 175                 180

gcg ctg ccg gcg gat ttt gtg gag tcc acg gag atc gat ggc cgt gag   691
Ala Leu Pro Ala Asp Phe Val Glu Ser Thr Glu Ile Asp Gly Arg Glu
            185                 190                 195

gtg ctg cat tac cgt cag gtg att gat aac gtg aat gtg gcg gag tat   739
Val Leu His Tyr Arg Gln Val Ile Asp Asn Val Asn Val Ala Glu Tyr
        200                 205                 210

ttc gcg gat gcc aac aac acc acc acg ttg act aaa gag gat ggc ggt   787
Phe Ala Asp Ala Asn Asn Thr Thr Thr Leu Thr Lys Glu Asp Gly Gly
    215                 220                 225

acc acg acg ggc tat ttt tat cac aat gtg act cgt gat ttt tgg gtg   835
Thr Thr Thr Gly Tyr Phe Tyr His Asn Val Thr Arg Asp Phe Trp Val
230                 235                 240                 245

gat cag cgt acc ggt ttg gtt gtc gat cta gct gaa aat att gat gat   883
Asp Gln Arg Thr Gly Leu Val Val Asp Leu Ala Glu Asn Ile Asp Asp
                250                 255                 260

ttt tac ggc gac cgc agc ggc cag aag tac gaa cag aaa ttg ctt ttc   931
Phe Tyr Gly Asp Arg Ser Gly Gln Lys Tyr Glu Gln Lys Leu Leu Phe
            265                 270                 275

gac gcc tcc ctc gac gat gca gct gtc tct aag ctg gtt gca cag gcc   979
Asp Ala Ser Leu Asp Asp Ala Ala Val Ser Lys Leu Val Ala Gln Ala
        280                 285                 290

gaa agc atc cct gat gga gat gtg agc aaa atc gca aat acc gta ggt   1027
Glu Ser Ile Pro Asp Gly Asp Val Ser Lys Ile Ala Asn Thr Val Gly
    295                 300                 305

att gtg atc ggt gcg gta ttg gct ctc gtg ggc ctg gcc ggg tgt ttt   1075
Ile Val Ile Gly Ala Val Leu Ala Leu Val Gly Leu Ala Gly Cys Phe
310                 315                 320                 325

ggg gcg ttt ggg aag aaa cgt cga gaa gct taacctgctg ttcaaataga     1125
Gly Ala Phe Gly Lys Lys Arg Arg Glu Ala
                330                 335

ttt                                                               1128
```

<210> 2184
<211> 335
<212> PRT
<213> Corynebacterium glutamicum

<400> 2184

```
Met Pro Gly Gly Cys Ser Gly Asn Ile Val Arg Met Leu Pro Lys Ser
  1               5                  10                  15

Arg Ile Phe Ser Ala Ile Leu Leu Gly Ile Gly Val Ala Leu Val Val
             20                  25                  30

Trp Gly Leu Val Ala Pro Arg Phe Val His Ala Asp Gly Arg Leu Pro
         35                  40                  45

Leu Asp Leu Glu Ala Thr Thr Tyr Val Leu His Asp Ser Asp Ala Gln
     50                  55                  60

Thr Thr Ile Asn Ser Asp Pro Leu Ala Gly Val Val Thr Thr Pro Val
 65                  70                  75                  80

Thr Arg Gln Leu His Phe Glu Val Met Asp Pro Ala Ser Ala Asp Asp
                 85                  90                  95

Ala Thr Ile Arg Ile Gly Asp Ser Met Leu Arg Gly Asn Pro Asp Thr
            100                 105                 110

Gln Gly Phe Glu Gln Glu Arg Leu Leu Ser Ala Thr Val Ser Ser Phe
        115                 120                 125

Arg Ile Asp Arg Thr Ser Gly Glu Val Leu Ser Asp Ile Ala Leu Thr
    130                 135                 140

Asn Gln Leu Ala Ser Pro Thr Val Gln Tyr Ser Val Asp Gly Ile Trp
145                 150                 155                 160

Leu Lys Phe Pro Thr Asp Ala Gln Glu Thr Thr Tyr Asn Val Val Asp
                165                 170                 175

Pro Val Leu Arg Ser Ala Leu Pro Ala Asp Phe Val Glu Ser Thr Glu
            180                 185                 190

Ile Asp Gly Arg Glu Val Leu His Tyr Arg Gln Val Ile Asp Asn Val
        195                 200                 205

Asn Val Ala Glu Tyr Phe Ala Asp Ala Asn Asn Thr Thr Thr Leu Thr
    210                 215                 220

Lys Glu Asp Gly Gly Thr Thr Thr Gly Tyr Phe Tyr His Asn Val Thr
225                 230                 235                 240

Arg Asp Phe Trp Val Asp Gln Arg Thr Gly Leu Val Val Asp Leu Ala
                245                 250                 255

Glu Asn Ile Asp Asp Phe Tyr Gly Asp Arg Ser Gly Gln Lys Tyr Glu
            260                 265                 270

Gln Lys Leu Leu Phe Asp Ala Ser Leu Asp Asp Ala Ala Val Ser Lys
        275                 280                 285
```

```
Leu Val Ala Gln Ala Glu Ser Ile Pro Asp Gly Asp Val Ser Lys Ile
    290                 295                 300

Ala Asn Thr Val Gly Ile Val Ile Gly Ala Val Leu Ala Leu Val Gly
305                 310                 315                 320

Leu Ala Gly Cys Phe Gly Ala Phe Gly Lys Lys Arg Arg Glu Ala
                325                 330                 335


<210> 2185
<211> 726
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(703)
<223> RXA01336

<400> 2185
catggcatcc gcctccaacg cgccgggcgg gggagtccac ggaatgcccg gctggtgggc 60

agcgcaagcc gttttagcag atcacaggta gaattgcgac atg gag ccc acc gta   115
                                        Met Glu Pro Thr Val
                                          1               5

aaa gcc agc gcg cgc cac acc atc cac gtc acc gcc gac acc tgg cgc   163
Lys Ala Ser Ala Arg His Thr Ile His Val Thr Ala Asp Thr Trp Arg
                10                  15                  20

atc cgc ctg agt gcc tca gcc cac tca cac ccc aac gac gcg tac gcg   211
Ile Arg Leu Ser Ala Ser Ala His Ser His Pro Asn Asp Ala Tyr Ala
            25                  30                  35

cgc cgg gct acg gca att tcc gcc ata ggc agc gtg ctt atc gac gtc   259
Arg Arg Ala Thr Ala Ile Ser Ala Ile Gly Ser Val Leu Ile Asp Val
        40                  45                  50

ccc ctc caa ggc gaa cgc atc tct gaa tcc act gca tac gac ggc caa   307
Pro Leu Gln Gly Glu Arg Ile Ser Glu Ser Thr Ala Tyr Asp Gly Gln
    55                  60                  65

atc aac gcc gac tgg aac gca gaa gtc acc ggc acc gat gtg aac atc   355
Ile Asn Ala Asp Trp Asn Ala Glu Val Thr Gly Thr Asp Val Asn Ile
70                  75                  80                  85

gca cgc gac atc atc tcc cgg ctc gca gcg gtg cca gac gtt caa gtc   403
Ala Arg Asp Ile Ile Ser Arg Leu Ala Ala Val Pro Asp Val Gln Val
                90                  95                  100

gac ggc ccg ttg tgg tcc ttg agt gac agt ttg gct gca gag gct gct   451
Asp Gly Pro Leu Trp Ser Leu Ser Asp Ser Leu Ala Ala Glu Ala Ala
            105                 110                 115

gtg gag gca ttg caa ggt gct gcc gac act gcg cgg aac acc gcg acc   499
Val Glu Ala Leu Gln Gly Ala Ala Asp Thr Ala Arg Asn Thr Ala Thr
        120                 125                 130

gcc atc gca gaa tcc ctc ggc ggg cag cta ggt gca ctt ctc tac gca   547
Ala Ile Ala Glu Ser Leu Gly Gly Gln Leu Gly Ala Leu Leu Tyr Ala
```

```
    135                 140                 145

aca acc gac acc cac agc tcc aca ccg ata cca gca cgc gca gaa atg   595
Thr Thr Asp Thr His Ser Ser Thr Pro Ile Pro Ala Arg Ala Glu Met
150                 155                 160                 165

atg gca gca aaa gcc tcc ata cca ccg cgc aca ctc gac cta gaa ctc   643
Met Ala Ala Lys Ala Ser Ile Pro Pro Arg Thr Leu Asp Leu Glu Leu
                170                 175                 180

gcc ccc tct gac atc gaa gtc acc aaa gaa atc gcc gtg acc ttt gaa   691
Ala Pro Ser Asp Ile Glu Val Thr Lys Glu Ile Ala Val Thr Phe Glu
            185                 190                 195

ttc ctt gca ggc taaaccgcga tttggtattt cgg                        726
Phe Leu Ala Gly
        200


<210> 2186
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 2186
Met Glu Pro Thr Val Lys Ala Ser Ala Arg His Thr Ile His Val Thr
  1               5                  10                  15

Ala Asp Thr Trp Arg Ile Arg Leu Ser Ala Ser Ala His Ser His Pro
             20                  25                  30

Asn Asp Ala Tyr Ala Arg Arg Ala Thr Ala Ile Ser Ala Ile Gly Ser
         35                  40                  45

Val Leu Ile Asp Val Pro Leu Gln Gly Glu Arg Ile Ser Glu Ser Thr
     50                  55                  60

Ala Tyr Asp Gly Gln Ile Asn Ala Asp Trp Asn Ala Glu Val Thr Gly
 65                  70                  75                  80

Thr Asp Val Asn Ile Ala Arg Asp Ile Ile Ser Arg Leu Ala Ala Val
                 85                  90                  95

Pro Asp Val Gln Val Asp Gly Pro Leu Trp Ser Leu Ser Asp Ser Leu
            100                 105                 110

Ala Ala Glu Ala Ala Val Glu Ala Leu Gln Gly Ala Ala Asp Thr Ala
        115                 120                 125

Arg Asn Thr Ala Thr Ala Ile Ala Glu Ser Leu Gly Gly Gln Leu Gly
    130                 135                 140

Ala Leu Leu Tyr Ala Thr Thr Asp Thr His Ser Ser Thr Pro Ile Pro
145                 150                 155                 160

Ala Arg Ala Glu Met Met Ala Ala Lys Ala Ser Ile Pro Pro Arg Thr
                165                 170                 175

Leu Asp Leu Glu Leu Ala Pro Ser Asp Ile Glu Val Thr Lys Glu Ile
            180                 185                 190
```

```
Ala Val Thr Phe Glu Phe Leu Ala Gly
        195                 200


<210> 2187
<211> 1635
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1612)
<223> RXA01342

<400> 2187
gatgagtatt ctctccgagg caacgaagtt aatatgtcca tgagggcgaa gttgtagaca 60

atatttggcc catatggata attgacagga gtttaacgcc atg gaa acc cca acc   115
                                              Met Glu Thr Pro Thr
                                                1               5

caa gac atg gat gtc cgc tgg tta tac acc caa agc cag ctc aaa ctc   163
Gln Asp Met Asp Val Arg Trp Leu Tyr Thr Gln Ser Gln Leu Lys Leu
                10                  15                  20

cgc gaa att ctc ccc aca aac aaa acc ttc gat gtc atc caa atc agc   211
Arg Glu Ile Leu Pro Thr Asn Lys Thr Phe Asp Val Ile Gln Ile Ser
            25                  30                  35

gaa ctc gtt gac ccc acc gac ttc atc agg ccc aac agc gtg gtc tta   259
Glu Leu Val Asp Pro Thr Asp Phe Ile Arg Pro Asn Ser Val Val Leu
        40                  45                  50

tcc gtt ggc atc gcc ttc gca gaa acg ccc gac ggg ctt cgc gat tgg   307
Ser Val Gly Ile Ala Phe Ala Glu Thr Pro Asp Gly Leu Arg Asp Trp
    55                  60                  65

gca cac cga ctc gcc gac gca ggg gtc atc gcg atc ggg ttc ggc tcc   355
Ala His Arg Leu Ala Asp Ala Gly Val Ile Ala Ile Gly Phe Gly Ser
70                  75                  80                  85

ggc ctc acc ttc cca cag gtt ccg cag gcg ctt atc gac gcc tcc ctc   403
Gly Leu Thr Phe Pro Gln Val Pro Gln Ala Leu Ile Asp Ala Ser Leu
                90                  95                  100

cac ctt ggc ctc ggc ctc ttt gaa gtc ccc cgt gaa att cca ttt atc   451
His Leu Gly Leu Gly Leu Phe Glu Val Pro Arg Glu Ile Pro Phe Ile
            105                 110                 115

tcg atc acc tcc agc gtg cgt gat gag caa acc cgc cgt gcc ggc cgc   499
Ser Ile Thr Ser Ser Val Arg Asp Glu Gln Thr Arg Arg Ala Gly Arg
        120                 125                 130

ctg caa caa gaa ctc ctc ctg gaa cag gaa cgg ctt aac tcc atc gcc   547
Leu Gln Gln Glu Leu Leu Leu Glu Gln Glu Arg Leu Asn Ser Ile Ala
    135                 140                 145

atc tcc ggt ggc atc gaa gcc ctg tgc cgt gct gcc gcc gac tat ttg   595
Ile Ser Gly Gly Ile Glu Ala Leu Cys Arg Ala Ala Ala Asp Tyr Leu
150                 155                 160                 165
```

```
ggt ggt gca gta acc atc gtg gac agc gac ggc cgc gtg gct tgc tct   643
Gly Gly Ala Val Thr Ile Val Asp Ser Asp Gly Arg Val Ala Cys Ser
                170                 175                 180

att acc acc gat gac cta gac gca ctc ccc caa gct gtc tcg cgc ctg   691
Ile Thr Thr Asp Asp Leu Asp Ala Leu Pro Gln Ala Val Ser Arg Leu
            185                 190                 195

aac gga tcc agt caa gca ctc acg gat gcc acc aac ttt gga ttc atc   739
Asn Gly Ser Ser Gln Ala Leu Thr Asp Ala Thr Asn Phe Gly Phe Ile
        200                 205                 210

cac cgc atg acc cgc tac ggc gac cgc cac cac gtg ctc tca gtc ctt   787
His Arg Met Thr Arg Tyr Gly Asp Arg His His Val Leu Ser Val Leu
    215                 220                 225

atg ccc acc cgc ccc aca gac caa cac cgc gcg ctg atc aga cac tgc   835
Met Pro Thr Arg Pro Thr Asp Gln His Arg Ala Leu Ile Arg His Cys
230                 235                 240                 245

gca ggc ctt gcc gat att ttg ctc caa cgc ccc gaa gcc atg cgc gac   883
Ala Gly Leu Ala Asp Ile Leu Leu Gln Arg Pro Glu Ala Met Arg Asp
                250                 255                 260

cga gaa atc gaa gtg cga tca ctt gcc atg tca cta ctt ctg ggt cga   931
Arg Glu Ile Glu Val Arg Ser Leu Ala Met Ser Leu Leu Leu Gly Arg
            265                 270                 275

agc gac gac ctg gcc acc att cac cgc gtg ttc gct gac atc act gat   979
Ser Asp Asp Leu Ala Thr Ile His Arg Val Phe Ala Asp Ile Thr Asp
        280                 285                 290

gct tcc gga aat atc cgc ccc atc ctc atc acc ggc aac aca ccc caa  1027
Ala Ser Gly Asn Ile Arg Pro Ile Leu Ile Thr Gly Asn Thr Pro Gln
    295                 300                 305

tca gta cga aaa gca ctc tcc agt gtc gcc acc gca ctg tac aaa cag  1075
Ser Val Arg Lys Ala Leu Ser Ser Val Ala Thr Ala Leu Tyr Lys Gln
310                 315                 320                 325

gaa cga gca cta gct cat cta cgc ctc gcc gaa tcc acc gaa ctc ctc  1123
Glu Arg Ala Leu Ala His Leu Arg Leu Ala Glu Ser Thr Glu Leu Leu
                330                 335                 340

ttc ctt cgc gga agc cgc agc gtg cac aac atc gtg caa ctt ttt ggt  1171
Phe Leu Arg Gly Ser Arg Ser Val His Asn Ile Val Gln Leu Phe Gly
            345                 350                 355

act gcc gca agc gga gtt cgc ctc tgc att ggt ctg ccc acc cga gcg  1219
Thr Ala Ala Ser Gly Val Arg Leu Cys Ile Gly Leu Pro Thr Arg Ala
        360                 365                 370

gaa aac atc gat aag aaa ctc atc cgc gaa ctc act gcc acc gca aaa  1267
Glu Asn Ile Asp Lys Lys Leu Ile Arg Glu Leu Thr Ala Thr Ala Lys
    375                 380                 385

acc cta caa ctt gga acc cac gcc gaa ccc cgt gac ggc acc ttg ctg  1315
Thr Leu Gln Leu Gly Thr His Ala Glu Pro Arg Asp Gly Thr Leu Leu
390                 395                 400                 405

tgg ctc caa aac ccc gag ctg cgc aaa atc ctt aag atc cga tcc cgc  1363
```

```
Trp Leu Gln Asn Pro Glu Leu Arg Lys Ile Leu Lys Ile Arg Ser Arg
                410                 415                 420

gac acc tac gac cgt ctc ctc gac cac gac cgc acc aac aac acc gag   1411
Asp Thr Tyr Asp Arg Leu Leu Asp His Asp Arg Thr Asn Asn Thr Glu
            425                 430                 435

ctc gcc ccc acc ttg gtg tct ttt act cag cac agc gga cat ata ggc   1459
Leu Ala Pro Thr Leu Val Ser Phe Thr Gln His Ser Gly His Ile Gly
        440                 445                 450

gac acc gcc aaa gaa ctg ggc atc cac cgc cac acc gtg cgc acc cgc   1507
Asp Thr Ala Lys Glu Leu Gly Ile His Arg His Thr Val Arg Thr Arg
    455                 460                 465

atg atc cgc att gaa gag atc tgc gaa atc gac ctc aat gat cca ctg   1555
Met Ile Arg Ile Glu Glu Ile Cys Glu Ile Asp Leu Asn Asp Pro Leu
470                 475                 480                 485

acc aga gcg gag ctg ctc tta gtg atc gca acg aag gag gga gac gtc   1603
Thr Arg Ala Glu Leu Leu Leu Val Ile Ala Thr Lys Glu Gly Asp Val
                490                 495                 500

gaa aag caa taaaaagacc ccatgcaaag cat                            1635
Glu Lys Gln
```

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<210> 2188
<211> 504
<212> PRT
<213> Corynebacterium glutamicum

<400> 2188

```
Met Glu Thr Pro Thr Gln Asp Met Asp Val Arg Trp Leu Tyr Thr Gln
  1               5                  10                  15

Ser Gln Leu Lys Leu Arg Glu Ile Leu Pro Thr Asn Lys Thr Phe Asp
             20                  25                  30

Val Ile Gln Ile Ser Glu Leu Val Asp Pro Thr Asp Phe Ile Arg Pro
         35                  40                  45

Asn Ser Val Val Leu Ser Val Gly Ile Ala Phe Ala Glu Thr Pro Asp
     50                  55                  60

Gly Leu Arg Asp Trp Ala His Arg Leu Ala Asp Ala Gly Val Ile Ala
 65                  70                  75                  80

Ile Gly Phe Gly Ser Gly Leu Thr Phe Pro Gln Val Pro Gln Ala Leu
                 85                  90                  95

Ile Asp Ala Ser Leu His Leu Gly Leu Gly Leu Phe Glu Val Pro Arg
            100                 105                 110

Glu Ile Pro Phe Ile Ser Ile Thr Ser Ser Val Arg Asp Glu Gln Thr
        115                 120                 125

Arg Arg Ala Gly Arg Leu Gln Gln Glu Leu Leu Leu Glu Gln Glu Arg
    130                 135                 140
```

```
Leu Asn Ser Ile Ala Ile Ser Gly Gly Ile Glu Ala Leu Cys Arg Ala
145                 150                 155                 160

Ala Ala Asp Tyr Leu Gly Gly Ala Val Thr Ile Val Asp Ser Asp Gly
                165                 170                 175

Arg Val Ala Cys Ser Ile Thr Thr Asp Asp Leu Asp Ala Leu Pro Gln
            180                 185                 190

Ala Val Ser Arg Leu Asn Gly Ser Ser Gln Ala Leu Thr Asp Ala Thr
        195                 200                 205

Asn Phe Gly Phe Ile His Arg Met Thr Arg Tyr Gly Asp Arg His His
    210                 215                 220

Val Leu Ser Val Leu Met Pro Thr Arg Pro Thr Asp Gln His Arg Ala
225                 230                 235                 240

Leu Ile Arg His Cys Ala Gly Leu Ala Asp Ile Leu Leu Gln Arg Pro
                245                 250                 255

Glu Ala Met Arg Asp Arg Glu Ile Glu Val Arg Ser Leu Ala Met Ser
            260                 265                 270

Leu Leu Leu Gly Arg Ser Asp Asp Leu Ala Thr Ile His Arg Val Phe
        275                 280                 285

Ala Asp Ile Thr Asp Ala Ser Gly Asn Ile Arg Pro Ile Leu Ile Thr
    290                 295                 300

Gly Asn Thr Pro Gln Ser Val Arg Lys Ala Leu Ser Ser Val Ala Thr
305                 310                 315                 320

Ala Leu Tyr Lys Gln Glu Arg Ala Leu Ala His Leu Arg Leu Ala Glu
                325                 330                 335

Ser Thr Glu Leu Leu Phe Leu Arg Gly Ser Arg Ser Val His Asn Ile
            340                 345                 350

Val Gln Leu Phe Gly Thr Ala Ala Ser Gly Val Arg Leu Cys Ile Gly
        355                 360                 365

Leu Pro Thr Arg Ala Glu Asn Ile Asp Lys Lys Leu Ile Arg Glu Leu
    370                 375                 380

Thr Ala Thr Ala Lys Thr Leu Gln Leu Gly Thr His Ala Glu Pro Arg
385                 390                 395                 400

Asp Gly Thr Leu Leu Trp Leu Gln Asn Pro Glu Leu Arg Lys Ile Leu
                405                 410                 415

Lys Ile Arg Ser Arg Asp Thr Tyr Asp Arg Leu Leu Asp His Asp Arg
            420                 425                 430

Thr Asn Asn Thr Glu Leu Ala Pro Thr Leu Val Ser Phe Thr Gln His
        435                 440                 445

Ser Gly His Ile Gly Asp Thr Ala Lys Glu Leu Gly Ile His Arg His
    450                 455                 460

Thr Val Arg Thr Arg Met Ile Arg Ile Glu Glu Ile Cys Glu Ile Asp
```

```
465                 470                 475                 480

Leu Asn Asp Pro Leu Thr Arg Ala Glu Leu Leu Leu Val Ile Ala Thr
                485                 490                 495

Lys Glu Gly Asp Val Glu Lys Gln
            500
```

<210> 2189
<211> 615
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(592)
<223> RXA01348

<400> 2189

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atgggacaat gagcacgtga ctctacgatc tgcattactt gcgctactaa gttccggacc 60

attgactggg tatgacgcct cccagcgatt tggggcctcg gtg ggc ttt gtg tgg   115
                                            Val Gly Phe Val Trp
                                              1               5

agt ggt tcc gat tcg cag att tat ccc gaa ctt cga aaa atg gaa gcc   163
Ser Gly Ser Asp Ser Gln Ile Tyr Pro Glu Leu Arg Lys Met Glu Ala
                10                  15                  20

gaa gaa ctc ctc gtg gga tcc gat gtt ccc tgg ggc tcc aaa ggc gcc   211
Glu Glu Leu Leu Val Gly Ser Asp Val Pro Trp Gly Ser Lys Gly Ala
            25                  30                  35

acc aaa acc gaa tac gcc ttg agt gaa aaa ggc tgg gaa gcg cta aga   259
Thr Lys Thr Glu Tyr Ala Leu Ser Glu Lys Gly Trp Glu Ala Leu Arg
        40                  45                  50

aaa gcg tgg tac gag cca gta acc tac ggt ccc acc aga gat cct gcc   307
Lys Ala Trp Tyr Glu Pro Val Thr Tyr Gly Pro Thr Arg Asp Pro Ala
    55                  60                  65

agg ctt aaa gcc gcc tat ttt gag gtc ggt aca aat ggc gat gca cgc   355
Arg Leu Lys Ala Ala Tyr Phe Glu Val Gly Thr Asn Gly Asp Ala Arg
70                  75                  80                  85

cga cat tta agg gcg cac atc gct cat ttt gaa cag cag aaa att caa   403
Arg His Leu Arg Ala His Ile Ala His Phe Glu Gln Gln Lys Ile Gln
                90                  95                  100

tca gaa tca atg att gat gag ctg aaa gca aaa act cat cca acc ttg   451
Ser Glu Ser Met Ile Asp Glu Leu Lys Ala Lys Thr His Pro Thr Leu
            105                 110                 115

gca cgg cga ctt gag cgc tcc ccg aaa aag gag cac gag cga ata gtc   499
Ala Arg Arg Leu Glu Arg Ser Pro Lys Lys Glu His Glu Arg Ile Val
        120                 125                 130

gcg ttt aaa gtg ctt gcc tat gag ggg cag att gca cgc gct cag gca   547
Ala Phe Lys Val Leu Ala Tyr Glu Gly Gln Ile Ala Arg Ala Gln Ala
    135                 140                 145
```

```
gag att gaa tgg gcg gaa aag ggc ttg aaa cta ctc gat acc ctt       592
Glu Ile Glu Trp Ala Glu Lys Gly Leu Lys Leu Leu Asp Thr Leu
150                 155                 160

tagttttcga acacgtccgt atc                                        615


<210> 2190
<211> 164
<212> PRT
<213> Corynebacterium glutamicum

<400> 2190
Val Gly Phe Val Trp Ser Gly Ser Asp Ser Gln Ile Tyr Pro Glu Leu
  1               5                  10                  15

Arg Lys Met Glu Ala Glu Glu Leu Leu Val Gly Ser Asp Val Pro Trp
             20                  25                  30

Gly Ser Lys Gly Ala Thr Lys Thr Glu Tyr Ala Leu Ser Glu Lys Gly
         35                  40                  45

Trp Glu Ala Leu Arg Lys Ala Trp Tyr Glu Pro Val Thr Tyr Gly Pro
     50                  55                  60

Thr Arg Asp Pro Ala Arg Leu Lys Ala Ala Tyr Phe Glu Val Gly Thr
 65                  70                  75                  80

Asn Gly Asp Ala Arg Arg His Leu Arg Ala His Ile Ala His Phe Glu
                 85                  90                  95

Gln Gln Lys Ile Gln Ser Glu Ser Met Ile Asp Glu Leu Lys Ala Lys
            100                 105                 110

Thr His Pro Thr Leu Ala Arg Arg Leu Glu Arg Ser Pro Lys Lys Glu
        115                 120                 125

His Glu Arg Ile Val Ala Phe Lys Val Leu Ala Tyr Glu Gly Gln Ile
    130                 135                 140

Ala Arg Ala Gln Ala Glu Ile Glu Trp Ala Glu Lys Gly Leu Lys Leu
145                 150                 155                 160

Leu Asp Thr Leu


<210> 2191
<211> 900
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(877)
<223> RXA01349

<400> 2191
agttgtcagc tgggatttgc cgatggtgtt atctttgata tttaccttaa ccccgtttct 60
```

```
aattcacgtt ttctcgttac ccgaaaggaa ttgatcgatt atg gcg aca tca cgt   115
                                              Met Ala Thr Ser Arg
                                                1               5

cga gat gcc gaa aac ata gac cag gcc ggt agc gaa ttc att gaa tct   163
Arg Asp Ala Glu Asn Ile Asp Gln Ala Gly Ser Glu Phe Ile Glu Ser
                10                  15                  20

gat tca gga cac acc gca acc cct gaa gag gta gta gcc acc gct ctg   211
Asp Ser Gly His Thr Ala Thr Pro Glu Glu Val Val Ala Thr Ala Leu
            25                  30                  35

aca ttt ttt gca gag gat ggt ttt agc gaa acc aaa ttg gag aaa atc   259
Thr Phe Phe Ala Glu Asp Gly Phe Ser Glu Thr Lys Leu Glu Lys Ile
        40                  45                  50

gcg aag gca tct ggc atg tcc aag cgc atg atc cac tat cac ttt ggc   307
Ala Lys Ala Ser Gly Met Ser Lys Arg Met Ile His Tyr His Phe Gly
    55                  60                  65

gat aag aaa ggc ctg tac atc aag gct gtt tcc tac gcg ttg cga ttg   355
Asp Lys Lys Gly Leu Tyr Ile Lys Ala Val Ser Tyr Ala Leu Arg Leu
70                  75                  80                  85

ctg cgc cca gag gct gaa gcg atg caa ctt gat tcc gcg gta cca gtt   403
Leu Arg Pro Glu Ala Glu Ala Met Gln Leu Asp Ser Ala Val Pro Val
                90                  95                  100

gat ggt gtc cgc aaa atc gtc gag gct tta tat acc tgc atc acc aag   451
Asp Gly Val Arg Lys Ile Val Glu Ala Leu Tyr Thr Cys Ile Thr Lys
            105                 110                 115

cac cca gaa gca gtg cgc ctg cta ttg atg gaa aac ctg cat agc caa   499
His Pro Glu Ala Val Arg Leu Leu Leu Met Glu Asn Leu His Ser Gln
        120                 125                 130

gac agc gtg gat tcc acc gcg gca tat tcc gat gaa tcc aat gtg ctg   547
Asp Ser Val Asp Ser Thr Ala Ala Tyr Ser Asp Glu Ser Asn Val Leu
    135                 140                 145

ctc aac ctg gat aag ctg ctc atg ctt ggc cag gat gcc ggc gcc ttc   595
Leu Asn Leu Asp Lys Leu Leu Met Leu Gly Gln Asp Ala Gly Ala Phe
150                 155                 160                 165

cgt cct gga atc tcc gca gaa gac gta ctg gtt ctt att agc tcc ctg   643
Arg Pro Gly Ile Ser Ala Glu Asp Val Leu Val Leu Ile Ser Ser Leu
                170                 175                 180

gcc tac ttc cgc gta tcc aac aag gtc acg ttg aag aac ctc tac tcc   691
Ala Tyr Phe Arg Val Ser Asn Lys Val Thr Leu Lys Asn Leu Tyr Ser
            185                 190                 195

ctt gat ttg gaa tca gag gcc aat att gaa ggc atg aag cgc atc gtc   739
Leu Asp Leu Glu Ser Glu Ala Asn Ile Glu Gly Met Lys Arg Ile Val
        200                 205                 210

gtt gac acg gtg ctg gca ttc ttg acc tca aat att caa aat tct ggc   787
Val Asp Thr Val Leu Ala Phe Leu Thr Ser Asn Ile Gln Asn Ser Gly
    215                 220                 225

aac tcc agc tac ctg gtt gtt ggt ggc aag act gca gaa cca gaa act   835
```

```
Asn Ser Ser Tyr Leu Val Val Gly Gly Lys Thr Ala Glu Pro Glu Thr
230                 235                 240                 245

gat gac agc gtc tac agc ttt gat acg gac gtg ttc gaa aac          877
Asp Asp Ser Val Tyr Ser Phe Asp Thr Asp Val Phe Glu Asn
                250                 255

taaagggtat cgagtagttt caa                                       900


<210> 2192
<211> 259
<212> PRT
<213> Corynebacterium glutamicum

<400> 2192
Met Ala Thr Ser Arg Arg Asp Ala Glu Asn Ile Asp Gln Ala Gly Ser
  1               5                  10                  15

Glu Phe Ile Glu Ser Asp Ser Gly His Thr Ala Thr Pro Glu Glu Val
             20                  25                  30

Val Ala Thr Ala Leu Thr Phe Phe Ala Glu Asp Gly Phe Ser Glu Thr
         35                  40                  45

Lys Leu Glu Lys Ile Ala Lys Ala Ser Gly Met Ser Lys Arg Met Ile
     50                  55                  60

His Tyr His Phe Gly Asp Lys Lys Gly Leu Tyr Ile Lys Ala Val Ser
 65                  70                  75                  80

Tyr Ala Leu Arg Leu Leu Arg Pro Glu Ala Glu Ala Met Gln Leu Asp
                 85                  90                  95

Ser Ala Val Pro Val Asp Gly Val Arg Lys Ile Val Glu Ala Leu Tyr
            100                 105                 110

Thr Cys Ile Thr Lys His Pro Glu Ala Val Arg Leu Leu Leu Met Glu
        115                 120                 125

Asn Leu His Ser Gln Asp Ser Val Asp Ser Thr Ala Ala Tyr Ser Asp
    130                 135                 140

Glu Ser Asn Val Leu Leu Asn Leu Asp Lys Leu Leu Met Leu Gly Gln
145                 150                 155                 160

Asp Ala Gly Ala Phe Arg Pro Gly Ile Ser Ala Glu Asp Val Leu Val
                165                 170                 175

Leu Ile Ser Ser Leu Ala Tyr Phe Arg Val Ser Asn Lys Val Thr Leu
            180                 185                 190

Lys Asn Leu Tyr Ser Leu Asp Leu Glu Ser Glu Ala Asn Ile Glu Gly
        195                 200                 205

Met Lys Arg Ile Val Val Asp Thr Val Leu Ala Phe Leu Thr Ser Asn
    210                 215                 220

Ile Gln Asn Ser Gly Asn Ser Ser Tyr Leu Val Val Gly Gly Lys Thr
225                 230                 235                 240
```

```
Ala Glu Pro Glu Thr Asp Asp Ser Val Tyr Ser Phe Asp Thr Asp Val
                245                 250                 255

Phe Glu Asn
```

<210> 2193
<211> 426
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(403)
<223> RXA01357

<400> 2193

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acggcgcaag tcccgagcac agatatagtt atgcaaatgt ggccaaggca caccaagaat 60

ggctacacgc tgcagataat gacacgacgg aaggtggagc atg agc gct gaa gaa   115
                                            Met Ser Ala Glu Glu
                                              1               5

ctc gac aac tac gaa gca gag gtt gaa ctc tct ctt tac cgc gaa tac   163
Leu Asp Asn Tyr Glu Ala Glu Val Glu Leu Ser Leu Tyr Arg Glu Tyr
                10                  15                  20

cgc gac gta gtc agc cag ttt tcc tat gtt gta gaa act gaa cgt cgc   211
Arg Asp Val Val Ser Gln Phe Ser Tyr Val Val Glu Thr Glu Arg Arg
            25                  30                  35

ttc tac tta gca aat gca gtg cag ctt att cca cac aac agc gga aac   259
Phe Tyr Leu Ala Asn Ala Val Gln Leu Ile Pro His Asn Ser Gly Asn
        40                  45                  50

gat gtc tac tac gaa gtc cgc atg tct gac gcc tgg gta tgg gac atg   307
Asp Val Tyr Tyr Glu Val Arg Met Ser Asp Ala Trp Val Trp Asp Met
    55                  60                  65

tac cgc tca gca cgc ttc gtt cgc tac gtc cga gtg atc acc tac aag   355
Tyr Arg Ser Ala Arg Phe Val Arg Tyr Val Arg Val Ile Thr Tyr Lys
70                  75                  80                  85

gac gtc aac atc gaa gaa tta gat aag cct gac atc atc atg cct gag   403
Asp Val Asn Ile Glu Glu Leu Asp Lys Pro Asp Ile Ile Met Pro Glu
                90                  95                  100

tagttcttag gtttaaaatc gct                                       426
```

<210> 2194
<211> 101
<212> PRT
<213> Corynebacterium glutamicum

<400> 2194

```
Met Ser Ala Glu Glu Leu Asp Asn Tyr Glu Ala Glu Val Glu Leu Ser
  1               5                  10                  15

Leu Tyr Arg Glu Tyr Arg Asp Val Val Ser Gln Phe Ser Tyr Val Val
```

```
            20                  25                  30

Glu Thr Glu Arg Arg Phe Tyr Leu Ala Asn Ala Val Gln Leu Ile Pro
         35                  40                  45

His Asn Ser Gly Asn Asp Val Tyr Tyr Glu Val Arg Met Ser Asp Ala
     50                  55                  60

Trp Val Trp Asp Met Tyr Arg Ser Ala Arg Phe Val Arg Tyr Val Arg
 65                  70                  75                  80

Val Ile Thr Tyr Lys Asp Val Asn Ile Glu Glu Leu Asp Lys Pro Asp
                 85                  90                  95

Ile Ile Met Pro Glu
            100


<210> 2195
<211> 1305
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1282)
<223> RXA01359

<400> 2195
gttggacctt gtgcgatttg gatggggaac agcagcccaa tcttgaccat attgcgcgag 60

ccatggagct tcggggcact acatacagtg aggtagcagc atg att gac tcc cgc   115
                                            Met Ile Asp Ser Arg
                                              1               5

ttg ctg gca tgg gcg tat ctc tca aaa gtg gtg gag ggt ccc aat gca   163
Leu Leu Ala Trp Ala Tyr Leu Ser Lys Val Val Glu Gly Pro Asn Ala
                10                  15                  20

cac ctg caa aag ctc ctg aaa gaa ggt cat gat gta gag cgg atc gca   211
His Leu Gln Lys Leu Leu Lys Glu Gly His Asp Val Glu Arg Ile Ala
            25                  30                  35

ttt ggt att aaa cac cgc gaa gag tgg att ggc gaa ggt ctg ctg aaa   259
Phe Gly Ile Lys His Arg Glu Glu Trp Ile Gly Glu Gly Leu Leu Lys
        40                  45                  50

aac acc gat tcc cgg tac tcg att gat acc gcg caa act gat ctg gaa   307
Asn Thr Asp Ser Arg Tyr Ser Ile Asp Thr Ala Gln Thr Asp Leu Glu
    55                  60                  65

act atc gcc aaa ctc ggt ggg cgg ctc atc aca cct gaa gac gac gaa   355
Thr Ile Ala Lys Leu Gly Gly Arg Leu Ile Thr Pro Glu Asp Asp Glu
70                  75                  80                  85

tgg ccg atg gaa gaa tta gac cat gct ttt gga ttt gcc gct tct ggc   403
Trp Pro Met Glu Glu Leu Asp His Ala Phe Gly Phe Ala Ala Ser Gly
                90                  95                 100

atg agt gat cat gtg cgt acc tat caa gat gat gcg ctg cca ccg cat   451
Met Ser Asp His Val Arg Thr Tyr Gln Asp Asp Ala Leu Pro Pro His
```

```
            105                 110                 115

gcg ttg tgg att agg gga gga aat ctc aga aca ctc agt gca cag tcc   499
Ala Leu Trp Ile Arg Gly Gly Asn Leu Arg Thr Leu Ser Ala Gln Ser
        120                 125                 130

gtc aca ctc gtg ggc acc agg gca ata agc caa tat ggc acg gaa gta   547
Val Thr Leu Val Gly Thr Arg Ala Ile Ser Gln Tyr Gly Thr Glu Val
    135                 140                 145

act cgg gaa ttc acc caa aac ctt gtg tct cat cag tgg aca atc atc   595
Thr Arg Glu Phe Thr Gln Asn Leu Val Ser His Gln Trp Thr Ile Ile
150                 155                 160                 165

tca ggt ggt gcc ttg gga gtt gat agc gtc gcc cat agt gaa gcc gta   643
Ser Gly Gly Ala Leu Gly Val Asp Ser Val Ala His Ser Glu Ala Val
                170                 175                 180

cgt gca caa ggc tcc acc atc gcg atc gca gca tgc gga ttg gat cgc   691
Arg Ala Gln Gly Ser Thr Ile Ala Ile Ala Ala Cys Gly Leu Asp Arg
            185                 190                 195

tcg tac ccc agc cac aat cga gat ctg ttc aac cag att gcc aaa tcc   739
Ser Tyr Pro Ser His Asn Arg Asp Leu Phe Asn Gln Ile Ala Lys Ser
        200                 205                 210

gga aag ggg gcg ttg gtg agt gaa tat cca ccg gga act cca cct caa   787
Gly Lys Gly Ala Leu Val Ser Glu Tyr Pro Pro Gly Thr Pro Pro Gln
    215                 220                 225

cgc cac cgc ttt ctc act cgc aat cgt ctc gtt gct gct cta tct caa   835
Arg His Arg Phe Leu Thr Arg Asn Arg Leu Val Ala Ala Leu Ser Gln
230                 235                 240                 245

gga act gtc gtg gtg gag gca gcc tgg agg tca ggc gcg cta aac act   883
Gly Thr Val Val Val Glu Ala Ala Trp Arg Ser Gly Ala Leu Asn Thr
                250                 255                 260

ttg agc tgg tgt gct ggt tta ggc agg att gct atg gcg gtc cct ggg   931
Leu Ser Trp Cys Ala Gly Leu Gly Arg Ile Ala Met Ala Val Pro Gly
            265                 270                 275

ccg gta aat act gct gga tca ctt ggg tgc cac gaa agg att cga aac   979
Pro Val Asn Thr Ala Gly Ser Leu Gly Cys His Glu Arg Ile Arg Asn
        280                 285                 290

ggc agc gca caa atg gtc acc agt gcg gat gac gtt cgg tca ctt ctg   1027
Gly Ser Ala Gln Met Val Thr Ser Ala Asp Asp Val Arg Ser Leu Leu
    295                 300                 305

ggt gca gtg ggt gca atg gat agc caa act cag tat gaa tta aac ttc   1075
Gly Ala Val Gly Ala Met Asp Ser Gln Thr Gln Tyr Glu Leu Asn Phe
310                 315                 320                 325

gcg gcc act cca gta cag ggt tta acc aga aat gag ctg cga gtt ttt   1123
Ala Ala Thr Pro Val Gln Gly Leu Thr Arg Asn Glu Leu Arg Val Phe
                330                 335                 340

gat gcg tta gac gac cga gga gag ggg agg gaa gcg gcg agt atc gct   1171
Asp Ala Leu Asp Asp Arg Gly Glu Gly Arg Glu Ala Ala Ser Ile Ala
            345                 350                 355
```

```
acc gaa gcc ggg ttg acc ttg cag tta aca att ttc ctt ctc att gca   1219
Thr Glu Ala Gly Leu Thr Leu Gln Leu Thr Ile Phe Leu Leu Ile Ala
        360                 365                 370

ttg aac aag cgc gga atc gtg aaa cgc gac gga act gct tgg tcg aga   1267
Leu Asn Lys Arg Gly Ile Val Lys Arg Asp Gly Thr Ala Trp Ser Arg
    375                 380                 385

aat gcg gaa atg cca taaaacctgg gggttatata aaa                    1305
Asn Ala Glu Met Pro
390
```

<210> 2196
<211> 394
<212> PRT
<213> Corynebacterium glutamicum

<400> 2196

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Met Ile Asp Ser Arg Leu Leu Ala Trp Ala Tyr Leu Ser Lys Val Val
  1               5                  10                  15

Glu Gly Pro Asn Ala His Leu Gln Lys Leu Leu Lys Glu Gly His Asp
             20                  25                  30

Val Glu Arg Ile Ala Phe Gly Ile Lys His Arg Glu Glu Trp Ile Gly
         35                  40                  45

Glu Gly Leu Leu Lys Asn Thr Asp Ser Arg Tyr Ser Ile Asp Thr Ala
     50                  55                  60

Gln Thr Asp Leu Glu Thr Ile Ala Lys Leu Gly Gly Arg Leu Ile Thr
 65                  70                  75                  80

Pro Glu Asp Asp Glu Trp Pro Met Glu Glu Leu Asp His Ala Phe Gly
                 85                  90                  95

Phe Ala Ala Ser Gly Met Ser Asp His Val Arg Thr Tyr Gln Asp Asp
            100                 105                 110

Ala Leu Pro Pro His Ala Leu Trp Ile Arg Gly Gly Asn Leu Arg Thr
        115                 120                 125

Leu Ser Ala Gln Ser Val Thr Leu Val Gly Thr Arg Ala Ile Ser Gln
    130                 135                 140

Tyr Gly Thr Glu Val Thr Arg Glu Phe Thr Gln Asn Leu Val Ser His
145                 150                 155                 160

Gln Trp Thr Ile Ile Ser Gly Gly Ala Leu Gly Val Asp Ser Val Ala
                165                 170                 175

His Ser Glu Ala Val Arg Ala Gln Gly Ser Thr Ile Ala Ile Ala Ala
            180                 185                 190

Cys Gly Leu Asp Arg Ser Tyr Pro Ser His Asn Arg Asp Leu Phe Asn
        195                 200                 205

Gln Ile Ala Lys Ser Gly Lys Gly Ala Leu Val Ser Glu Tyr Pro Pro
    210                 215                 220
```

```
Gly Thr Pro Pro Gln Arg His Arg Phe Leu Thr Arg Asn Arg Leu Val
225                 230                 235                 240

Ala Ala Leu Ser Gln Gly Thr Val Val Val Glu Ala Ala Trp Arg Ser
                245                 250                 255

Gly Ala Leu Asn Thr Leu Ser Trp Cys Ala Gly Leu Gly Arg Ile Ala
            260                 265                 270

Met Ala Val Pro Gly Pro Val Asn Thr Ala Gly Ser Leu Gly Cys His
        275                 280                 285

Glu Arg Ile Arg Asn Gly Ser Ala Gln Met Val Thr Ser Ala Asp Asp
    290                 295                 300

Val Arg Ser Leu Leu Gly Ala Val Gly Ala Met Asp Ser Gln Thr Gln
305                 310                 315                 320

Tyr Glu Leu Asn Phe Ala Ala Thr Pro Val Gln Gly Leu Thr Arg Asn
                325                 330                 335

Glu Leu Arg Val Phe Asp Ala Leu Asp Asp Arg Gly Glu Gly Arg Glu
            340                 345                 350

Ala Ala Ser Ile Ala Thr Glu Ala Gly Leu Thr Leu Gln Leu Thr Ile
        355                 360                 365

Phe Leu Leu Ile Ala Leu Asn Lys Arg Gly Ile Val Lys Arg Asp Gly
    370                 375                 380

Thr Ala Trp Ser Arg Asn Ala Glu Met Pro
385                 390


<210> 2197
<211> 513
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(490)
<223> RXA01366

<400> 2197
atgcatgaaa acaaattcta tgtgtgttga gctgccaaaa ggggttggcg cgccgatgat 60

gactgtccaa acctaaacca aaggtctaaa ctttggcttc gtg agt cag ttt cgt   115
                                          Val Ser Gln Phe Arg
                                            1               5

cgt tgt tcc cgc cct ggt tgt ggc aag cct gcc gtc gca acc ctc acc   163
Arg Cys Ser Arg Pro Gly Cys Gly Lys Pro Ala Val Ala Thr Leu Thr
                10                  15                  20

tac gca tat tcg gat tcc act gcg gtg gtt ggt cct ttg gcg cct gca   211
Tyr Ala Tyr Ser Asp Ser Thr Ala Val Val Gly Pro Leu Ala Pro Ala
            25                  30                  35

gca gag ccc cat agt tgg gat ctg tgt gag cat cat gcc gag cgt att   259
```

```
Ala Glu Pro His Ser Trp Asp Leu Cys Glu His His Ala Glu Arg Ile
         40                  45                  50

act gcg ccc ctt ggt tgg gag atg ctg cgg gtg aac gac atc aaa gtc   307
Thr Ala Pro Leu Gly Trp Glu Met Leu Arg Val Asn Asp Ile Lys Val
     55                  60                  65

gat gac gat gag gat ctg acg gct ctt gct cag gct gtt cgt gag gct   355
Asp Asp Asp Glu Asp Leu Thr Ala Leu Ala Gln Ala Val Arg Glu Ala
 70                  75                  80                  85

gga cgc act gtg agt ggt ctg gtt cct gaa gac gaa gtg ggc ggc aac   403
Gly Arg Thr Val Ser Gly Leu Val Pro Glu Asp Glu Val Gly Gly Asn
                 90                  95                 100

cat ccg gtg aac cgg agt gcg cgg atc gcg gaa cag aag gtt cac cgc   451
His Pro Val Asn Arg Ser Ala Arg Ile Ala Glu Gln Lys Val His Arg
            105                 110                 115

agg ggt cat ctc tat gtt gtg cct gat cag gac gaa tca taaggtttgc    500
Arg Gly His Leu Tyr Val Val Pro Asp Gln Asp Glu Ser
        120                 125                 130

tattcggatt gga                                                   513


<210> 2198
<211> 130
<212> PRT
<213> Corynebacterium glutamicum

<400> 2198
Val Ser Gln Phe Arg Arg Cys Ser Arg Pro Gly Cys Gly Lys Pro Ala
  1               5                  10                  15

Val Ala Thr Leu Thr Tyr Ala Tyr Ser Asp Ser Thr Ala Val Val Gly
             20                  25                  30

Pro Leu Ala Pro Ala Ala Glu Pro His Ser Trp Asp Leu Cys Glu His
         35                  40                  45

His Ala Glu Arg Ile Thr Ala Pro Leu Gly Trp Glu Met Leu Arg Val
     50                  55                  60

Asn Asp Ile Lys Val Asp Asp Asp Glu Asp Leu Thr Ala Leu Ala Gln
 65                  70                  75                  80

Ala Val Arg Glu Ala Gly Arg Thr Val Ser Gly Leu Val Pro Glu Asp
                 85                  90                  95

Glu Val Gly Gly Asn His Pro Val Asn Arg Ser Ala Arg Ile Ala Glu
            100                 105                 110

Gln Lys Val His Arg Arg Gly His Leu Tyr Val Val Pro Asp Gln Asp
        115                 120                 125

Glu Ser
    130


<210> 2199
```

<211> 525
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(502)
<223> RXA01367

<400> 2199
cgcgccaacc ccttttggca gctcaacaca catagaattt gttttcatgc atacgagaac 60

tttccgcaat cggcacggac gcggtctccg cggcccactc atg ccc gtc gaa gtt 115
Met Pro Val Glu Val
1 5

ccc cgc cac gcc tct aga cgc caa gcc ttc gac cgc gca gtc tta gag 163
Pro Arg His Ala Ser Arg Arg Gln Ala Phe Asp Arg Ala Val Leu Glu
10 15 20

gcc tac tcc cct ctt tac ggg att tac caa aaa gag ctc agc aat cta 211
Ala Tyr Ser Pro Leu Tyr Gly Ile Tyr Gln Lys Glu Leu Ser Asn Leu
25 30 35

gac atc gct gtc gat acc gtt cct cgc atg cga ctc agc gcc gac ctt 259
Asp Ile Ala Val Asp Thr Val Pro Arg Met Arg Leu Ser Ala Asp Leu
40 45 50

gcc att ctc ccc gat gaa atc acc gcc gac ggc ccc gtt cca ctt ggt 307
Ala Ile Leu Pro Asp Glu Ile Thr Ala Asp Gly Pro Val Pro Leu Gly
55 60 65

cgc gtc atc cca ccg gcg atc gat acc aag gga aac ccc acg aga gcg 355
Arg Val Ile Pro Pro Ala Ile Asp Thr Lys Gly Asn Pro Thr Arg Ala
70 75 80 85

cgc atc gtt att ttc aga atg ccg atc gag caa cga gtc acc aac gct 403
Arg Ile Val Ile Phe Arg Met Pro Ile Glu Gln Arg Val Thr Asn Ala
90 95 100

gtg gaa cgc cac gag cta ttg act cat gtt ctc acc tct ttg gtg gcg 451
Val Glu Arg His Glu Leu Leu Thr His Val Leu Thr Ser Leu Val Ala
105 110 115

aac tat ctg aat att gat cca cga gac atc gat ccg gga ttc cag gat 499
Asn Tyr Leu Asn Ile Asp Pro Arg Asp Ile Asp Pro Gly Phe Gln Asp
120 125 130

ctc tagcgtggcc ggtgcaccat ggg 525
Leu

<210> 2200
<211> 134
<212> PRT
<213> Corynebacterium glutamicum

<400> 2200
Met Pro Val Glu Val Pro Arg His Ala Ser Arg Arg Gln Ala Phe Asp
1 5 10 15

```
Arg Ala Val Leu Glu Ala Tyr Ser Pro Leu Tyr Gly Ile Tyr Gln Lys
            20                  25                  30

Glu Leu Ser Asn Leu Asp Ile Ala Val Asp Thr Val Pro Arg Met Arg
        35                  40                  45

Leu Ser Ala Asp Leu Ala Ile Leu Pro Asp Glu Ile Thr Ala Asp Gly
    50                  55                  60

Pro Val Pro Leu Gly Arg Val Ile Pro Pro Ala Ile Asp Thr Lys Gly
65                  70                  75                  80

Asn Pro Thr Arg Ala Arg Ile Val Ile Phe Arg Met Pro Ile Glu Gln
                85                  90                  95

Arg Val Thr Asn Ala Val Glu Arg His Glu Leu Leu Thr His Val Leu
            100                 105                 110

Thr Ser Leu Val Ala Asn Tyr Leu Asn Ile Asp Pro Arg Asp Ile Asp
        115                 120                 125

Pro Gly Phe Gln Asp Leu
    130
```

Sequence Listing

<210> 2201
<211> 474
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(451)
<223> RXA01370

<400> 2201

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ctgtctgaat cgtgtgggcg ttagatgaat tgttataaac cggatgttta acggaattta 60

atacgtgtct tattacgcgg actagaaagg ttttagggac atg ggt gca tgg gac   115
                                            Met Gly Ala Trp Asp
                                              1               5

gat gca atc ttg act gag gaa gtc aac gtt gat ttt ctc gac gag atc   163
Asp Ala Ile Leu Thr Glu Glu Val Asn Val Asp Phe Leu Asp Glu Ile
                10                  15                  20

tca gaa tta gat act caa gac att ctt gag gcg ttg gaa gac gca tgt   211
Ser Glu Leu Asp Thr Gln Asp Ile Leu Glu Ala Leu Glu Asp Ala Cys
            25                  30                  35

ttg ctg gtg gtt aac cag gac aac gcc act gaa gac gaa cac ctc aac   259
Leu Leu Val Val Asn Gln Asp Asn Ala Thr Glu Asp Glu His Leu Asn
        40                  45                  50

ggt cag gcg gct gcg acg atc gcg gcc atc atg ttt ggc gct cca tat   307
Gly Gln Ala Ala Ala Thr Ile Ala Ala Ile Met Phe Gly Ala Pro Tyr
    55                  60                  65

tct gcg ggc cag gtg ctg gag aat tac cca ttt atc cgc gaa ctc gtc   355
Ser Ala Gly Gln Val Leu Glu Asn Tyr Pro Phe Ile Arg Glu Leu Val
```

```
 70                  75                  80                  85

ggt gag ggc tct gaa gct ctt cgc ggt gct gca gcg cag gtt ttg gaa   403
Gly Glu Gly Ser Glu Ala Leu Arg Gly Ala Ala Ala Gln Val Leu Glu
                90                  95                  100

gag gca gat gtg gaa tat gac ctc gaa gct tat tta gag gcc ctc aac   451
Glu Ala Asp Val Glu Tyr Asp Leu Glu Ala Tyr Leu Glu Ala Leu Asn
            105                 110                 115

tagccctcca ctaaacagct tca                                        474


<210> 2202
<211> 117
<212> PRT
<213> Corynebacterium glutamicum

<400> 2202
Met Gly Ala Trp Asp Asp Ala Ile Leu Thr Glu Glu Val Asn Val Asp
  1               5                  10                  15

Phe Leu Asp Glu Ile Ser Glu Leu Asp Thr Gln Asp Ile Leu Glu Ala
             20                  25                  30

Leu Glu Asp Ala Cys Leu Leu Val Val Asn Gln Asp Asn Ala Thr Glu
         35                  40                  45

Asp Glu His Leu Asn Gly Gln Ala Ala Ala Thr Ile Ala Ala Ile Met
     50                  55                  60

Phe Gly Ala Pro Tyr Ser Ala Gly Gln Val Leu Glu Asn Tyr Pro Phe
 65                  70                  75                  80

Ile Arg Glu Leu Val Gly Glu Gly Ser Glu Ala Leu Arg Gly Ala Ala
                85                  90                  95

Ala Gln Val Leu Glu Glu Ala Asp Val Glu Tyr Asp Leu Glu Ala Tyr
            100                 105                 110

Leu Glu Ala Leu Asn
        115


<210> 2203
<211> 614
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(591)
<223> RXA01372

<400> 2203
cag gac acc ttc gtc ctt ccc acc ttg ccc acg gcc gca ggc ttg tcg   48
Gln Asp Thr Phe Val Leu Pro Thr Leu Pro Thr Ala Ala Gly Leu Ser
  1               5                  10                  15

cct gcc cgc atc gtg gcg tcg ata agc act ctt tta gat ctt tta gaa   96
Pro Ala Arg Ile Val Ala Ser Ile Ser Thr Leu Leu Asp Leu Leu Glu
```

```
          20                  25                  30

gca gac ccc agc att att tcc gac cgc ttg gaa cac ctc gcc gac tgc   144
Ala Asp Pro Ser Ile Ile Ser Asp Arg Leu Glu His Leu Ala Asp Cys
        35                  40                  45

att gat gag gaa gtg gaa tcg cta tcg ccg gaa cgt gac gaa cta gtc   192
Ile Asp Glu Glu Val Glu Ser Leu Ser Pro Glu Arg Asp Glu Leu Val
    50                  55                  60

aat ccc ggc cga aaa ctg cgc gca tac gta gat cac gca cgg atc gtg   240
Asn Pro Gly Arg Lys Leu Arg Ala Tyr Val Asp His Ala Arg Ile Val
65                  70                  75                  80

cat acc ggc cga act gat gtg gga ctc gcg att gcc aac gtt atc gcc   288
His Thr Gly Arg Thr Asp Val Gly Leu Ala Ile Ala Asn Val Ile Ala
                85                  90                  95

cca atc tgg acc cga cga ggc ctg gta tca gcc gtg ctg gat ttt ccc   336
Pro Ile Trp Thr Arg Arg Gly Leu Val Ser Ala Val Leu Asp Phe Pro
            100                 105                 110

gag ctc atg gaa tca ttg ccg gaa ctc cgc gga ccc gag cca att acc   384
Glu Leu Met Glu Ser Leu Pro Glu Leu Arg Gly Pro Glu Pro Ile Thr
        115                 120                 125

gac gat ata ttc cat gac cca ttc ata gat gac gaa ccc ggg gtg gta   432
Asp Asp Ile Phe His Asp Pro Phe Ile Asp Asp Glu Pro Gly Val Val
    130                 135                 140

ccg ttt agg gct gtt gtc tgg gcc gaa gag gaa ccc gga atc ccc gat   480
Pro Phe Arg Ala Val Val Trp Ala Glu Glu Glu Pro Gly Ile Pro Asp
145                 150                 155                 160

gcc atg gcg caa agc tgc gac gga cct agc aaa ggg gcg ctg aca caa   528
Ala Met Ala Gln Ser Cys Asp Gly Pro Ser Lys Gly Ala Leu Thr Gln
                165                 170                 175

gca ctg cgt ttg ctg gtg cgc gga cag tca gcc acg acc tat tcc att   576
Ala Leu Arg Leu Leu Val Arg Gly Gln Ser Ala Thr Thr Tyr Ser Ile
            180                 185                 190

gaa gaa aag gac ttg taaatggagc tattggaagg ctc                    614
Glu Glu Lys Asp Leu
        195
```

<210> 2204
<211> 197
<212> PRT
<213> Corynebacterium glutamicum

<400> 2204

```
Gln Asp Thr Phe Val Leu Pro Thr Leu Pro Thr Ala Ala Gly Leu Ser
  1               5                  10                  15

Pro Ala Arg Ile Val Ala Ser Ile Ser Thr Leu Leu Asp Leu Leu Glu
             20                  25                  30

Ala Asp Pro Ser Ile Ile Ser Asp Arg Leu Glu His Leu Ala Asp Cys
         35                  40                  45
```

```
Ile Asp Glu Glu Val Glu Ser Leu Ser Pro Glu Arg Asp Glu Leu Val
     50                  55                  60

Asn Pro Gly Arg Lys Leu Arg Ala Tyr Val Asp His Ala Arg Ile Val
 65                  70                  75                  80

His Thr Gly Arg Thr Asp Val Gly Leu Ala Ile Ala Asn Val Ile Ala
                 85                  90                  95

Pro Ile Trp Thr Arg Arg Gly Leu Val Ser Ala Val Leu Asp Phe Pro
            100                 105                 110

Glu Leu Met Glu Ser Leu Pro Glu Leu Arg Gly Pro Glu Pro Ile Thr
        115                 120                 125

Asp Asp Ile Phe His Asp Pro Phe Ile Asp Asp Glu Pro Gly Val Val
    130                 135                 140

Pro Phe Arg Ala Val Val Trp Ala Glu Glu Glu Pro Gly Ile Pro Asp
145                 150                 155                 160

Ala Met Ala Gln Ser Cys Asp Gly Pro Ser Lys Gly Ala Leu Thr Gln
                165                 170                 175

Ala Leu Arg Leu Leu Val Arg Gly Gln Ser Ala Thr Thr Tyr Ser Ile
            180                 185                 190

Glu Glu Lys Asp Leu
        195
```

Sequence Listing

<210> 2205
<211> 1278
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1278)
<223> RXA01378

<400> 2205

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cat gtg tgg att tca cca ggt gcg agc aat ccg atc aag gat cgc ctc   48
His Val Trp Ile Ser Pro Gly Ala Ser Asn Pro Ile Lys Asp Arg Leu
  1               5                  10                  15

ttc cct tgg aca ttg gtg aag gct ttt ctc tcc tcc cct gca gcc ttg   96
Phe Pro Trp Thr Leu Val Lys Ala Phe Leu Ser Ser Pro Ala Ala Leu
             20                  25                  30

ggc gaa aca gtg tcc aat cgc ctc aaa aag gcc tct gca cca gaa gaa   144
Gly Glu Thr Val Ser Asn Arg Leu Lys Lys Ala Ser Ala Pro Glu Glu
         35                  40                  45

aaa cgc gcc cta gaa acc ctt tca caa ctt aat tct gcg atc acc ccg   192
Lys Arg Ala Leu Glu Thr Leu Ser Gln Leu Asn Ser Ala Ile Thr Pro
     50                  55                  60

cag acc tca cag aag tac caa tct cta ctg agc tac ctc ggt gac atc   240
Gln Thr Ser Gln Lys Tyr Gln Ser Leu Leu Ser Tyr Leu Gly Asp Ile
```

```
65                  70                  75                  80

gga gtg aag aag aac tcc gat acc cgc gtg gtg att ttc tct gag cgt   288
Gly Val Lys Lys Asn Ser Asp Thr Arg Val Val Ile Phe Ser Glu Arg
                85                  90                  95

gtc gct act ttg cac tgg ctg cag gaa aac ctc atc cgt gat ctc aag   336
Val Ala Thr Leu His Trp Leu Gln Glu Asn Leu Ile Arg Asp Leu Lys
            100                 105                 110

atg cca ccc aac tct att gct gtt atg cac ggc ggt ctc ccc gac cag   384
Met Pro Pro Asn Ser Ile Ala Val Met His Gly Gly Leu Pro Asp Gln
        115                 120                 125

gag caa atg cgc ctg gtg gat gag ttt aaa aag acg gat tct ccc atc   432
Glu Gln Met Arg Leu Val Asp Glu Phe Lys Lys Thr Asp Ser Pro Ile
    130                 135                 140

cgc atc atg atc acc ggc gat gtt gcc tca gaa ggt gtg aac ctg cat   480
Arg Ile Met Ile Thr Gly Asp Val Ala Ser Glu Gly Val Asn Leu His
145                 150                 155                 160

act ctc tgc cac aac ttg gtg cac tat gac atc ccg tgg tca ctg atc   528
Thr Leu Cys His Asn Leu Val His Tyr Asp Ile Pro Trp Ser Leu Ile
                165                 170                 175

cgc att cag cag cgc aat ggc cgt att gat cgt tat ggt caa acc cac   576
Arg Ile Gln Gln Arg Asn Gly Arg Ile Asp Arg Tyr Gly Gln Thr His
            180                 185                 190

aac cct tcc atc gtt acc ttc ttg ctc gat ccc gcc gag gat tcc aaa   624
Asn Pro Ser Ile Val Thr Phe Leu Leu Asp Pro Ala Glu Asp Ser Lys
        195                 200                 205

gta ggt gaa gtc cat gtg ctg gag agg ctc atg gag cgc gaa cat gag   672
Val Gly Glu Val His Val Leu Glu Arg Leu Met Glu Arg Glu His Glu
    210                 215                 220

gcg cac tct ttg ctc ggt gat gcc gca tct ctc atg ggc aag cac tct   720
Ala His Ser Leu Leu Gly Asp Ala Ala Ser Leu Met Gly Lys His Ser
225                 230                 235                 240

gag cgt ttg gaa gaa gaa acc atc cgc gaa gtc ctg cgc ggt gcc caa   768
Glu Arg Leu Glu Glu Glu Thr Ile Arg Glu Val Leu Arg Gly Ala Gln
                245                 250                 255

aac ttt aat gat gca gtg gct gat cca gcg gaa gtc cta gaa aac cca   816
Asn Phe Asn Asp Ala Val Ala Asp Pro Ala Glu Val Leu Glu Asn Pro
            260                 265                 270

gca ggc cta gat gat att gat tgg ttg cta gcc caa atc gcc caa gcc   864
Ala Gly Leu Asp Asp Ile Asp Trp Leu Leu Ala Gln Ile Ala Gln Ala
        275                 280                 285

gat gcc aag gca gaa aca gaa gca gaa gca gaa aca gaa aac caa aca   912
Asp Ala Lys Ala Glu Thr Glu Ala Glu Ala Glu Thr Glu Asn Gln Thr
    290                 295                 300

gca cca gat gca gct tcc aat agc acg cag cat gca caa cgc cgg ttg   960
Ala Pro Asp Ala Ala Ser Asn Ser Thr Gln His Ala Gln Arg Arg Leu
305                 310                 315                 320
```

```
tat gca cag gaa agc tct ttc ctc tat gac tgc ctc ctc gaa ggt ttc   1008
Tyr Ala Gln Glu Ser Ser Phe Leu Tyr Asp Cys Leu Leu Glu Gly Phe
                325                 330                 335

aat aac gta ccg gag gat tcc atc aac cgc ggt ggc gtg ggg ttc aaa   1056
Asn Asn Val Pro Glu Asp Ser Ile Asn Arg Gly Gly Val Gly Phe Lys
            340                 345                 350

aaa cac gat aat gac atc gtg gag ctc acc ccc acc gat gat ctg cgc   1104
Lys His Asp Asn Asp Ile Val Glu Leu Thr Pro Thr Asp Asp Leu Arg
        355                 360                 365

cgt cgt cta gat ttc ctc ccg cag gat tat gtg gct gct cgg aaa gtt   1152
Arg Arg Leu Asp Phe Leu Pro Gln Asp Tyr Val Ala Ala Arg Lys Val
    370                 375                 380

aag gaa gat ctc cta cta gct tcc aca ctg atg cgt ggc caa gaa cgc   1200
Lys Glu Asp Leu Leu Leu Ala Ser Thr Leu Met Arg Gly Gln Glu Arg
385                 390                 395                 400

ctc aac gct gcg cgc act ggt gaa gat ggc agt acc tgg cca agt gcc   1248
Leu Asn Ala Ala Arg Thr Gly Glu Asp Gly Ser Thr Trp Pro Ser Ala
                405                 410                 415

cac tat cta ggc ccc ctg cac cca gtc act                          1278
His Tyr Leu Gly Pro Leu His Pro Val Thr
            420                 425
```

<210> 2206
<211> 426
<212> PRT
<213> Corynebacterium glutamicum

<400> 2206

```
His Val Trp Ile Ser Pro Gly Ala Ser Asn Pro Ile Lys Asp Arg Leu
  1               5                  10                  15

Phe Pro Trp Thr Leu Val Lys Ala Phe Leu Ser Ser Pro Ala Ala Leu
             20                  25                  30

Gly Glu Thr Val Ser Asn Arg Leu Lys Lys Ala Ser Ala Pro Glu Glu
         35                  40                  45

Lys Arg Ala Leu Glu Thr Leu Ser Gln Leu Asn Ser Ala Ile Thr Pro
     50                  55                  60

Gln Thr Ser Gln Lys Tyr Gln Ser Leu Leu Ser Tyr Leu Gly Asp Ile
 65                  70                  75                  80

Gly Val Lys Lys Asn Ser Asp Thr Arg Val Val Ile Phe Ser Glu Arg
                 85                  90                  95

Val Ala Thr Leu His Trp Leu Gln Glu Asn Leu Ile Arg Asp Leu Lys
            100                 105                 110

Met Pro Pro Asn Ser Ile Ala Val Met His Gly Gly Leu Pro Asp Gln
        115                 120                 125

Glu Gln Met Arg Leu Val Asp Glu Phe Lys Lys Thr Asp Ser Pro Ile
```

```
    130                 135                 140

Arg Ile Met Ile Thr Gly Asp Val Ala Ser Glu Gly Val Asn Leu His
145                 150                 155                 160

Thr Leu Cys His Asn Leu Val His Tyr Asp Ile Pro Trp Ser Leu Ile
                165                 170                 175

Arg Ile Gln Gln Arg Asn Gly Arg Ile Asp Arg Tyr Gly Gln Thr His
            180                 185                 190

Asn Pro Ser Ile Val Thr Phe Leu Leu Asp Pro Ala Glu Asp Ser Lys
        195                 200                 205

Val Gly Glu Val His Val Leu Glu Arg Leu Met Glu Arg Glu His Glu
    210                 215                 220

Ala His Ser Leu Leu Gly Asp Ala Ala Ser Leu Met Gly Lys His Ser
225                 230                 235                 240

Glu Arg Leu Glu Glu Glu Thr Ile Arg Glu Val Leu Arg Gly Ala Gln
                245                 250                 255

Asn Phe Asn Asp Ala Val Ala Asp Pro Ala Glu Val Leu Glu Asn Pro
            260                 265                 270

Ala Gly Leu Asp Asp Ile Asp Trp Leu Leu Ala Gln Ile Ala Gln Ala
        275                 280                 285

Asp Ala Lys Ala Glu Thr Glu Ala Glu Ala Glu Thr Glu Asn Gln Thr
    290                 295                 300

Ala Pro Asp Ala Ala Ser Asn Ser Thr Gln His Ala Gln Arg Arg Leu
305                 310                 315                 320

Tyr Ala Gln Glu Ser Ser Phe Leu Tyr Asp Cys Leu Leu Glu Gly Phe
                325                 330                 335

Asn Asn Val Pro Glu Asp Ser Ile Asn Arg Gly Gly Val Gly Phe Lys
            340                 345                 350

Lys His Asp Asn Asp Ile Val Glu Leu Thr Pro Thr Asp Asp Leu Arg
        355                 360                 365

Arg Arg Leu Asp Phe Leu Pro Gln Asp Tyr Val Ala Ala Arg Lys Val
    370                 375                 380

Lys Glu Asp Leu Leu Leu Ala Ser Thr Leu Met Arg Gly Gln Glu Arg
385                 390                 395                 400

Leu Asn Ala Ala Arg Thr Gly Glu Asp Gly Ser Thr Trp Pro Ser Ala
                405                 410                 415

His Tyr Leu Gly Pro Leu His Pro Val Thr
            420                 425
```

<210> 2207
<211> 2039
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(2016)
<223> RXA01380

<400> 2207

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tcg ctg att ttg gga tgc gac acc aag gct cgc ctg gag gat ctg tac   48
Ser Leu Ile Leu Gly Cys Asp Thr Lys Ala Arg Leu Glu Asp Leu Tyr
  1               5                  10                  15

ctg ccg ttc aaa aaa cgg cgc aag acg aag gcc gat atc gct agg gag   96
Leu Pro Phe Lys Lys Arg Arg Lys Thr Lys Ala Asp Ile Ala Arg Glu
             20                  25                  30

gcg ggc ctg gag ggg ctc gtc gat aag ctt atc gac gcc ccg tcc ctc   144
Ala Gly Leu Glu Gly Leu Val Asp Lys Leu Ile Asp Ala Pro Ser Leu
         35                  40                  45

gac gcc gca gcg cag gca gct gca ttt acg act gag ggc ttt gag gat   192
Asp Ala Ala Ala Gln Ala Ala Ala Phe Thr Thr Glu Gly Phe Glu Asp
     50                  55                  60

tcc aaa aaa gtt ttg gat ggc gct cgc gcc att ttg att gac cgc ttc   240
Ser Lys Lys Val Leu Asp Gly Ala Arg Ala Ile Leu Ile Asp Arg Phe
 65                  70                  75                  80

gcg ctc gat gcc gat ttg gtg ggc gag gtg cgt gag caa atg tat cgc   288
Ala Leu Asp Ala Asp Leu Val Gly Glu Val Arg Glu Gln Met Tyr Arg
                 85                  90                  95

gcg ggt tcc atg gcg gca tcg gtg gtg gcg ggc aag gag cag gaa ggc   336
Ala Gly Ser Met Ala Ala Ser Val Val Ala Gly Lys Glu Gln Glu Gly
            100                 105                 110

gca aag ttc aag gac tac ttt gag ttt tcc gaa cct ttt gac aag ctt   384
Ala Lys Phe Lys Asp Tyr Phe Glu Phe Ser Glu Pro Phe Asp Lys Leu
        115                 120                 125

cca tct cac cga att ttg gcg ctg ctg cgc ggt gaa aac gaa ggt gtg   432
Pro Ser His Arg Ile Leu Ala Leu Leu Arg Gly Glu Asn Glu Gly Val
    130                 135                 140

ctg agc ctc aac ctc gat gcg ggc gac gac ata atc tac gaa ggt ttg   480
Leu Ser Leu Asn Leu Asp Ala Gly Asp Asp Ile Ile Tyr Glu Gly Leu
145                 150                 155                 160

atc gcc gac cga ttc tcc ctg gac acc cac act tct agc tgg ctg gct   528
Ile Ala Asp Arg Phe Ser Leu Asp Thr His Thr Ser Ser Trp Leu Ala
                165                 170                 175

gag gct gtg cgc tgg ggt tgg cgc acc aaa ctg tat gtg tcc tcc gga   576
Glu Ala Val Arg Trp Gly Trp Arg Thr Lys Leu Tyr Val Ser Ser Gly
            180                 185                 190

ttg gat gtg cgc atg cgt ctg aaa gaa aaa gca gag gaa ggc gca ctc   624
Leu Asp Val Arg Met Arg Leu Lys Glu Lys Ala Glu Glu Gly Ala Leu
        195                 200                 205

gat gtg ttt gcc acc aac ctc cgc gac gtt ctc ctt gca gct ccc gct   672
Asp Val Phe Ala Thr Asn Leu Arg Asp Val Leu Leu Ala Ala Pro Ala
```

```
    210                 215                 220

ggt cag cgc tcc aca att ggc ctt gac ccg gga ttc cgc aac ggt gtg   720
Gly Gln Arg Ser Thr Ile Gly Leu Asp Pro Gly Phe Arg Asn Gly Val
225                 230                 235                 240

aaa gta gct gtc gtg gat tcc acc ggt aag gat gtt gcc acc acg atc   768
Lys Val Ala Val Val Asp Ser Thr Gly Lys Asp Val Ala Thr Thr Ile
                245                 250                 255

gtc tac cca cac cag ccc caa aac cgc tgg aag gaa gcc gta tcc gaa   816
Val Tyr Pro His Gln Pro Gln Asn Arg Trp Lys Glu Ala Val Ser Glu
            260                 265                 270

ctg gct aac ctg tgc gcg acc cac ggt gtg gaa ctc atg gcg atc ggc   864
Leu Ala Asn Leu Cys Ala Thr His Gly Val Glu Leu Met Ala Ile Gly
        275                 280                 285

aac gga acc gcc tcg agg gaa acg gaa aaa ctc gcc ggc gaa gta gct   912
Asn Gly Thr Ala Ser Arg Glu Thr Glu Lys Leu Ala Gly Glu Val Ala
    290                 295                 300

gac atg atc aaa gcc gca ggt ggc acg cga cca acc ccc gtg gtg gtc   960
Asp Met Ile Lys Ala Ala Gly Gly Thr Arg Pro Thr Pro Val Val Val
305                 310                 315                 320

tcc gaa tcg ggc gca tcc gtg tac tcg gca tca ccg atc gca gcc gaa  1008
Ser Glu Ser Gly Ala Ser Val Tyr Ser Ala Ser Pro Ile Ala Ala Glu
                325                 330                 335

gaa ttc ccc gac atg gac gtc tcc ctc cgc ggt gca gtt tct atc gcg  1056
Glu Phe Pro Asp Met Asp Val Ser Leu Arg Gly Ala Val Ser Ile Ala
            340                 345                 350

agg cga ctc cag gat cca ctg gcg gag ctc gtc aag att gag ccc aaa  1104
Arg Arg Leu Gln Asp Pro Leu Ala Glu Leu Val Lys Ile Glu Pro Lys
        355                 360                 365

gcc atc gga gtc ggc cag tac caa cac gat gtc aac cag gtt gca ctt  1152
Ala Ile Gly Val Gly Gln Tyr Gln His Asp Val Asn Gln Val Ala Leu
    370                 375                 380

gcc aaa acc ctt gat ggt gtc gtc gaa gac gca gta aac gca gtc gga  1200
Ala Lys Thr Leu Asp Gly Val Val Glu Asp Ala Val Asn Ala Val Gly
385                 390                 395                 400

gtt aac ctc aac acc gca tcc gca cca ctt ctt acc cga gtt gcc gga  1248
Val Asn Leu Asn Thr Ala Ser Ala Pro Leu Leu Thr Arg Val Ala Gly
                405                 410                 415

gtg acc tcc acc ttg gca aac aat atc gtg gcc tac cgc aac gaa aac  1296
Val Thr Ser Thr Leu Ala Asn Asn Ile Val Ala Tyr Arg Asn Glu Asn
            420                 425                 430

ggt gga ttc tcc tcc cga aaa gaa ctg aac aaa gtt cct cgc ctg gga  1344
Gly Gly Phe Ser Ser Arg Lys Glu Leu Asn Lys Val Pro Arg Leu Gly
        435                 440                 445

ccc aaa gcc ttt gaa cag tgt gct ggc ttc ctc cgc att tct gga tcc  1392
Pro Lys Ala Phe Glu Gln Cys Ala Gly Phe Leu Arg Ile Ser Gly Ser
    450                 455                 460
```

```
acc gac cct ctc gac gcc tcc gct gtt cac ccc gag gcg tac cca gtt   1440
Thr Asp Pro Leu Asp Ala Ser Ala Val His Pro Glu Ala Tyr Pro Val
465                 470                 475                 480

gtt cgc aac att gcg aaa gcc aca gga ttg gat gtc tcg gga ctg atc   1488
Val Arg Asn Ile Ala Lys Ala Thr Gly Leu Asp Val Ser Gly Leu Ile
                485                 490                 495

gga aac tct gcg gtg ctc acc aaa ttg aag ccc gct gat ttc gct gat   1536
Gly Asn Ser Ala Val Leu Thr Lys Leu Lys Pro Ala Asp Phe Ala Asp
            500                 505                 510

gaa cga ttc ggc atc ccc acc gtc acc gac atc atc gcc gag ctg gat   1584
Glu Arg Phe Gly Ile Pro Thr Val Thr Asp Ile Ile Ala Glu Leu Asp
        515                 520                 525

aaa ccc gga cgt gac ccc cgc cca gaa ttc aaa acc gcc agc ttc aaa   1632
Lys Pro Gly Arg Asp Pro Arg Pro Glu Phe Lys Thr Ala Ser Phe Lys
    530                 535                 540

gaa ggc gtg gag aaa atc tcc gac ctc aca ccc ggc atg atc ctg gaa   1680
Glu Gly Val Glu Lys Ile Ser Asp Leu Thr Pro Gly Met Ile Leu Glu
545                 550                 555                 560

gga act gtc acc aac gtt gcg gcg ttc ggc gca ttc gtt gac gtg gga   1728
Gly Thr Val Thr Asn Val Ala Ala Phe Gly Ala Phe Val Asp Val Gly
                565                 570                 575

gtg cac cga gat ggc ctc gtt cac gtt tcc gcg atg agc gac aaa ttc   1776
Val His Arg Asp Gly Leu Val His Val Ser Ala Met Ser Asp Lys Phe
            580                 585                 590

atc tcc aac ccc cac gaa gtt gtt cgc tct ggt gag gtc gtg aag gta   1824
Ile Ser Asn Pro His Glu Val Val Arg Ser Gly Glu Val Val Lys Val
        595                 600                 605

aag gtc atg gaa gtt gac gtc gac cgc aaa cgc atc ggc ctt tcc ctc   1872
Lys Val Met Glu Val Asp Val Asp Arg Lys Arg Ile Gly Leu Ser Leu
    610                 615                 620

cgc ttg acc gat gaa ccc ggt gcc cca gct ccg caa aag cgc gga aac   1920
Arg Leu Thr Asp Glu Pro Gly Ala Pro Ala Pro Gln Lys Arg Gly Asn
625                 630                 635                 640

cga cca gcc aaa cag cag cga gct ccg caa aaa cag tcc gct aag ccc   1968
Arg Pro Ala Lys Gln Gln Arg Ala Pro Gln Lys Gln Ser Ala Lys Pro
                645                 650                 655

gcc aca ggt tcc atg gca gat gct tta cga cgc gcc ggc ctc ggt ggc   2016
Ala Thr Gly Ser Met Ala Asp Ala Leu Arg Arg Ala Gly Leu Gly Gly
            660                 665                 670

taaggcaact ttcaaaccaa gcg                                        2039
```

<210> 2208
<211> 672
<212> PRT
<213> Corynebacterium glutamicum

<400> 2208

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Ser Leu Ile Leu Gly Cys Asp Thr Lys Ala Arg Leu Glu Asp Leu Tyr
  1               5                  10                  15

Leu Pro Phe Lys Lys Arg Arg Lys Thr Lys Ala Asp Ile Ala Arg Glu
            20                  25                  30

Ala Gly Leu Glu Gly Leu Val Asp Lys Leu Ile Asp Ala Pro Ser Leu
        35                  40                  45

Asp Ala Ala Ala Gln Ala Ala Ala Phe Thr Thr Glu Gly Phe Glu Asp
    50                  55                  60

Ser Lys Lys Val Leu Asp Gly Ala Arg Ala Ile Leu Ile Asp Arg Phe
65                  70                  75                  80

Ala Leu Asp Ala Asp Leu Val Gly Glu Val Arg Glu Gln Met Tyr Arg
                85                  90                  95

Ala Gly Ser Met Ala Ala Ser Val Val Ala Gly Lys Glu Gln Glu Gly
            100                 105                 110

Ala Lys Phe Lys Asp Tyr Phe Glu Phe Ser Glu Pro Phe Asp Lys Leu
        115                 120                 125

Pro Ser His Arg Ile Leu Ala Leu Leu Arg Gly Glu Asn Glu Gly Val
    130                 135                 140

Leu Ser Leu Asn Leu Asp Ala Gly Asp Asp Ile Ile Tyr Glu Gly Leu
145                 150                 155                 160

Ile Ala Asp Arg Phe Ser Leu Asp Thr His Thr Ser Ser Trp Leu Ala
                165                 170                 175

Glu Ala Val Arg Trp Gly Trp Arg Thr Lys Leu Tyr Val Ser Ser Gly
            180                 185                 190

Leu Asp Val Arg Met Arg Leu Lys Glu Lys Ala Glu Glu Gly Ala Leu
        195                 200                 205

Asp Val Phe Ala Thr Asn Leu Arg Asp Val Leu Leu Ala Ala Pro Ala
    210                 215                 220

Gly Gln Arg Ser Thr Ile Gly Leu Asp Pro Gly Phe Arg Asn Gly Val
225                 230                 235                 240

Lys Val Ala Val Val Asp Ser Thr Gly Lys Asp Val Ala Thr Thr Ile
                245                 250                 255

Val Tyr Pro His Gln Pro Gln Asn Arg Trp Lys Glu Ala Val Ser Glu
            260                 265                 270

Leu Ala Asn Leu Cys Ala Thr His Gly Val Glu Leu Met Ala Ile Gly
        275                 280                 285

Asn Gly Thr Ala Ser Arg Glu Thr Glu Lys Leu Ala Gly Glu Val Ala
    290                 295                 300

Asp Met Ile Lys Ala Ala Gly Gly Thr Arg Pro Thr Pro Val Val Val
305                 310                 315                 320
```

```
Ser Glu Ser Gly Ala Ser Val Tyr Ser Ala Ser Pro Ile Ala Ala Glu
                325                 330                 335

Glu Phe Pro Asp Met Asp Val Ser Leu Arg Gly Ala Val Ser Ile Ala
            340                 345                 350

Arg Arg Leu Gln Asp Pro Leu Ala Glu Leu Val Lys Ile Glu Pro Lys
        355                 360                 365

Ala Ile Gly Val Gly Gln Tyr Gln His Asp Val Asn Gln Val Ala Leu
    370                 375                 380

Ala Lys Thr Leu Asp Gly Val Val Glu Asp Ala Val Asn Ala Val Gly
385                 390                 395                 400

Val Asn Leu Asn Thr Ala Ser Ala Pro Leu Leu Thr Arg Val Ala Gly
                405                 410                 415

Val Thr Ser Thr Leu Ala Asn Asn Ile Val Ala Tyr Arg Asn Glu Asn
            420                 425                 430

Gly Gly Phe Ser Ser Arg Lys Glu Leu Asn Lys Val Pro Arg Leu Gly
        435                 440                 445

Pro Lys Ala Phe Glu Gln Cys Ala Gly Phe Leu Arg Ile Ser Gly Ser
    450                 455                 460

Thr Asp Pro Leu Asp Ala Ser Ala Val His Pro Glu Ala Tyr Pro Val
465                 470                 475                 480

Val Arg Asn Ile Ala Lys Ala Thr Gly Leu Asp Val Ser Gly Leu Ile
                485                 490                 495

Gly Asn Ser Ala Val Leu Thr Lys Leu Lys Pro Ala Asp Phe Ala Asp
            500                 505                 510

Glu Arg Phe Gly Ile Pro Thr Val Thr Asp Ile Ile Ala Glu Leu Asp
        515                 520                 525

Lys Pro Gly Arg Asp Pro Arg Pro Glu Phe Lys Thr Ala Ser Phe Lys
    530                 535                 540

Glu Gly Val Glu Lys Ile Ser Asp Leu Thr Pro Gly Met Ile Leu Glu
545                 550                 555                 560

Gly Thr Val Thr Asn Val Ala Ala Phe Gly Ala Phe Val Asp Val Gly
                565                 570                 575

Val His Arg Asp Gly Leu Val His Val Ser Ala Met Ser Asp Lys Phe
            580                 585                 590

Ile Ser Asn Pro His Glu Val Val Arg Ser Gly Glu Val Val Lys Val
        595                 600                 605

Lys Val Met Glu Val Asp Val Asp Arg Lys Arg Ile Gly Leu Ser Leu
    610                 615                 620

Arg Leu Thr Asp Glu Pro Gly Ala Pro Ala Pro Gln Lys Arg Gly Asn
625                 630                 635                 640

Arg Pro Ala Lys Gln Gln Arg Ala Pro Gln Lys Gln Ser Ala Lys Pro
```

```
                645                 650                 655

Ala Thr Gly Ser Met Ala Asp Ala Leu Arg Arg Ala Gly Leu Gly Gly
            660                 665                 670
```

<210> 2209
<211> 1839
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1816)
<223> RXA01384

<400> 2209

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actgtccctc actctgcgag cagccattgc gctatcggca gctacctgca aggtgcgctg 60

gtgggaagcg tcgacaagca tctttaagta gcgttgatgt atg cgc tca ctt caa   115
                                              Met Arg Ser Leu Gln
                                                1               5

tcg gtc ctt gac ctg ctg act tct aag tcc aaa gtg gct acc aaa att   163
Ser Val Leu Asp Leu Leu Thr Ser Lys Ser Lys Val Ala Thr Lys Ile
                10                  15                  20

gtg gtg gaa cga att gaa aag cat cct gtt cat gga ttg gga tgg atg   211
Val Val Glu Arg Ile Glu Lys His Pro Val His Gly Leu Gly Trp Met
            25                  30                  35

atg tat ccg cca ttt cat cca tgg act gat gct tcg acc ttg acg att   259
Met Tyr Pro Pro Phe His Pro Trp Thr Asp Ala Ser Thr Leu Thr Ile
        40                  45                  50

gag cga aac gga acc agt cgg cgc gcg agt cag aat ggc gtt gcg gtt   307
Glu Arg Asn Gly Thr Ser Arg Arg Ala Ser Gln Asn Gly Val Ala Val
    55                  60                  65

ctt cat cag cat gag caa gtt caa act atc ggt cta gcc agc tat ttt   355
Leu His Gln His Glu Gln Val Gln Thr Ile Gly Leu Ala Ser Tyr Phe
70                  75                  80                  85

atc gac tcc aag att tgg gta aac gag ctg gct ggc ctt gat cgt atc   403
Ile Asp Ser Lys Ile Trp Val Asn Glu Leu Ala Gly Leu Asp Arg Ile
                90                  95                  100

aac att tct gag agt gaa gtt gct ggt cgt gac gta tta gtt ctg ccg   451
Asn Ile Ser Glu Ser Glu Val Ala Gly Arg Asp Val Leu Val Leu Pro
            105                 110                 115

tta tct gat ctg act tta agc atc gat gcg aaa tac ggc gtg gtt ttg   499
Leu Ser Asp Leu Thr Leu Ser Ile Asp Ala Lys Tyr Gly Val Val Leu
        120                 125                 130

gct gcg gaa gac agc gat gaa tca gtg cgc gcg gta tcc gtg gag ttc   547
Ala Ala Glu Asp Ser Asp Glu Ser Val Arg Ala Val Ser Val Glu Phe
    135                 140                 145
```

```
ctg gac cag tgg gta gat gaa gaa gaa ccc cca gcg gaa gaa gtg cct   595
Leu Asp Gln Trp Val Asp Glu Glu Glu Pro Pro Ala Glu Glu Val Pro
150                 155                 160                 165

aaa tat acg gaa acc agg gag gaa ctt cct cca ctt gag att cct ccg   643
Lys Tyr Thr Glu Thr Arg Glu Glu Leu Pro Pro Leu Glu Ile Pro Pro
                170                 175                 180

gct cct tcc gga aat cgt aat ctc cga gtt ctg tgc acg tgg gga gcg   691
Ala Pro Ser Gly Asn Arg Asn Leu Arg Val Leu Cys Thr Trp Gly Ala
            185                 190                 195

atg gaa gga att att cct gag tgg aaa ccc ggc gat caa gtt tca ctg   739
Met Glu Gly Ile Ile Pro Glu Trp Lys Pro Gly Asp Gln Val Ser Leu
        200                 205                 210

ttt ttg tct ttc gac ctc gac gat ccg ccg ttc gaa cag ctc aaa acc   787
Phe Leu Ser Phe Asp Leu Asp Asp Pro Pro Phe Glu Gln Leu Lys Thr
    215                 220                 225

act cgt cgc ggg tac acc gaa cct ggc gag att tat gga aac cag cgc   835
Thr Arg Arg Gly Tyr Thr Glu Pro Gly Glu Ile Tyr Gly Asn Gln Arg
230                 235                 240                 245

agc tat aaa ttt cac gct gat ggt tgg aac gct gtt att tcc gcc aaa   883
Ser Tyr Lys Phe His Ala Asp Gly Trp Asn Ala Val Ile Ser Ala Lys
                250                 255                 260

gtg cca ctg cgc acc gaa gaa aac ctc acc ggc tac ttc acc cac agc   931
Val Pro Leu Arg Thr Glu Glu Asn Leu Thr Gly Tyr Phe Thr His Ser
            265                 270                 275

tcc tac gcg gac acg agc cgc cgc acg tca gcg gtc atc acc gca gtc   979
Ser Tyr Ala Asp Thr Ser Arg Arg Thr Ser Ala Val Ile Thr Ala Val
        280                 285                 290

tac cgc cac ggt aag gac gca att atc gac gtg acc ctc gac ggt gcg   1027
Tyr Arg His Gly Lys Asp Ala Ile Ile Asp Val Thr Leu Asp Gly Ala
    295                 300                 305

aaa cct cct aga tat caa gaa tcc ttg gat tgg agc agc acc agt acc   1075
Lys Pro Pro Arg Tyr Gln Glu Ser Leu Asp Trp Ser Ser Thr Ser Thr
310                 315                 320                 325

tgt gac ggt gaa aca atc tgg ctg tcc gat aag agc ttg ccc ttc gtc   1123
Cys Asp Gly Glu Thr Ile Trp Leu Ser Asp Lys Ser Leu Pro Phe Val
                330                 335                 340

cgc ggt ttc aat gtc tcc aca ggc aag cta gta cac gag atc tcc ata   1171
Arg Gly Phe Asn Val Ser Thr Gly Lys Leu Val His Glu Ile Ser Ile
            345                 350                 355

ccc acc ttc aat gag atc gcc ctc gaa tcc ggc aat aga gcc cgc gca   1219
Pro Thr Phe Asn Glu Ile Ala Leu Glu Ser Gly Asn Arg Ala Arg Ala
        360                 365                 370

gcg aaa aaa ctt tgg gaa ctt cca gat ctt aaa gag gca acc gac cct   1267
Ala Lys Lys Leu Trp Glu Leu Pro Asp Leu Lys Glu Ala Thr Asp Pro
    375                 380                 385
```

```
gtc cca gcg atc ccc gcg ggc tgg aaa cta cac aaa aga ttc ggg aaa   1315
Val Pro Ala Ile Pro Ala Gly Trp Lys Leu His Lys Arg Phe Gly Lys
390                 395                 400                 405

aac ttc cat atc gta agc gct gac aac gga acc tgg aaa caa acc atc   1363
Asn Phe His Ile Val Ser Ala Asp Asn Gly Thr Trp Lys Gln Thr Ile
                410                 415                 420

ctt agg atc aaa ccc ttc aaa gca att gag ctt gat ctt gga tac gcc   1411
Leu Arg Ile Lys Pro Phe Lys Ala Ile Glu Leu Asp Leu Gly Tyr Ala
            425                 430                 435

aag att tcg acg att tac caa tac ggt gaa cga att tat ctg cgt tcc   1459
Lys Ile Ser Thr Ile Tyr Gln Tyr Gly Glu Arg Ile Tyr Leu Arg Ser
        440                 445                 450

gat ctt cac cag atc acg ttt aat cag gat ctt gaa atc ctc agt gta   1507
Asp Leu His Gln Ile Thr Phe Asn Gln Asp Leu Glu Ile Leu Ser Val
    455                 460                 465

gag gtc cac gga aat ccc gat gca ggt tat tgg cca ctt tcc gat ctt   1555
Glu Val His Gly Asn Pro Asp Ala Gly Tyr Trp Pro Leu Ser Asp Leu
470                 475                 480                 485

cca cca ggg gat tct cca acg ctg gga ttt cct atc gga tca ctc atg   1603
Pro Pro Gly Asp Ser Pro Thr Leu Gly Phe Pro Ile Gly Ser Leu Met
                490                 495                 500

atg ttc cac gaa caa caa gat atc tac gct ttc cac gat cct aaa aca   1651
Met Phe His Glu Gln Gln Asp Ile Tyr Ala Phe His Asp Pro Lys Thr
            505                 510                 515

aca aag caa cta aca act gtg aac ttg ccc aaa agg cag ttt gaa gtg   1699
Thr Lys Gln Leu Thr Thr Val Asn Leu Pro Lys Arg Gln Phe Glu Val
        520                 525                 530

gaa tat gct tct cag aac aga att gtt att tcg ctg aaa aat cca gaa   1747
Glu Tyr Ala Ser Gln Asn Arg Ile Val Ile Ser Leu Lys Asn Pro Glu
    535                 540                 545

agc cgc ctc att gac aaa ctg ttg gtg tgg gaa cca caa acc agg tgg   1795
Ser Arg Leu Ile Asp Lys Leu Leu Val Trp Glu Pro Gln Thr Arg Trp
550                 555                 560                 565

cgg gaa caa aac ctg gag agc tgagcacggt ttgattaacg tcg            1839
Arg Glu Gln Asn Leu Glu Ser
                570
```

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<210> 2210
<211> 572
<212> PRT
<213> Corynebacterium glutamicum

<400> 2210

```
Met Arg Ser Leu Gln Ser Val Leu Asp Leu Leu Thr Ser Lys Ser Lys
  1               5                  10                  15

Val Ala Thr Lys Ile Val Val Glu Arg Ile Glu Lys His Pro Val His
             20                  25                  30
```

```
Gly Leu Gly Trp Met Met Tyr Pro Pro Phe His Pro Trp Thr Asp Ala
          35                  40                  45

Ser Thr Leu Thr Ile Glu Arg Asn Gly Thr Ser Arg Arg Ala Ser Gln
      50                  55                  60

Asn Gly Val Ala Val Leu His Gln His Glu Gln Val Gln Thr Ile Gly
 65                  70                  75                  80

Leu Ala Ser Tyr Phe Ile Asp Ser Lys Ile Trp Val Asn Glu Leu Ala
                85                  90                  95

Gly Leu Asp Arg Ile Asn Ile Ser Glu Ser Glu Val Ala Gly Arg Asp
            100                 105                 110

Val Leu Val Leu Pro Leu Ser Asp Leu Thr Leu Ser Ile Asp Ala Lys
        115                 120                 125

Tyr Gly Val Val Leu Ala Ala Glu Asp Ser Asp Glu Ser Val Arg Ala
    130                 135                 140

Val Ser Val Glu Phe Leu Asp Gln Trp Val Asp Glu Glu Glu Pro Pro
145                 150                 155                 160

Ala Glu Glu Val Pro Lys Tyr Thr Glu Thr Arg Glu Glu Leu Pro Pro
                165                 170                 175

Leu Glu Ile Pro Pro Ala Pro Ser Gly Asn Arg Asn Leu Arg Val Leu
            180                 185                 190

Cys Thr Trp Gly Ala Met Glu Gly Ile Ile Pro Glu Trp Lys Pro Gly
        195                 200                 205

Asp Gln Val Ser Leu Phe Leu Ser Phe Asp Leu Asp Asp Pro Pro Phe
    210                 215                 220

Glu Gln Leu Lys Thr Thr Arg Arg Gly Tyr Thr Glu Pro Gly Glu Ile
225                 230                 235                 240

Tyr Gly Asn Gln Arg Ser Tyr Lys Phe His Ala Asp Gly Trp Asn Ala
                245                 250                 255

Val Ile Ser Ala Lys Val Pro Leu Arg Thr Glu Glu Asn Leu Thr Gly
            260                 265                 270

Tyr Phe Thr His Ser Ser Tyr Ala Asp Thr Ser Arg Arg Thr Ser Ala
        275                 280                 285

Val Ile Thr Ala Val Tyr Arg His Gly Lys Asp Ala Ile Ile Asp Val
    290                 295                 300

Thr Leu Asp Gly Ala Lys Pro Pro Arg Tyr Gln Glu Ser Leu Asp Trp
305                 310                 315                 320

Ser Ser Thr Ser Thr Cys Asp Gly Glu Thr Ile Trp Leu Ser Asp Lys
                325                 330                 335

Ser Leu Pro Phe Val Arg Gly Phe Asn Val Ser Thr Gly Lys Leu Val
            340                 345                 350

His Glu Ile Ser Ile Pro Thr Phe Asn Glu Ile Ala Leu Glu Ser Gly
```

```
        355                 360                 365

Asn Arg Ala Arg Ala Ala Lys Lys Leu Trp Glu Leu Pro Asp Leu Lys
    370                 375                 380

Glu Ala Thr Asp Pro Val Pro Ala Ile Pro Ala Gly Trp Lys Leu His
385                 390                 395                 400

Lys Arg Phe Gly Lys Asn Phe His Ile Val Ser Ala Asp Asn Gly Thr
                405                 410                 415

Trp Lys Gln Thr Ile Leu Arg Ile Lys Pro Phe Lys Ala Ile Glu Leu
            420                 425                 430

Asp Leu Gly Tyr Ala Lys Ile Ser Thr Ile Tyr Gln Tyr Gly Glu Arg
        435                 440                 445

Ile Tyr Leu Arg Ser Asp Leu His Gln Ile Thr Phe Asn Gln Asp Leu
    450                 455                 460

Glu Ile Leu Ser Val Glu Val His Gly Asn Pro Asp Ala Gly Tyr Trp
465                 470                 475                 480

Pro Leu Ser Asp Leu Pro Pro Gly Asp Ser Pro Thr Leu Gly Phe Pro
                485                 490                 495

Ile Gly Ser Leu Met Met Phe His Glu Gln Gln Asp Ile Tyr Ala Phe
            500                 505                 510

His Asp Pro Lys Thr Thr Lys Gln Leu Thr Thr Val Asn Leu Pro Lys
        515                 520                 525

Arg Gln Phe Glu Val Glu Tyr Ala Ser Gln Asn Arg Ile Val Ile Ser
    530                 535                 540

Leu Lys Asn Pro Glu Ser Arg Leu Ile Asp Lys Leu Leu Val Trp Glu
545                 550                 555                 560

Pro Gln Thr Arg Trp Arg Glu Gln Asn Leu Glu Ser
                565                 570
```

<210> 2211
<211> 381
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(358)
<223> RXA01396

<400> 2211
tcaccaaccc acttaacttc gagaccttcg attccctcgt cgttccagtt ggttcttctg 60

caaccgctga gatccaggct cagcttcaac ctcccgcgtt ttg aag gct ttc aac 115
                                              Leu Lys Ala Phe Asn
                                                1   5

acc aac ttc gca gcc act ttg gct acc gga aag gtt ggc gat atc acc 163
Thr Asn Phe Ala Ala Thr Leu Ala Thr Gly Lys Val Gly Asp Ile Thr

```
                10                  15                  20

acc acc gtt tta gtt gca ggc gat gat gaa gac gca aag aac gct ctt   211
Thr Thr Val Leu Val Ala Gly Asp Asp Glu Asp Ala Lys Asn Ala Leu
            25                  30                  35

atc acc gac gtc aac gct ggc ggc ctc gac gcc ctt gac gct ggt tcc   259
Ile Thr Asp Val Asn Ala Gly Gly Leu Asp Ala Leu Asp Ala Gly Ser
        40                  45                  50

ctc aag cgt gca cac gag ctt gaa gca gtt ggt ttc ctg cag ctc acc   307
Leu Lys Arg Ala His Glu Leu Glu Ala Val Gly Phe Leu Gln Leu Thr
    55                  60                  65

ctt gca ggt tcc gag aag att gga tgg acc ggc gga ttc ggc ctg gtc   355
Leu Ala Gly Ser Glu Lys Ile Gly Trp Thr Gly Gly Phe Gly Leu Val
70                  75                  80                  85

aag taacacccag cctcaaaagc act                                     381
Lys
```

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<210> 2212
<211> 86
<212> PRT
<213> Corynebacterium glutamicum

<400> 2212

```
Leu Lys Ala Phe Asn Thr Asn Phe Ala Ala Thr Leu Ala Thr Gly Lys
  1               5                  10                  15

Val Gly Asp Ile Thr Thr Thr Val Leu Val Ala Gly Asp Asp Glu Asp
            20                  25                  30

Ala Lys Asn Ala Leu Ile Thr Asp Val Asn Ala Gly Gly Leu Asp Ala
        35                  40                  45

Leu Asp Ala Gly Ser Leu Lys Arg Ala His Glu Leu Glu Ala Val Gly
    50                  55                  60

Phe Leu Gln Leu Thr Leu Ala Gly Ser Glu Lys Ile Gly Trp Thr Gly
65                  70                  75                  80

Gly Phe Gly Leu Val Lys
                85
```

<210> 2213
<211> 543
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(520)
<223> RXA01397

<400> 2213

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tgagctgcta aaagtctcgc attaaaggac tgcttccctt cgggggagca tttcttttta 60
```

```
actaattact tgacacgtca agtaattagg gtctagtgtt gtg ttc atg atc aaa   115
                                              Val Phe Met Ile Lys
                                                1               5

gaa ctg ctc aac aag ctc ttc gga aac aag aag gct tcc ccg gca atg   163
Glu Leu Leu Asn Lys Leu Phe Gly Asn Lys Lys Ala Ser Pro Ala Met
                10                  15                  20

aca caa tct gaa acc att tca cac aag gag aac aac aca atg acc act   211
Thr Gln Ser Glu Thr Ile Ser His Lys Glu Asn Asn Thr Met Thr Thr
            25                  30                  35

tac acc atc ttc ggc cgc ggc aac atg ggc acc gca atc gca ggc gtc   259
Tyr Thr Ile Phe Gly Arg Gly Asn Met Gly Thr Ala Ile Ala Gly Val
        40                  45                  50

ctc acc aag ggt ggt gca act gta gaa cac atc ggt tct gca gat tct   307
Leu Thr Lys Gly Gly Ala Thr Val Glu His Ile Gly Ser Ala Asp Ser
    55                  60                  65

gac atc gca acc atc aac ggt gac gtt gtt atc ctt gct gtt cct tac   355
Asp Ile Ala Thr Ile Asn Gly Asp Val Val Ile Leu Ala Val Pro Tyr
70                  75                  80                  85

cca gca gta gag tcc atc att gca agc cac aag gat gct ctc gca ggc   403
Pro Ala Val Glu Ser Ile Ile Ala Ser His Lys Asp Ala Leu Ala Gly
                90                  95                  100

aag acc gtt atc gat atc acc aac cca ctt aac ttc gag acc ttc gat   451
Lys Thr Val Ile Asp Ile Thr Asn Pro Leu Asn Phe Glu Thr Phe Asp
            105                 110                 115

tcc ctc gtc gtt cca gtt ggt tct tct gca acc gct gag atc cag gct   499
Ser Leu Val Val Pro Val Gly Ser Ser Ala Thr Ala Glu Ile Gln Ala
        120                 125                 130

cag ctt caa cct ccc gcg ttt tgaaggcttt caacaccaac ttc            543
Gln Leu Gln Pro Pro Ala Phe
    135                 140
```

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<210> 2214
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

<400> 2214

```
Val Phe Met Ile Lys Glu Leu Leu Asn Lys Leu Phe Gly Asn Lys Lys
  1               5                  10                  15

Ala Ser Pro Ala Met Thr Gln Ser Glu Thr Ile Ser His Lys Glu Asn
            20                  25                  30

Asn Thr Met Thr Thr Tyr Thr Ile Phe Gly Arg Gly Asn Met Gly Thr
        35                  40                  45

Ala Ile Ala Gly Val Leu Thr Lys Gly Gly Ala Thr Val Glu His Ile
    50                  55                  60

Gly Ser Ala Asp Ser Asp Ile Ala Thr Ile Asn Gly Asp Val Val Ile
65                  70                  75                  80
```

```
Leu Ala Val Pro Tyr Pro Ala Val Glu Ser Ile Ile Ala Ser His Lys
                 85                  90                  95

Asp Ala Leu Ala Gly Lys Thr Val Ile Asp Ile Thr Asn Pro Leu Asn
            100                 105                 110

Phe Glu Thr Phe Asp Ser Leu Val Val Pro Val Gly Ser Ser Ala Thr
        115                 120                 125

Ala Glu Ile Gln Ala Gln Leu Gln Pro Pro Ala Phe
    130                 135                 140


<210> 2215
<211> 384
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(361)
<223> RXA01401

<400> 2215
tgccaaacgg aaggtttaat tggtctacat gtgtcagtct catggcacta taatagacct 60

agtatctata gattgataga aaataattta ggaagtttcc atg aac tct ccc cta   115
                                            Met Asn Ser Pro Leu
                                              1               5

caa cac agc gcc ttc ccc gtc ccc ggc gcg caa ctc tcc acc tca tac   163
Gln His Ser Ala Phe Pro Val Pro Gly Ala Gln Leu Ser Thr Ser Tyr
                 10                  15                  20

agc gac gaa cac ggc caa gcc gtc atc caa ctt cac ggc ctc acc tcc   211
Ser Asp Glu His Gly Gln Ala Val Ile Gln Leu His Gly Leu Thr Ser
             25                  30                  35

tcc cgc caa cgc gac cgc ctc ctc gac ctc gac ctc ggc cgt ggc ctt   259
Ser Arg Gln Arg Asp Arg Leu Leu Asp Leu Asp Leu Gly Arg Gly Leu
         40                  45                  50

tcc ggc acg cgc ctt ttg cgt tac gac gcc cgc ggc cac ggc acc tcc   307
Ser Gly Thr Arg Leu Leu Arg Tyr Asp Ala Arg Gly His Gly Thr Ser
     55                  60                  65

acc ggc cgc gct gcc tcc acc gat tat cag tgg gac acc cta gcg ggt   355
Thr Gly Arg Ala Ala Ser Thr Asp Tyr Gln Trp Asp Thr Leu Ala Gly
 70                  75                  80                  85

gac ctt taatgcttct cgacgcccac ttc                                384
Asp Leu


<210> 2216
<211> 87
<212> PRT
<213> Corynebacterium glutamicum
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<400> 2216
Met Asn Ser Pro Leu Gln His Ser Ala Phe Pro Val Pro Gly Ala Gln
1 5 10 15

Leu Ser Thr Ser Tyr Ser Asp Glu His Gly Gln Ala Val Ile Gln Leu
20 25 30

His Gly Leu Thr Ser Ser Arg Gln Arg Asp Arg Leu Leu Asp Leu Asp
35 40 45

Leu Gly Arg Gly Leu Ser Gly Thr Arg Leu Leu Arg Tyr Asp Ala Arg
50 55 60

Gly His Gly Thr Ser Thr Gly Arg Ala Ala Ser Thr Asp Tyr Gln Trp
65 70 75 80

Asp Thr Leu Ala Gly Asp Leu
85

<210> 2217
<211> 597
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(574)
<223> RXA01402

<400> 2217
cgctgcctcc accgattatc agtgggacac cctagcgggt gacctttaat gcttctcgac 60

gcccacttcc ccacgaacaa gtccacggcg tcggcccctc atg ggt tgc gcc acc 115
Met Gly Cys Ala Thr
1 5

ctc ctc aaa gcc gcg gtg tta aac ccc gac cgc ttc agt gga ttc aca 163
Leu Leu Lys Ala Ala Val Leu Asn Pro Asp Arg Phe Ser Gly Phe Thr
10 15 20

ctc atg ctc cca ccc acc gcc tgg gaa tcc cga aaa gcc caa gcc tcc 211
Leu Met Leu Pro Pro Thr Ala Trp Glu Ser Arg Lys Ala Gln Ala Ser
25 30 35

gaa tac cta tcc cga gca gaa ttc cta gaa acc cac ggc atg gac gcc 259
Glu Tyr Leu Ser Arg Ala Glu Phe Leu Glu Thr His Gly Met Asp Ala
40 45 50

ttc ctc aac gcc gaa aaa ctc cac gcc caa cca cca gca acc gta gga 307
Phe Leu Asn Ala Glu Lys Leu His Ala Gln Pro Pro Ala Thr Val Gly
55 60 65

acc ccc gac aca gtc ccc gac att tcc gcc gaa ctc ctc ccc tgg gct 355
Thr Pro Asp Thr Val Pro Asp Ile Ser Ala Glu Leu Leu Pro Trp Ala
70 75 80 85

tac cga ggc gcc gcc caa agc gac ctc ccc tca aag aaa gaa atc gcc 403
Tyr Arg Gly Ala Ala Gln Ser Asp Leu Pro Ser Lys Lys Glu Ile Ala
90 95 100

```
aaa ata aca gcc ccc acc act att ctg agc tgg acc gac gat ccc gga   451
Lys Ile Thr Ala Pro Thr Thr Ile Leu Ser Trp Thr Asp Asp Pro Gly
            105                 110                 115

cac ccc gta tcc acg gca atc gag cta acc cgc ctc atg cca aac gcc   499
His Pro Val Ser Thr Ala Ile Glu Leu Thr Arg Leu Met Pro Asn Ala
        120                 125                 130

caa ctg cgc att gcc act acc cca gcg gaa gtc gcg cgg tgg cca caa   547
Gln Leu Arg Ile Ala Thr Thr Pro Ala Glu Val Ala Arg Trp Pro Gln
    135                 140                 145

cac ctt cgc gat gac ctg cag ttg gac taaaaacctt cattatctgg         594
His Leu Arg Asp Asp Leu Gln Leu Asp
150                 155

ttt                                                               597
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<210> 2218
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 2218

```
Met Gly Cys Ala Thr Leu Leu Lys Ala Ala Val Leu Asn Pro Asp Arg
  1               5                  10                  15

Phe Ser Gly Phe Thr Leu Met Leu Pro Pro Thr Ala Trp Glu Ser Arg
             20                  25                  30

Lys Ala Gln Ala Ser Glu Tyr Leu Ser Arg Ala Glu Phe Leu Glu Thr
         35                  40                  45

His Gly Met Asp Ala Phe Leu Asn Ala Glu Lys Leu His Ala Gln Pro
     50                  55                  60

Pro Ala Thr Val Gly Thr Pro Asp Thr Val Pro Asp Ile Ser Ala Glu
 65                  70                  75                  80

Leu Leu Pro Trp Ala Tyr Arg Gly Ala Ala Gln Ser Asp Leu Pro Ser
                 85                  90                  95

Lys Lys Glu Ile Ala Lys Ile Thr Ala Pro Thr Thr Ile Leu Ser Trp
            100                 105                 110

Thr Asp Asp Pro Gly His Pro Val Ser Thr Ala Ile Glu Leu Thr Arg
        115                 120                 125

Leu Met Pro Asn Ala Gln Leu Arg Ile Ala Thr Thr Pro Ala Glu Val
    130                 135                 140

Ala Arg Trp Pro Gln His Leu Arg Asp Asp Leu Gln Leu Asp
145                 150                 155
```

<210> 2219
<211> 579
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> RXA01405

<400> 2219
aattagacgt ctgtctctag ggatgccgca tcccgccggc gctcctagag tccgtttgta 60

aaacctagaa ttccgaatac gttccgaata gggtgggggt atg agt aag ata gtt 115
Met Ser Lys Ile Val
1 5

gat ctg cgc tat ggg acc cgg cgt tcc tcg gag ttg agc aaa cgc tct 163
Asp Leu Arg Tyr Gly Thr Arg Arg Ser Ser Glu Leu Ser Lys Arg Ser
10 15 20

gct gaa gtc ttt gcc gaa gct gaa gaa cat ccc att act gtg aca cgt 211
Ala Glu Val Phe Ala Glu Ala Glu Glu His Pro Ile Thr Val Thr Arg
25 30 35

cgt gat ggt gaa gcg ttg gta ttg atg tcg cag cgc gaa gct gac ggg 259
Arg Asp Gly Glu Ala Leu Val Leu Met Ser Gln Arg Glu Ala Asp Gly
40 45 50

cga gcc cgc ctg ctg gag ttg gct gca cag tta att act gtg gcc act 307
Arg Ala Arg Leu Leu Glu Leu Ala Ala Gln Leu Ile Thr Val Ala Thr
55 60 65

gat cat cag ggc acg tta gcc gaa cgt atg gcg aaa gta ttc ccg tgg 355
Asp His Gln Gly Thr Leu Ala Glu Arg Met Ala Lys Val Phe Pro Trp
70 75 80 85

atg ctg gcc ctg tca gtg gcg gat cgt gag gcg tgt gcc cgt gag att 403
Met Leu Ala Leu Ser Val Ala Asp Arg Glu Ala Cys Ala Arg Glu Ile
90 95 100

ctt gac gct gca cga gca tcg ttt gca acc gaa caa cct cac ctc gct 451
Leu Asp Ala Ala Arg Ala Ser Phe Ala Thr Glu Gln Pro His Leu Ala
105 110 115

ctt act gaa ctg acc tca tgg aaa gaa aca gca gca gct gtt gct gct 499
Leu Thr Glu Leu Thr Ser Trp Lys Glu Thr Ala Ala Ala Val Ala Ala
120 125 130

gga ttg agt aac act gat ctg cag tgg tac gac gat ccg cat ctg gtg 547
Gly Leu Ser Asn Thr Asp Leu Gln Trp Tyr Asp Asp Pro His Leu Val
135 140 145

gag cgt ccc taagcgtggc tggaaagaaa agc 579
Glu Arg Pro
150

<210> 2220
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 2220
Met Ser Lys Ile Val Asp Leu Arg Tyr Gly Thr Arg Arg Ser Ser Glu
1 5 10 15

```
Leu Ser Lys Arg Ser Ala Glu Val Phe Ala Glu Ala Glu Glu His Pro
            20                  25                  30

Ile Thr Val Thr Arg Arg Asp Gly Glu Ala Leu Val Leu Met Ser Gln
        35                  40                  45

Arg Glu Ala Asp Gly Arg Ala Arg Leu Leu Glu Leu Ala Ala Gln Leu
    50                  55                  60

Ile Thr Val Ala Thr Asp His Gln Gly Thr Leu Ala Glu Arg Met Ala
65                  70                  75                  80

Lys Val Phe Pro Trp Met Leu Ala Leu Ser Val Ala Asp Arg Glu Ala
                85                  90                  95

Cys Ala Arg Glu Ile Leu Asp Ala Ala Arg Ala Ser Phe Ala Thr Glu
            100                 105                 110

Gln Pro His Leu Ala Leu Thr Glu Leu Thr Ser Trp Lys Glu Thr Ala
        115                 120                 125

Ala Ala Val Ala Ala Gly Leu Ser Asn Thr Asp Leu Gln Trp Tyr Asp
    130                 135                 140

Asp Pro His Leu Val Glu Arg Pro
145                 150


<210> 2221
<211> 723
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(700)
<223> RXA01413

<400> 2221
tttgccctat tggaagaagt aaattccaca ccttcacttt ccaatacttc ttttggtgag 60

cgggtttcct cagcgtttaa ccatctgaaa ccatctgaga ttg acc cat ctg ttc  115
                                        Leu Thr His Leu Phe
                                          1               5

tta gaa ctc gat gag cgt tta gta ctg ggt gtt cag caa gat ggt tac  163
Leu Glu Leu Asp Glu Arg Leu Val Leu Gly Val Gln Gln Asp Gly Tyr
                10                  15                  20

caa tgg act gag cat ttg ttc cgg ctg cca ctg caa cat ctc cgt aac  211
Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu Gln His Leu Arg Asn
            25                  30                  35

tcg ccc aat gac ctg cag gga ttg aag ata cga tgg tgt gaa ctt tat  259
Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg Trp Cys Glu Leu Tyr
        40                  45                  50

tcc aca acg ggg aaa gat caa ggg gta gaa ctt ctg cct caa gca acc  307
Ser Thr Thr Gly Lys Asp Gln Gly Val Glu Leu Leu Pro Gln Ala Thr
    55                  60                  65
```

```
gtc gtt acc cca aat aac ttc gag gct tcc acc ctc tcc ggc ctt gag   355
Val Val Thr Pro Asn Asn Phe Glu Ala Ser Thr Leu Ser Gly Leu Glu
 70                  75                  80                  85

aag ctt gag acc gtc gag gac ctc aag gag gct gcc cgc ctc att tat   403
Lys Leu Glu Thr Val Glu Asp Leu Lys Glu Ala Ala Arg Leu Ile Tyr
                90                  95                 100

gag caa ggc ccc cag tac gta gtc gtc aag ggt ggc atg gac ttc ccc   451
Glu Gln Gly Pro Gln Tyr Val Val Val Lys Gly Gly Met Asp Phe Pro
            105                 110                 115

ggc gag aac gcc gtg gat gtg ctt ttc gac gga tcc tcc tac cac gtc   499
Gly Glu Asn Ala Val Asp Val Leu Phe Asp Gly Ser Ser Tyr His Val
        120                 125                 130

ttc tct gag cca aag att ggt gaa gag cgc gtt tcc ggc gca gtc tgc   547
Phe Ser Glu Pro Lys Ile Gly Glu Glu Arg Val Ser Gly Ala Val Cys
    135                 140                 145

acc ttc gca gct gtt atc acc gca gag cta gca aag ggt gct gag gtt   595
Thr Phe Ala Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Ala Glu Val
150                 155                 160                 165

gta gac cca gtg gca acc gca aag cgt gtg gtc acc cgt gcg gtt caa   643
Val Asp Pro Val Ala Thr Ala Lys Arg Val Val Thr Arg Ala Val Gln
                170                 175                 180

gat gct gtt gca tcc aac gca cct ttt acc tcc gta tgg ctt gct gag   691
Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu
            185                 190                 195

gac aac aag tagagtttta aaataccgat caa                            723
Asp Asn Lys
        200
```

<210> 2222
<211> 200
<212> PRT
<213> Corynebacterium glutamicum

<400> 2222

```
Leu Thr His Leu Phe Leu Glu Leu Asp Glu Arg Leu Val Leu Gly Val
  1               5                  10                  15

Gln Gln Asp Gly Tyr Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu
             20                  25                  30

Gln His Leu Arg Asn Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg
         35                  40                  45

Trp Cys Glu Leu Tyr Ser Thr Thr Gly Lys Asp Gln Gly Val Glu Leu
     50                  55                  60

Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu Ala Ser Thr
 65                  70                  75                  80

Leu Ser Gly Leu Glu Lys Leu Glu Thr Val Glu Asp Leu Lys Glu Ala
                 85                  90                  95
```

```
Ala Arg Leu Ile Tyr Glu Gln Gly Pro Gln Tyr Val Val Val Lys Gly
            100                 105                 110

Gly Met Asp Phe Pro Gly Glu Asn Ala Val Asp Val Leu Phe Asp Gly
        115                 120                 125

Ser Ser Tyr His Val Phe Ser Glu Pro Lys Ile Gly Glu Glu Arg Val
    130                 135                 140

Ser Gly Ala Val Cys Thr Phe Ala Ala Val Ile Thr Ala Glu Leu Ala
145                 150                 155                 160

Lys Gly Ala Glu Val Val Asp Pro Val Ala Thr Ala Lys Arg Val Val
                165                 170                 175

Thr Arg Ala Val Gln Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser
            180                 185                 190

Val Trp Leu Ala Glu Asp Asn Lys
        195                 200
```

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<210> 2223
<211> 630
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(607)
<223> RXA01414

<400> 2223

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tattgcctaa gtagaccaat aggtctatgc ttcatagaac aactagttca taagtgatta 60

gttttaagaa tttattacct ctctacagga gaacccagcg atg gcc gtt ttt gat   115
                                              Met Ala Val Phe Asp
                                                1               5

ttc cct aac ccc gtt aac gaa tat gca gct cgc tgc act gcg ggt ttg   163
Phe Pro Asn Pro Val Asn Glu Tyr Ala Ala Arg Cys Thr Ala Gly Leu
                10                  15                  20

gtt gtt ttg ctg agc gcc gcc acg ctt ttt gcc tct ggt gac ctt cgt   211
Val Val Leu Leu Ser Ala Ala Thr Leu Phe Ala Ser Gly Asp Leu Arg
            25                  30                  35

att att ttg gca agc atc ttg acc ttc ggc ttc gca ttg cgc gtg gcc   259
Ile Ile Leu Ala Ser Ile Leu Thr Phe Gly Phe Ala Leu Arg Val Ala
        40                  45                  50

ggc gga ccc cgt tac tcc ccc ttt gga cgt ctt tca gta cac gta ctt   307
Gly Gly Pro Arg Tyr Ser Pro Phe Gly Arg Leu Ser Val His Val Leu
    55                  60                  65

gta cca ctg ctg aag aaa gca ccg atc ctg acc cct ggc cca cca aag   355
Val Pro Leu Leu Lys Lys Ala Pro Ile Leu Thr Pro Gly Pro Pro Lys
70                  75                  80                  85

cgc ttc gcg cag acc atc ggc ctg ggc ttt agc ggt act tcc ctt atc   403
```

```
Arg Phe Ala Gln Thr Ile Gly Leu Gly Phe Ser Gly Thr Ser Leu Ile
                 90                  95                 100

ctt atg gcc ttt gga ttt aac gtt gca gct tcc gta gtc cta gtc atg   451
Leu Met Ala Phe Gly Phe Asn Val Ala Ala Ser Val Val Leu Val Met
            105                 110                 115

ctc atc gca gca gcc acc tta gaa tcc gtc ttt ggt atc tgc ctc ggt   499
Leu Ile Ala Ala Ala Thr Leu Glu Ser Val Phe Gly Ile Cys Leu Gly
        120                 125                 130

tgc tgg gga ttc ggc aag ctc atg cgc tac ggc gtc atc cca gaa gac   547
Cys Trp Gly Phe Gly Lys Leu Met Arg Tyr Gly Val Ile Pro Glu Asp
    135                 140                 145

gtt tgc gag cag tgc ttc cag aag gaa tcc tcc cgc acc ggc tgg ctc   595
Val Cys Glu Gln Cys Phe Gln Lys Glu Ser Ser Arg Thr Gly Trp Leu
150                 155                 160                 165

gtt agc ctg aag tagcacttcg aatctaagac cac                        630
Val Ser Leu Lys
```

Sequence Listing.ST25.txt

<210> 2224
<211> 169
<212> PRT
<213> Corynebacterium glutamicum

<400> 2224

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Met Ala Val Phe Asp Phe Pro Asn Pro Val Asn Glu Tyr Ala Ala Arg
  1               5                  10                  15

Cys Thr Ala Gly Leu Val Val Leu Leu Ser Ala Ala Thr Leu Phe Ala
             20                  25                  30

Ser Gly Asp Leu Arg Ile Ile Leu Ala Ser Ile Leu Thr Phe Gly Phe
         35                  40                  45

Ala Leu Arg Val Ala Gly Gly Pro Arg Tyr Ser Pro Phe Gly Arg Leu
     50                  55                  60

Ser Val His Val Leu Val Pro Leu Leu Lys Lys Ala Pro Ile Leu Thr
 65                  70                  75                  80

Pro Gly Pro Pro Lys Arg Phe Ala Gln Thr Ile Gly Leu Gly Phe Ser
                 85                  90                  95

Gly Thr Ser Leu Ile Leu Met Ala Phe Gly Phe Asn Val Ala Ala Ser
            100                 105                 110

Val Val Leu Val Met Leu Ile Ala Ala Ala Thr Leu Glu Ser Val Phe
        115                 120                 125

Gly Ile Cys Leu Gly Cys Trp Gly Phe Gly Lys Leu Met Arg Tyr Gly
    130                 135                 140

Val Ile Pro Glu Asp Val Cys Glu Gln Cys Phe Gln Lys Glu Ser Ser
145                 150                 155                 160

Arg Thr Gly Trp Leu Val Ser Leu Lys
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165

<210> 2225
<211> 720
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(697)
<223> RXA01417

<400> 2225
agcctcccca aggctggtta gtcccactat cctctcagag agaagcaaaa ctgaaataac 60

ttcagcctca gctatccccg caatttaagg aaaataggat atg act gac aag ttt 115
Met Thr Asp Lys Phe
1 5

gac aga gtc ctt gct gta gag gtg tgc att cag gag tgg atc gac gag 163
Asp Arg Val Leu Ala Val Glu Val Cys Ile Gln Glu Trp Ile Asp Glu
10 15 20

caa aac ctc acg cta gag gtg cca tta atg att gca cgt ttg cag ctt 211
Gln Asn Leu Thr Leu Glu Val Pro Leu Met Ile Ala Arg Leu Gln Leu
25 30 35

aga gac gtc gcg aag gat atc act gct gtt cac gaa gaa aaa ttc tac 259
Arg Asp Val Ala Lys Asp Ile Thr Ala Val His Glu Glu Lys Phe Tyr
40 45 50

gac ctc act gat atc gat act gat gcc ttt gtg aaa aac atc aaa ctg 307
Asp Leu Thr Asp Ile Asp Thr Asp Ala Phe Val Lys Asn Ile Lys Leu
55 60 65

gga tgg aat gaa cgc ttg atc aag aaa agc ctc ttt cca caa ccg gac 355
Gly Trp Asn Glu Arg Leu Ile Lys Lys Ser Leu Phe Pro Gln Pro Asp
70 75 80 85

gtg cat aaa caa cat ttc aca gaa act gaa cat ggc att gac gcg act 403
Val His Lys Gln His Phe Thr Glu Thr Glu His Gly Ile Asp Ala Thr
90 95 100

gtg acg gtc tgg tcg aag ggc ttc gat ccg gaa agt ggc ccc gac ttc 451
Val Thr Val Trp Ser Lys Gly Phe Asp Pro Glu Ser Gly Pro Asp Phe
105 110 115

ttg gtt tcc tat gtg gat ggt ctt tgg tca gcc gat att aga aac cgc 499
Leu Val Ser Tyr Val Asp Gly Leu Trp Ser Ala Asp Ile Arg Asn Arg
120 125 130

atc acg aaa ttt cag aat aga gaa atc gtt agc aaa ttc tat ttt act 547
Ile Thr Lys Phe Gln Asn Arg Glu Ile Val Ser Lys Phe Tyr Phe Thr
135 140 145

cca gaa cat att aag gag gat gga gat ttc tcc gca gag att ttt att 595
Pro Glu His Ile Lys Glu Asp Gly Asp Phe Ser Ala Glu Ile Phe Ile
150 155 160 165

aac cga cca gaa aat gac gac gac tca caa gat ttg gtc gag gtg tgg 643

```
Asn Arg Pro Glu Asn Asp Asp Asp Ser Gln Asp Leu Val Glu Val Trp
                170                 175                 180

act gat caa gac acc aga tac tgc ggt gaa atg atc atc tat ttc aaa   691
Thr Asp Gln Asp Thr Arg Tyr Cys Gly Glu Met Ile Ile Tyr Phe Lys
            185                 190                 195

tgg ctc taaattccac ttttctgcat cag                                 720
Trp Leu
```

<210> 2226
<211> 199
<212> PRT
<213> Corynebacterium glutamicum

<400> 2226

```
Met Thr Asp Lys Phe Asp Arg Val Leu Ala Val Glu Val Cys Ile Gln
  1               5                  10                  15

Glu Trp Ile Asp Glu Gln Asn Leu Thr Leu Glu Val Pro Leu Met Ile
             20                  25                  30

Ala Arg Leu Gln Leu Arg Asp Val Ala Lys Asp Ile Thr Ala Val His
         35                  40                  45

Glu Glu Lys Phe Tyr Asp Leu Thr Asp Ile Asp Thr Asp Ala Phe Val
     50                  55                  60

Lys Asn Ile Lys Leu Gly Trp Asn Glu Arg Leu Ile Lys Lys Ser Leu
 65                  70                  75                  80

Phe Pro Gln Pro Asp Val His Lys Gln His Phe Thr Glu Thr Glu His
                 85                  90                  95

Gly Ile Asp Ala Thr Val Thr Val Trp Ser Lys Gly Phe Asp Pro Glu
            100                 105                 110

Ser Gly Pro Asp Phe Leu Val Ser Tyr Val Asp Gly Leu Trp Ser Ala
        115                 120                 125

Asp Ile Arg Asn Arg Ile Thr Lys Phe Gln Asn Arg Glu Ile Val Ser
    130                 135                 140

Lys Phe Tyr Phe Thr Pro Glu His Ile Lys Glu Asp Gly Asp Phe Ser
145                 150                 155                 160

Ala Glu Ile Phe Ile Asn Arg Pro Glu Asn Asp Asp Asp Ser Gln Asp
                165                 170                 175

Leu Val Glu Val Trp Thr Asp Gln Asp Thr Arg Tyr Cys Gly Glu Met
            180                 185                 190

Ile Ile Tyr Phe Lys Trp Leu
        195
```

<210> 2227
<211> 510
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(487)
<223> RXA01421

<400> 2227
ttgatgcacg tgcagaaatc gtcggcggtc cgtggcaccc atctgttaag ggagactcgg 60

ttactgcagg gatcctgcga gatcgagtaa acgcctaaag atg acg tcg aaa agc 115
Met Thr Ser Lys Ser
1 5

att agc ggc aag cgc ccg aat ctg ccg tcg ctc act gga gcg cgg tgg 163
Ile Ser Gly Lys Arg Pro Asn Leu Pro Ser Leu Thr Gly Ala Arg Trp
10 15 20

ctc gcg gcg ctc gct gtt tat ttt ttg cat gcg ttg gtg ttt ttg tcg 211
Leu Ala Ala Leu Ala Val Tyr Phe Leu His Ala Leu Val Phe Leu Ser
25 30 35

gtg tat ccg ttc cag cag tcg gaa ctg ttt gcc aca atc cat aaa ttt 259
Val Tyr Pro Phe Gln Gln Ser Glu Leu Phe Ala Thr Ile His Lys Phe
40 45 50

gtc ccc atg cag ctg ggt tca gct ggt gta acc ttc ttc ttt atc ttg 307
Val Pro Met Gln Leu Gly Ser Ala Gly Val Thr Phe Phe Phe Ile Leu
55 60 65

tcc gga ttt ttg atc tat tgg tca aat agc cag ctc aag ggc atg aag 355
Ser Gly Phe Leu Ile Tyr Trp Ser Asn Ser Gln Leu Lys Gly Met Lys
70 75 80 85

aat gtg ctg tat tac tgc aag cgc cgc atc acc aag att tat ccc atg 403
Asn Val Leu Tyr Tyr Cys Lys Arg Arg Ile Thr Lys Ile Tyr Pro Met
90 95 100

cac ttg att gcg ttg ccg atg ttt att gag gcg tcg gcg aag ttc acg 451
His Leu Ile Ala Leu Pro Met Phe Ile Glu Ala Ser Ala Lys Phe Thr
105 110 115

act aca ggc att acc tgg gtg ctg att ttg cgc gag taaagctgtg 497
Thr Thr Gly Ile Thr Trp Val Leu Ile Leu Arg Glu
120 125

gctgcggaat gcg 510

<210> 2228
<211> 129
<212> PRT
<213> Corynebacterium glutamicum

<400> 2228
Met Thr Ser Lys Ser Ile Ser Gly Lys Arg Pro Asn Leu Pro Ser Leu
1 5 10 15

Thr Gly Ala Arg Trp Leu Ala Ala Leu Ala Val Tyr Phe Leu His Ala
20 25 30

```
Leu Val Phe Leu Ser Val Tyr Pro Phe Gln Gln Ser Glu Leu Phe Ala
         35                  40                  45

Thr Ile His Lys Phe Val Pro Met Gln Leu Gly Ser Ala Gly Val Thr
     50                  55                  60

Phe Phe Phe Ile Leu Ser Gly Phe Leu Ile Tyr Trp Ser Asn Ser Gln
 65                  70                  75                  80

Leu Lys Gly Met Lys Asn Val Leu Tyr Tyr Cys Lys Arg Arg Ile Thr
                85                  90                  95

Lys Ile Tyr Pro Met His Leu Ile Ala Leu Pro Met Phe Ile Glu Ala
            100                 105                 110

Ser Ala Lys Phe Thr Thr Thr Gly Ile Thr Trp Val Leu Ile Leu Arg
        115                 120                 125

Glu
```

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<210> 2229
<211> 1008
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(985)
<223> RXA01425

<400> 2229

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agtccctatt aatcccaagg agtttcgact cacagtgctc aatttcattt attggccaat 60

ttcggccatt ctgtggttct ggcataaagc gttcagcttt gtg ctg agc cca gat   115
                                              Val Leu Ser Pro Asp
                                                1               5

tcc gga att acc tgg gcc ttg tcg atc atg ttc ttg acc ttc acc gtg   163
Ser Gly Ile Thr Trp Ala Leu Ser Ile Met Phe Leu Thr Phe Thr Val
                10                  15                  20

cgt atg gtt ctg gtc aag ccg atg gtc aac acc atg cgt tca cag cgc   211
Arg Met Val Leu Val Lys Pro Met Val Asn Thr Met Arg Ser Gln Arg
            25                  30                  35

aag atg caa gac atg gct cca aag atg cag gcc atc cgc gag aag tac   259
Lys Met Gln Asp Met Ala Pro Lys Met Gln Ala Ile Arg Glu Lys Tyr
        40                  45                  50

aaa aat gac cag cag aag atg atg gag gag acc cgc aaa ctt caa aaa   307
Lys Asn Asp Gln Gln Lys Met Met Glu Glu Thr Arg Lys Leu Gln Lys
    55                  60                  65

gaa gtg ggc gtt aac ccc atc gca ggc tgt ttg cca atg ttg gtg cag   355
Glu Val Gly Val Asn Pro Ile Ala Gly Cys Leu Pro Met Leu Val Gln
70                  75                  80                  85

atc cca gtg ttc ctg ggt ctg ttc cac gtg ctg cgc tcc ttc aac cgc   403
Ile Pro Val Phe Leu Gly Leu Phe His Val Leu Arg Ser Phe Asn Arg
```

```
                90                  95                 100

acc ggt tct ggc gtt ggc cag ctg gaa atg acc gtt gag caa aac gcg   451
Thr Gly Ser Gly Val Gly Gln Leu Glu Met Thr Val Glu Gln Asn Ala
            105                 110                 115

aac acc ccg aac tac atc ttc ggt gtc gac gag gtt cag tcc ttc ctg   499
Asn Thr Pro Asn Tyr Ile Phe Gly Val Asp Glu Val Gln Ser Phe Leu
        120                 125                 130

cgt gca gac ctg ttc ggt gcg cca ctg tcg tcc tac atc acc atg cct   547
Arg Ala Asp Leu Phe Gly Ala Pro Leu Ser Ser Tyr Ile Thr Met Pro
    135                 140                 145

gct gac gcg ttc gac gcg ttc ctt ggc ctg gat gtc tcc cgc ctc aac   595
Ala Asp Ala Phe Asp Ala Phe Leu Gly Leu Asp Val Ser Arg Leu Asn
150                 155                 160                 165

atc gcg ctg gtt gca gct cca atg att ttg atc att gtc gtg gca act   643
Ile Ala Leu Val Ala Ala Pro Met Ile Leu Ile Ile Val Val Ala Thr
                170                 175                 180

cac atg aac gcg cgt ctg tcc gtc aac cgc cag gaa gct cgc aag gca   691
His Met Asn Ala Arg Leu Ser Val Asn Arg Gln Glu Ala Arg Lys Ala
            185                 190                 195

gcc ggc aag cag cag gcc gct tcc agc gat cag atg gcc atg cag atg   739
Ala Gly Lys Gln Gln Ala Ala Ser Ser Asp Gln Met Ala Met Gln Met
        200                 205                 210

caa atg atg aac aag atg atg ctc tgg ttc atg cca gcc acc att ttg   787
Gln Met Met Asn Lys Met Met Leu Trp Phe Met Pro Ala Thr Ile Leu
    215                 220                 225

ttc acc ggc ttc atc tgg acc atc ggt ctt ctt gtc tac atg atg tcc   835
Phe Thr Gly Phe Ile Trp Thr Ile Gly Leu Leu Val Tyr Met Met Ser
230                 235                 240                 245

aac aac gtg tgg acc ttc ttc cag cag cgc tac atc ttc gcc aag atg   883
Asn Asn Val Trp Thr Phe Phe Gln Gln Arg Tyr Ile Phe Ala Lys Met
                250                 255                 260

gac gct gag gaa gca gct gag gag gag gaa aag cgc gca gca aag cgc   931
Asp Ala Glu Glu Ala Ala Glu Glu Glu Glu Lys Arg Ala Ala Lys Arg
            265                 270                 275

act acc gct cca aag cct ggc gtg aag cca gaa aac ccc aag aag cgt   979
Thr Thr Ala Pro Lys Pro Gly Val Lys Pro Glu Asn Pro Lys Lys Arg
        280                 285                 290

aag aag taaaacttca ctaaaaaccg cca                                1008
Lys Lys
    295
```

<210> 2230
<211> 295
<212> PRT
<213> Corynebacterium glutamicum

<400> 2230

```
Val Leu Ser Pro Asp Ser Gly Ile Thr Trp Ala Leu Ser Ile Met Phe
  1               5                  10                  15

Leu Thr Phe Thr Val Arg Met Val Leu Val Lys Pro Met Val Asn Thr
            20                  25                  30

Met Arg Ser Gln Arg Lys Met Gln Asp Met Ala Pro Lys Met Gln Ala
        35                  40                  45

Ile Arg Glu Lys Tyr Lys Asn Asp Gln Gln Lys Met Met Glu Glu Thr
    50                  55                  60

Arg Lys Leu Gln Lys Glu Val Gly Val Asn Pro Ile Ala Gly Cys Leu
65                  70                  75                  80

Pro Met Leu Val Gln Ile Pro Val Phe Leu Gly Leu Phe His Val Leu
                85                  90                  95

Arg Ser Phe Asn Arg Thr Gly Ser Gly Val Gly Gln Leu Glu Met Thr
            100                 105                 110

Val Glu Gln Asn Ala Asn Thr Pro Asn Tyr Ile Phe Gly Val Asp Glu
        115                 120                 125

Val Gln Ser Phe Leu Arg Ala Asp Leu Phe Gly Ala Pro Leu Ser Ser
    130                 135                 140

Tyr Ile Thr Met Pro Ala Asp Ala Phe Asp Ala Phe Leu Gly Leu Asp
145                 150                 155                 160

Val Ser Arg Leu Asn Ile Ala Leu Val Ala Ala Pro Met Ile Leu Ile
                165                 170                 175

Ile Val Val Ala Thr His Met Asn Ala Arg Leu Ser Val Asn Arg Gln
            180                 185                 190

Glu Ala Arg Lys Ala Ala Gly Lys Gln Gln Ala Ala Ser Ser Asp Gln
        195                 200                 205

Met Ala Met Gln Met Gln Met Met Asn Lys Met Met Leu Trp Phe Met
    210                 215                 220

Pro Ala Thr Ile Leu Phe Thr Gly Phe Ile Trp Thr Ile Gly Leu Leu
225                 230                 235                 240

Val Tyr Met Met Ser Asn Asn Val Trp Thr Phe Phe Gln Gln Arg Tyr
                245                 250                 255

Ile Phe Ala Lys Met Asp Ala Glu Glu Ala Ala Glu Glu Glu Glu Lys
            260                 265                 270

Arg Ala Ala Lys Arg Thr Thr Ala Pro Lys Pro Gly Val Lys Pro Glu
        275                 280                 285

Asn Pro Lys Lys Arg Lys Lys
    290                 295
```

<210> 2231
<211> 741
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(718)
<223> RXA01429

<400> 2231
ggtaagaaga agggcaagct cgtggtggaa ttcggcgaca aggatgattt cgagcgcatc 60

atgtccttga tccagggcca ataattttaa gtttggcgcc atg ctc cag gct tcc 115
Met Leu Gln Ala Ser
1 5

ctt ttc ccg atc gtg cag gaa cac ata gat ttc ctg cac ccc cag gcc 163
Leu Phe Pro Ile Val Gln Glu His Ile Asp Phe Leu His Pro Gln Ala
10 15 20

cgc aag tcg gtg ttt tgg gag ctc gca cct gag gtt gca gct aaa gct 211
Arg Lys Ser Val Phe Trp Glu Leu Ala Pro Glu Val Ala Ala Lys Ala
25 30 35

gat ccg gtg ttt gag aag gaa gcc tgg ctg tcc acc acg ctg ctg gaa 259
Asp Pro Val Phe Glu Lys Glu Ala Trp Leu Ser Thr Thr Leu Leu Glu
40 45 50

tat gaa tcc tgc ggt ttc aac att ggt tac cgc aat gga act ccg gcg 307
Tyr Glu Ser Cys Gly Phe Asn Ile Gly Tyr Arg Asn Gly Thr Pro Ala
55 60 65

ttg gcg tcg gtc att ttc tgc gag cgc gat gcc gcc ccg ggc gcg aag 355
Leu Ala Ser Val Ile Phe Cys Glu Arg Asp Ala Ala Pro Gly Ala Lys
70 75 80 85

gcg ctg cct acg gca ccg gtg tct agc gac gct gcg atc atc agc agc 403
Ala Leu Pro Thr Ala Pro Val Ser Ser Asp Ala Ala Ile Ile Ser Ser
90 95 100

ctg ttc atc gac gag gtt ttc cgg ggc acg ggc atg gaa tcg gcg ctt 451
Leu Phe Ile Asp Glu Val Phe Arg Gly Thr Gly Met Glu Ser Ala Leu
105 110 115

ctc gac gct tcc ctc atg gaa ctc att cgg cgc gac tac cca gcc gtt 499
Leu Asp Ala Ser Leu Met Glu Leu Ile Arg Arg Asp Tyr Pro Ala Val
120 125 130

gag gcg ttt gga tac cgc tcg gaa aac aca gaa gcg gat gcg atc gca 547
Glu Ala Phe Gly Tyr Arg Ser Glu Asn Thr Glu Ala Asp Ala Ile Ala
135 140 145

gct agg cgt tta gaa atc ggc ctg att gat gtg gag gcg tta gaa tca 595
Ala Arg Arg Leu Glu Ile Gly Leu Ile Asp Val Glu Ala Leu Glu Ser
150 155 160 165

gcc ggt ttc gaa gtg gtt gct gac cat ccc gtg tta ccc cgt ctg cgg 643
Ala Gly Phe Glu Val Val Ala Asp His Pro Val Leu Pro Arg Leu Arg
170 175 180

atg gaa tta cca ccc gca acg gtg ctg ctc aca gct aag gat gcc cag 691
Met Glu Leu Pro Pro Ala Thr Val Leu Leu Thr Ala Lys Asp Ala Gln
185 190 195

```
cga ctc ctt caa gag atg ggc gcg att tagccagcct gctctgattg          738
Arg Leu Leu Gln Glu Met Gly Ala Ile
        200                 205

caa                                                                741
```

<210> 2232
<211> 206
<212> PRT
<213> Corynebacterium glutamicum

<400> 2232

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Met Leu Gln Ala Ser Leu Phe Pro Ile Val Gln Glu His Ile Asp Phe
  1               5                  10                  15

Leu His Pro Gln Ala Arg Lys Ser Val Phe Trp Glu Leu Ala Pro Glu
             20                  25                  30

Val Ala Ala Lys Ala Asp Pro Val Phe Glu Lys Glu Ala Trp Leu Ser
         35                  40                  45

Thr Thr Leu Leu Glu Tyr Glu Ser Cys Gly Phe Asn Ile Gly Tyr Arg
     50                  55                  60

Asn Gly Thr Pro Ala Leu Ala Ser Val Ile Phe Cys Glu Arg Asp Ala
 65                  70                  75                  80

Ala Pro Gly Ala Lys Ala Leu Pro Thr Ala Pro Val Ser Ser Asp Ala
                 85                  90                  95

Ala Ile Ile Ser Ser Leu Phe Ile Asp Glu Val Phe Arg Gly Thr Gly
            100                 105                 110

Met Glu Ser Ala Leu Leu Asp Ala Ser Leu Met Glu Leu Ile Arg Arg
        115                 120                 125

Asp Tyr Pro Ala Val Glu Ala Phe Gly Tyr Arg Ser Glu Asn Thr Glu
    130                 135                 140

Ala Asp Ala Ile Ala Ala Arg Arg Leu Glu Ile Gly Leu Ile Asp Val
145                 150                 155                 160

Glu Ala Leu Glu Ser Ala Gly Phe Glu Val Val Ala Asp His Pro Val
                165                 170                 175

Leu Pro Arg Leu Arg Met Glu Leu Pro Pro Ala Thr Val Leu Leu Thr
            180                 185                 190

Ala Lys Asp Ala Gln Arg Leu Leu Gln Glu Met Gly Ala Ile
        195                 200                 205
```

<210> 2233
<211> 669
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(646)
<223> RXA01439

<400> 2233
gttaatccac agcgccctgt gtgcactcta ttagtgaata tccggtgaat gctcgtccct 60

cgactgtcta cttagtaggt ttgcaggcta gtcttttgtc atg acc cga tac ttt 115
Met Thr Arg Tyr Phe
1 5

gca gtt tcc aat ctt cag gag ctt ggc tcc ctc gaa gta cac aaa ttg 163
Ala Val Ser Asn Leu Gln Glu Leu Gly Ser Leu Glu Val His Lys Leu
10 15 20

tac aaa ctt cgt gta gat att ttc gtc cac gag cag cag act ccg tac 211
Tyr Lys Leu Arg Val Asp Ile Phe Val His Glu Gln Gln Thr Pro Tyr
25 30 35

gcg gag atc gat gac acc gat gct gcc cca acc acc aat cac atc ctg 259
Ala Glu Ile Asp Asp Thr Asp Ala Ala Pro Thr Thr Asn His Ile Leu
40 45 50

gtt tgg gag cgc gcc gac gcc acc cca acc aac ctc atc ggc tgc gca 307
Val Trp Glu Arg Ala Asp Ala Thr Pro Thr Asn Leu Ile Gly Cys Ala
55 60 65

cgc ctc gcg ccc atc acc gcc gcc gag ctt aag gcg tac acc ggc aag 355
Arg Leu Ala Pro Ile Thr Ala Ala Glu Leu Lys Ala Tyr Thr Gly Lys
70 75 80 85

ggc att tcg ctt gac gac gcc acc ccg ctc tca caa ctc ggc cgc gta 403
Gly Ile Ser Leu Asp Asp Ala Thr Pro Leu Ser Gln Leu Gly Arg Val
90 95 100

gcg gtg gca cag gaa ggg cgg ggc tcg ggg ctc tca ggt gag ctc atg 451
Ala Val Ala Gln Glu Gly Arg Gly Ser Gly Leu Ser Gly Glu Leu Met
105 110 115

cgc aac gcg ctg cgt ctt gca tat gag cag tac ccc gac cgc gat gtt 499
Arg Asn Ala Leu Arg Leu Ala Tyr Glu Gln Tyr Pro Asp Arg Asp Val
120 125 130

gtc ctg acc gcg cag aag cct ttg gta gat ttc tac gca gaa tac ggc 547
Val Leu Thr Ala Gln Lys Pro Leu Val Asp Phe Tyr Ala Glu Tyr Gly
135 140 145

ttt gag gtc ttg ggt gag gaa tac ctt gac tcg ggt gtt cct cac ctt 595
Phe Glu Val Leu Gly Glu Glu Tyr Leu Asp Ser Gly Val Pro His Leu
150 155 160 165

ccg atg ttg ctc aag gct gat gag ctt gaa agg ttc tca gac cta gac 643
Pro Met Leu Leu Lys Ala Asp Glu Leu Glu Arg Phe Ser Asp Leu Asp
170 175 180

gcc taatccgtag tcactggaac tca 669
Ala

<210> 2234
<211> 182

<212> PRT
<213> Corynebacterium glutamicum

<400> 2234
Met Thr Arg Tyr Phe Ala Val Ser Asn Leu Gln Glu Leu Gly Ser Leu
1 5 10 15

Glu Val His Lys Leu Tyr Lys Leu Arg Val Asp Ile Phe Val His Glu
20 25 30

Gln Gln Thr Pro Tyr Ala Glu Ile Asp Asp Thr Asp Ala Ala Pro Thr
35 40 45

Thr Asn His Ile Leu Val Trp Glu Arg Ala Asp Ala Thr Pro Thr Asn
50 55 60

Leu Ile Gly Cys Ala Arg Leu Ala Pro Ile Thr Ala Ala Glu Leu Lys
65 70 75 80

Ala Tyr Thr Gly Lys Gly Ile Ser Leu Asp Asp Ala Thr Pro Leu Ser
85 90 95

Gln Leu Gly Arg Val Ala Val Ala Gln Glu Gly Arg Gly Ser Gly Leu
100 105 110

Ser Gly Glu Leu Met Arg Asn Ala Leu Arg Leu Ala Tyr Glu Gln Tyr
115 120 125

Pro Asp Arg Asp Val Val Leu Thr Ala Gln Lys Pro Leu Val Asp Phe
130 135 140

Tyr Ala Glu Tyr Gly Phe Glu Val Leu Gly Glu Glu Tyr Leu Asp Ser
145 150 155 160

Gly Val Pro His Leu Pro Met Leu Leu Lys Ala Asp Glu Leu Glu Arg
165 170 175

Phe Ser Asp Leu Asp Ala
180

<210> 2235
<211> 1131
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1108)
<223> RXA01440

<400> 2235
ttgatggaac caccctcacg ctgaccacgc ctcaggggaa tcagtattgg gcaaacacac 60

acgattttgg agccggcaca cactaatttt aggagcactg atg aaa acc aag tgg 115
Met Lys Thr Lys Trp
1 5

tta gcg atc att cca ttc gtg gcg ctt gcg gtg gtt gca tgc tct gat 163
Leu Ala Ile Ile Pro Phe Val Ala Leu Ala Val Val Ala Cys Ser Asp
10 15 20

```
acg cag ccg ccg gtt aca gaa aca gtg aca gaa acc gcc ccg caa cct   211
Thr Gln Pro Pro Val Thr Glu Thr Val Thr Glu Thr Ala Pro Gln Pro
             25                  30                  35

act tct gaa acg gca gcg cag cca cca caa ccc acg aca cct gcg gaa   259
Thr Ser Glu Thr Ala Ala Gln Pro Pro Gln Pro Thr Thr Pro Ala Glu
         40                  45                  50

acg acc acg cag cag gca gaa ggt atc aac ttg acg cct cgc tac act   307
Thr Thr Thr Gln Gln Ala Glu Gly Ile Asn Leu Thr Pro Arg Tyr Thr
     55                  60                  65

cgc caa aat gtg ggg cac ttt tcc agt ggt tat cag cct gga cag gtg   355
Arg Gln Asn Val Gly His Phe Ser Ser Gly Tyr Gln Pro Gly Gln Val
 70                  75                  80                  85

agt ttt tcc tca gct gat gga acc att aaa tgt gag ttt cgc ccc atg   403
Ser Phe Ser Ser Ala Asp Gly Thr Ile Lys Cys Glu Phe Arg Pro Met
                 90                  95                 100

gaa cag gac gca cct atc aac cgg gag ccc tcc acc gat tgg cgg ttg   451
Glu Gln Asp Ala Pro Ile Asn Arg Glu Pro Ser Thr Asp Trp Arg Leu
            105                 110                 115

agt ttc gtg cag ggt gcg tgc caa ttc gac gat ggt tac gta gtg gcg   499
Ser Phe Val Gln Gly Ala Cys Gln Phe Asp Asp Gly Tyr Val Val Ala
        120                 125                 130

gat aca aat gtg gaa aac aga cca ggt ttt gct gag tac acc acg gcg   547
Asp Thr Asn Val Glu Asn Arg Pro Gly Phe Ala Glu Tyr Thr Thr Ala
    135                 140                 145

att tct cat gtc atg ccg gaa aat tac acc acg ttg ccg ccg gga acc   595
Ile Ser His Val Met Pro Glu Asn Tyr Thr Thr Leu Pro Pro Gly Thr
150                 155                 160                 165

tac atc gat tta cac acc atg gct tgt ttc acc gag tct gcc gat gaa   643
Tyr Ile Asp Leu His Thr Met Ala Cys Phe Thr Glu Ser Ala Asp Glu
                170                 175                 180

att tcc tgc att aag tac gcg acc aat gaa aca ttc cgc atc agc gcg   691
Ile Ser Cys Ile Lys Tyr Ala Thr Asn Glu Thr Phe Arg Ile Ser Ala
            185                 190                 195

cag ggt ttt gag atg ctc tca aat gcc cag cgc gac gcg gaa cta acc   739
Gln Gly Phe Glu Met Leu Ser Asn Ala Gln Arg Asp Ala Glu Leu Thr
        200                 205                 210

aca caa ggt ggc ttg tac cag gca ttt tcc aac atc gcg gaa tta cgg   787
Thr Gln Gly Gly Leu Tyr Gln Ala Phe Ser Asn Ile Ala Glu Leu Arg
    215                 220                 225

ttc agt gac ggc aac gcc atg tca tgt ttc ttt gac gcg ccg gga tcg   835
Phe Ser Asp Gly Asn Ala Met Ser Cys Phe Phe Asp Ala Pro Gly Ser
230                 235                 240                 245

caa gat ttc tgg tgc caa aca ctc agc acc ccc ggc tgg gac gac ggc   883
Gln Asp Phe Trp Cys Gln Thr Leu Ser Thr Pro Gly Trp Asp Asp Gly
                250                 255                 260
```

```
agc aac ctc att cat ttg acg gtc acc ggc gga aaa ctc agc ctg atg   931
Ser Asn Leu Ile His Leu Thr Val Thr Gly Gly Lys Leu Ser Leu Met
            265                 270                 275

ggc acc caa gtg ggc aac ccc ggc ctc gac tat ttc cgc ggc cgc cag   979
Gly Thr Gln Val Gly Asn Pro Gly Leu Asp Tyr Phe Arg Gly Arg Gln
        280                 285                 290

ctc att gag gcg cca aat tcg ctt ctc gac gcc tcc ctc tcc gta aca   1027
Leu Ile Glu Ala Pro Asn Ser Leu Leu Asp Ala Ser Leu Ser Val Thr
    295                 300                 305

ctc gac ggc gat cgg gtg cgt ttc cgc acc gcg acc ggc gag gag atg   1075
Leu Asp Gly Asp Arg Val Arg Phe Arg Thr Ala Thr Gly Glu Glu Met
310                 315                 320                 325

tgg gtg agt tcc agt gac tac gga tta ggc gtc taggtctgag aacctttcaa 1128
Trp Val Ser Ser Ser Asp Tyr Gly Leu Gly Val
                330                 335

gct                                                               1131
```

<210> 2236
<211> 336
<212> PRT
<213> Corynebacterium glutamicum

<400> 2236

```
Met Lys Thr Lys Trp Leu Ala Ile Ile Pro Phe Val Ala Leu Ala Val
  1               5                  10                  15

Val Ala Cys Ser Asp Thr Gln Pro Pro Val Thr Glu Thr Val Thr Glu
             20                  25                  30

Thr Ala Pro Gln Pro Thr Ser Glu Thr Ala Ala Gln Pro Pro Gln Pro
         35                  40                  45

Thr Thr Pro Ala Glu Thr Thr Thr Gln Gln Ala Glu Gly Ile Asn Leu
     50                  55                  60

Thr Pro Arg Tyr Thr Arg Gln Asn Val Gly His Phe Ser Ser Gly Tyr
 65                  70                  75                  80

Gln Pro Gly Gln Val Ser Phe Ser Ser Ala Asp Gly Thr Ile Lys Cys
                 85                  90                  95

Glu Phe Arg Pro Met Glu Gln Asp Ala Pro Ile Asn Arg Glu Pro Ser
            100                 105                 110

Thr Asp Trp Arg Leu Ser Phe Val Gln Gly Ala Cys Gln Phe Asp Asp
        115                 120                 125

Gly Tyr Val Val Ala Asp Thr Asn Val Glu Asn Arg Pro Gly Phe Ala
    130                 135                 140

Glu Tyr Thr Thr Ala Ile Ser His Val Met Pro Glu Asn Tyr Thr Thr
145                 150                 155                 160

Leu Pro Pro Gly Thr Tyr Ile Asp Leu His Thr Met Ala Cys Phe Thr
                165                 170                 175
```

```
Glu Ser Ala Asp Glu Ile Ser Cys Ile Lys Tyr Ala Thr Asn Glu Thr
            180                 185                 190

Phe Arg Ile Ser Ala Gln Gly Phe Glu Met Leu Ser Asn Ala Gln Arg
        195                 200                 205

Asp Ala Glu Leu Thr Thr Gln Gly Gly Leu Tyr Gln Ala Phe Ser Asn
    210                 215                 220

Ile Ala Glu Leu Arg Phe Ser Asp Gly Asn Ala Met Ser Cys Phe Phe
225                 230                 235                 240

Asp Ala Pro Gly Ser Gln Asp Phe Trp Cys Gln Thr Leu Ser Thr Pro
                245                 250                 255

Gly Trp Asp Asp Gly Ser Asn Leu Ile His Leu Thr Val Thr Gly Gly
            260                 265                 270

Lys Leu Ser Leu Met Gly Thr Gln Val Gly Asn Pro Gly Leu Asp Tyr
        275                 280                 285

Phe Arg Gly Arg Gln Leu Ile Glu Ala Pro Asn Ser Leu Leu Asp Ala
    290                 295                 300

Ser Leu Ser Val Thr Leu Asp Gly Asp Arg Val Arg Phe Arg Thr Ala
305                 310                 315                 320

Thr Gly Glu Glu Met Trp Val Ser Ser Ser Asp Tyr Gly Leu Gly Val
                325                 330                 335
```

Application as filed - Sequence Listing

<210> 2237
<211> 1152
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1129)
<223> RXA01441

<400> 2237
ttataacaat tagccgtgag ggtattaatc aaggtttcgg gagactaacg ttttagaaac 60

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aagtggactc cagcacacct cgtgagatgg caggttcatc atg gct aga acg aca   115
                                            Met Ala Arg Thr Thr
                                              1               5

aca gcg cac gca gtt ctc atg gcg ctt agt tca gtc ggg ctt ttg atg   163
Thr Ala His Ala Val Leu Met Ala Leu Ser Ser Val Gly Leu Leu Met
                 10                  15                  20

ctc cag gcc tgc tcc gaa cag gaa caa acc cca gaa caa acg cca gcg   211
Leu Gln Ala Cys Ser Glu Gln Glu Gln Thr Pro Glu Gln Thr Pro Ala
             25                  30                  35

ccc acc ctg act tcg cag gct ccc gag act cct caa gcc tca aca acc   259
```

```
Pro Thr Leu Thr Ser Gln Ala Pro Glu Thr Pro Gln Ala Ser Thr Thr
         40                  45                  50

tcc tca gca agc tcc aca gca act ccc ata gca act ccc ata gca gcc   307
Ser Ser Ala Ser Ser Thr Ala Thr Pro Ile Ala Thr Pro Ile Ala Ala
     55                  60                  65

acc gag ttg gat tat ctc cac atc gat cca gca acg tat gac atc ggt   355
Thr Glu Leu Asp Tyr Leu His Ile Asp Pro Ala Thr Tyr Asp Ile Gly
 70                  75                  80                  85

gtc caa gac caa gaa act gcc gta ttt acc act ggc gat ggg atc aca   403
Val Gln Asp Gln Glu Thr Ala Val Phe Thr Thr Gly Asp Gly Ile Thr
                 90                  95                 100

gcg cag tgt ttc ttc gag gca aca ccg ggg gag acc agc tat cag atc   451
Ala Gln Cys Phe Phe Glu Ala Thr Pro Gly Glu Thr Ser Tyr Gln Ile
            105                 110                 115

aag gag ttt gat ttc gac gaa act gcg gga acg tgc gct ttt ggt gat   499
Lys Glu Phe Asp Phe Asp Glu Thr Ala Gly Thr Cys Ala Phe Gly Asp
        120                 125                 130

caa cac atc agc gtc acc acg gat gaa aat gtc cgg gaa cgc ttt gcc   547
Gln His Ile Ser Val Thr Thr Asp Glu Asn Val Arg Glu Arg Phe Ala
    135                 140                 145

gaa ttg agt gaa acc gaa gaa gaa tta cca gaa gcg caa gcg act ctc   595
Glu Leu Ser Glu Thr Glu Glu Glu Leu Pro Glu Ala Gln Ala Thr Leu
150                 155                 160                 165

gat gtt ggt gag atg gtg cat ctt ggt cac atg ggt tgt tgg gcg ccg   643
Asp Val Gly Glu Met Val His Leu Gly His Met Gly Cys Trp Ala Pro
                170                 175                 180

agt gta tcg gag ttt agt tgt ctc gat ttc gcc tcc aac cag gcg ttc   691
Ser Val Ser Glu Phe Ser Cys Leu Asp Phe Ala Ser Asn Gln Ala Phe
            185                 190                 195

acc atg aat gaa cag ggc ttc cat gag ctt gat cct gca aaa gcc act   739
Thr Met Asn Glu Gln Gly Phe His Glu Leu Asp Pro Ala Lys Ala Thr
        200                 205                 210

gag cag cta att aat tcg agt ggc cag gtt caa acg tta tcg aaa atg   787
Glu Gln Leu Ile Asn Ser Ser Gly Gln Val Gln Thr Leu Ser Lys Met
    215                 220                 225

acg aat ttc cag ttc acc gat ggc acc agc atc acc tgt gtc agt gag   835
Thr Asn Phe Gln Phe Thr Asp Gly Thr Ser Ile Thr Cys Val Ser Glu
230                 235                 240                 245

ttg cag gcg gaa gag ttc ttg tgc cac aac agt ggt cct gga ggc tgg   883
Leu Gln Ala Glu Glu Phe Leu Cys His Asn Ser Gly Pro Gly Gly Trp
                250                 255                 260

tca act tca gct ggc cct gcc aac acc ctg tgg tgg aat ctg aac cag   931
Ser Thr Ser Ala Gly Pro Ala Asn Thr Leu Trp Trp Asn Leu Asn Gln
            265                 270                 275

gcc gac tcc gag ttt gag ggt gct cgc ccc acg aat cca acg caa agc   979
Ala Asp Ser Glu Phe Glu Gly Ala Arg Pro Thr Asn Pro Thr Gln Ser
```

```
        280                 285                 290

gtt tat aaa tct caa caa ata ttc ggt ccg gga tcg tat ctc ctc gcg   1027
Val Tyr Lys Ser Gln Gln Ile Phe Gly Pro Gly Ser Tyr Leu Leu Ala
    295                 300                 305

aac ggt gtg agt gca gaa ttt gat gga acc acc ctc acg ctg acc acg   1075
Asn Gly Val Ser Ala Glu Phe Asp Gly Thr Thr Leu Thr Leu Thr Thr
310                 315                 320                 325

cct cag ggg aat cag tat tgg gca aac aca cac gat ttt gga gcc ggc   1123
Pro Gln Gly Asn Gln Tyr Trp Ala Asn Thr His Asp Phe Gly Ala Gly
                330                 335                 340

aca cac taattttagg agcactgatg aaa                                1152
Thr His
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<210> 2238
<211> 343
<212> PRT
<213> Corynebacterium glutamicum

<400> 2238

```
Met Ala Arg Thr Thr Thr Ala His Ala Val Leu Met Ala Leu Ser Ser
  1               5                  10                  15

Val Gly Leu Leu Met Leu Gln Ala Cys Ser Glu Gln Glu Gln Thr Pro
             20                  25                  30

Glu Gln Thr Pro Ala Pro Thr Leu Thr Ser Gln Ala Pro Glu Thr Pro
         35                  40                  45

Gln Ala Ser Thr Thr Ser Ser Ala Ser Ser Thr Ala Thr Pro Ile Ala
     50                  55                  60

Thr Pro Ile Ala Ala Thr Glu Leu Asp Tyr Leu His Ile Asp Pro Ala
 65                  70                  75                  80

Thr Tyr Asp Ile Gly Val Gln Asp Gln Glu Thr Ala Val Phe Thr Thr
                 85                  90                  95

Gly Asp Gly Ile Thr Ala Gln Cys Phe Phe Glu Ala Thr Pro Gly Glu
            100                 105                 110

Thr Ser Tyr Gln Ile Lys Glu Phe Asp Phe Asp Glu Thr Ala Gly Thr
        115                 120                 125

Cys Ala Phe Gly Asp Gln His Ile Ser Val Thr Thr Asp Glu Asn Val
    130                 135                 140

Arg Glu Arg Phe Ala Glu Leu Ser Glu Thr Glu Glu Glu Leu Pro Glu
145                 150                 155                 160

Ala Gln Ala Thr Leu Asp Val Gly Glu Met Val His Leu Gly His Met
                165                 170                 175

Gly Cys Trp Ala Pro Ser Val Ser Glu Phe Ser Cys Leu Asp Phe Ala
            180                 185                 190
```

```
Ser Asn Gln Ala Phe Thr Met Asn Glu Gln Gly Phe His Glu Leu Asp
        195                 200                 205

Pro Ala Lys Ala Thr Glu Gln Leu Ile Asn Ser Ser Gly Gln Val Gln
    210                 215                 220

Thr Leu Ser Lys Met Thr Asn Phe Gln Phe Thr Asp Gly Thr Ser Ile
225                 230                 235                 240

Thr Cys Val Ser Glu Leu Gln Ala Glu Glu Phe Leu Cys His Asn Ser
                245                 250                 255

Gly Pro Gly Gly Trp Ser Thr Ser Ala Gly Pro Ala Asn Thr Leu Trp
            260                 265                 270

Trp Asn Leu Asn Gln Ala Asp Ser Glu Phe Glu Gly Ala Arg Pro Thr
        275                 280                 285

Asn Pro Thr Gln Ser Val Tyr Lys Ser Gln Gln Ile Phe Gly Pro Gly
    290                 295                 300

Ser Tyr Leu Leu Ala Asn Gly Val Ser Ala Glu Phe Asp Gly Thr Thr
305                 310                 315                 320

Leu Thr Leu Thr Thr Pro Gln Gly Asn Gln Tyr Trp Ala Asn Thr His
                325                 330                 335

Asp Phe Gly Ala Gly Thr His
            340
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Added at 2005-10-20 20:20:20 (GMT)

<210> 2239
<211> 1116
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1093)
<223> RXA01445

<400> 2239

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gagtctcgaa tgtataacga gtttgttcct aataacttta tcattaacta tgcctgcaat 60

aggcttggga aattttggca tccaggtaat cgcgctgtca atg atc cca ctt att   115
                                            Met Ile Pro Leu Ile
                                              1               5

aat gta cgt ttt ccc gtt gcc gcc tta cct ctc gca tta gtg gcg act   163
Asn Val Arg Phe Pro Val Ala Ala Leu Pro Leu Ala Leu Val Ala Thr
                 10                  15                  20

gta tgg ctt aat gct tgg gca gac cat ctt ctc cta act ggt ttt att   211
Val Trp Leu Asn Ala Trp Ala Asp His Leu Leu Leu Thr Gly Phe Ile
             25                  30                  35

gtt tat ctt gct gtg gaa tac gca aca agc cgt ggg cgc ttc gct ctc   259
Val Tyr Leu Ala Val Glu Tyr Ala Thr Ser Arg Gly Arg Phe Ala Leu
         40                  45                  50

gca ttg att ttg gga gtt gaa tgg atc tta att gct tat ggg gta gct   307
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Ala Leu Ile Leu Gly Val Glu Trp Ile Leu Ile Ala Tyr Gly Val Ala
     55                  60                  65

ttg gaa agg cct ctt gag gct aaa gac tct cca tct ctc att acc gaa   355
Leu Glu Arg Pro Leu Glu Ala Lys Asp Ser Pro Ser Leu Ile Thr Glu
 70                  75                  80                  85

att ttg ctc ata ctt gta gca gct ggc aca ggg gca ggt cgg tgg aaa   403
Ile Leu Leu Ile Leu Val Ala Ala Gly Thr Gly Ala Gly Arg Trp Lys
                 90                  95                 100

att ttg agt gaa cgc aag caa cgt gca att act cag cag gaa atc atc   451
Ile Leu Ser Glu Arg Lys Gln Arg Ala Ile Thr Gln Gln Glu Ile Ile
            105                 110                 115

aaa aaa atc cgt act gat ata gcg cac tat ttg cat gac agt atg gca   499
Lys Lys Ile Arg Thr Asp Ile Ala His Tyr Leu His Asp Ser Met Ala
        120                 125                 130

aga tcg ttg gca ata atg ata gtt caa tca aag ctg act gaa cta gag   547
Arg Ser Leu Ala Ile Met Ile Val Gln Ser Lys Leu Thr Glu Leu Glu
    135                 140                 145

cct gat cca aaa aag att caa gaa aaa cta aac agt att gcc aaa att   595
Pro Asp Pro Lys Lys Ile Gln Glu Lys Leu Asn Ser Ile Ala Lys Ile
150                 155                 160                 165

gga caa gag gca gtg gct gat ttg cat caa tta gtt aga cac ctc gtg   643
Gly Gln Glu Ala Val Ala Asp Leu His Gln Leu Val Arg His Leu Val
                170                 175                 180

gtc gag gag tct gct gaa aaa gcc aca gcg ttt gga gca tgg gct gca   691
Val Glu Glu Ser Ala Glu Lys Ala Thr Ala Phe Gly Ala Trp Ala Ala
            185                 190                 195

gtt tct att cat gac acg gtt aat tct gcc att cag tta tta gta gat   739
Val Ser Ile His Asp Thr Val Asn Ser Ala Ile Gln Leu Leu Val Asp
        200                 205                 210

gca gga cat gtc gtt tcc ttt gac agt aga aaa aag aac tat aag ctg   787
Ala Gly His Val Val Ser Phe Asp Ser Arg Lys Lys Asn Tyr Lys Leu
    215                 220                 225

gac cat att gct gaa acg gcg ttt gct tta gcc ttc aat gag gca gtc   835
Asp His Ile Ala Glu Thr Ala Phe Ala Leu Ala Phe Asn Glu Ala Val
230                 235                 240                 245

tgt aat gca att aaa cat tct ccg ccc aag gca aac gtt act att cgc   883
Cys Asn Ala Ile Lys His Ser Pro Pro Lys Ala Asn Val Thr Ile Arg
                250                 255                 260

ata aca gaa aaa gca cag tct ctt cag att cta gta atg aat cct att   931
Ile Thr Glu Lys Ala Gln Ser Leu Gln Ile Leu Val Met Asn Pro Ile
            265                 270                 275

gga gat tgg cat gca aat ggg gag tcc gca att cca ggt gtg ggc att   979
Gly Asp Trp His Ala Asn Gly Glu Ser Ala Ile Pro Gly Val Gly Ile
        280                 285                 290

ggc gta gaa agc tta acc aga agg ata cgt aat att aaa gga cag gtc   1027
Gly Val Glu Ser Leu Thr Arg Arg Ile Arg Asn Ile Lys Gly Gln Val
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    295                 300                 305

tgt gtg act tca ctg caa gga tac tgg aaa gta gtt att tca cta cct   1075
Cys Val Thr Ser Leu Gln Gly Tyr Trp Lys Val Val Ile Ser Leu Pro
310                 315                 320                 325

ttg aaa tgt gag gat tct taaattgtct ctatttgttg aac                 1116
Leu Lys Cys Glu Asp Ser
                330
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<210> 2240
<211> 331
<212> PRT
<213> Corynebacterium glutamicum

<400> 2240

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Met Ile Pro Leu Ile Asn Val Arg Phe Pro Val Ala Ala Leu Pro Leu
  1               5                  10                  15

Ala Leu Val Ala Thr Val Trp Leu Asn Ala Trp Ala Asp His Leu Leu
             20                  25                  30

Leu Thr Gly Phe Ile Val Tyr Leu Ala Val Glu Tyr Ala Thr Ser Arg
         35                  40                  45

Gly Arg Phe Ala Leu Ala Leu Ile Leu Gly Val Glu Trp Ile Leu Ile
     50                  55                  60

Ala Tyr Gly Val Ala Leu Glu Arg Pro Leu Glu Ala Lys Asp Ser Pro
 65                  70                  75                  80

Ser Leu Ile Thr Glu Ile Leu Leu Ile Leu Val Ala Ala Gly Thr Gly
                 85                  90                  95

Ala Gly Arg Trp Lys Ile Leu Ser Glu Arg Lys Gln Arg Ala Ile Thr
            100                 105                 110

Gln Gln Glu Ile Ile Lys Lys Ile Arg Thr Asp Ile Ala His Tyr Leu
        115                 120                 125

His Asp Ser Met Ala Arg Ser Leu Ala Ile Met Ile Val Gln Ser Lys
    130                 135                 140

Leu Thr Glu Leu Glu Pro Asp Pro Lys Lys Ile Gln Glu Lys Leu Asn
145                 150                 155                 160

Ser Ile Ala Lys Ile Gly Gln Glu Ala Val Ala Asp Leu His Gln Leu
                165                 170                 175

Val Arg His Leu Val Val Glu Glu Ser Ala Glu Lys Ala Thr Ala Phe
            180                 185                 190

Gly Ala Trp Ala Ala Val Ser Ile His Asp Thr Val Asn Ser Ala Ile
        195                 200                 205

Gln Leu Leu Val Asp Ala Gly His Val Val Ser Phe Asp Ser Arg Lys
    210                 215                 220

Lys Asn Tyr Lys Leu Asp His Ile Ala Glu Thr Ala Phe Ala Leu Ala
225                 230                 235                 240
```

```
Phe Asn Glu Ala Val Cys Asn Ala Ile Lys His Ser Pro Pro Lys Ala
                245                 250                 255

Asn Val Thr Ile Arg Ile Thr Glu Lys Ala Gln Ser Leu Gln Ile Leu
            260                 265                 270

Val Met Asn Pro Ile Gly Asp Trp His Ala Asn Gly Glu Ser Ala Ile
        275                 280                 285

Pro Gly Val Gly Ile Gly Val Glu Ser Leu Thr Arg Arg Ile Arg Asn
    290                 295                 300

Ile Lys Gly Gln Val Cys Val Thr Ser Leu Gln Gly Tyr Trp Lys Val
305                 310                 315                 320

Val Ile Ser Leu Pro Leu Lys Cys Glu Asp Ser
                325                 330


<210> 2241
<211> 972
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(949)
<223> RXA01447

<400> 2241
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catgtgaggt ttttaatcat cgcgatacta agcttgcggt atg cgt ctt ctg gtt   115
                                            Met Arg Leu Leu Val
                                              1               5

ttg cgg tgc gat gcc cca cac atc aac gaa ttc cct gcc ctt tcc acc   163
Leu Arg Cys Asp Ala Pro His Ile Asn Glu Phe Pro Ala Leu Ser Thr
                  10                  15                  20

tct gtg gag atc cac gat ttg cct gcg gtg ccc acc cga aaa gac ctc   211
Ser Val Glu Ile His Asp Leu Pro Ala Val Pro Thr Arg Lys Asp Leu
              25                  30                  35

aaa att ctt gat gat gtg gcc ttt gat gtg ctc cct cag gat ccc acg   259
Lys Ile Leu Asp Asp Val Ala Phe Asp Val Leu Pro Gln Asp Pro Thr
          40                  45                  50

cct tct ctc gat gag atc gcc aag cag cct gat gtc gag cat ttg agc   307
Pro Ser Leu Asp Glu Ile Ala Lys Gln Pro Asp Val Glu His Leu Ser
      55                  60                  65

agc cct aag ttt gcg cca caa cag cct gaa acc cgt ttg cgc atc gtg   355
Ser Pro Lys Phe Ala Pro Gln Gln Pro Glu Thr Arg Leu Arg Ile Val
  70                  75                  80                  85

gtg atc ggt tcg gat gca gcg ctg tct gcg gtc ctg act cgt ctc atg   403
Val Ile Gly Ser Asp Ala Ala Leu Ser Ala Val Leu Thr Arg Leu Met
                  90                  95                 100
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cgc gcc gat aat ttg tgg gcg gag att gga ttc gtg ccc gtt ggt cct   451
Arg Ala Asp Asn Leu Trp Ala Glu Ile Gly Phe Val Pro Val Gly Pro
            105                 110                 115

tca acg gct gcg aag aac tgg ggt ctg ccc gcc gat gag gct gcc gcg   499
Ser Thr Ala Ala Lys Asn Trp Gly Leu Pro Ala Asp Glu Ala Ala Ala
        120                 125                 130

ctt gag ctc gca ctg acc gga ttg gtc aat cct gcc ccg ctc atc cgc   547
Leu Glu Leu Ala Leu Thr Gly Leu Val Asn Pro Ala Pro Leu Ile Arg
    135                 140                 145

gat gac gtt gcg gtc gcc gtc gcc ggt tca gcc acc atc acc aac tgg   595
Asp Asp Val Ala Val Ala Val Ala Gly Ser Ala Thr Ile Thr Asn Trp
150                 155                 160                 165

gag ccg ggt gag atc acc ggc gaa gtc atc gtc gat gat cat gtt ctc   643
Glu Pro Gly Glu Ile Thr Gly Glu Val Ile Val Asp Asp His Val Leu
                170                 175                 180

atc cgc cac gag gct gcc tcg aag gcc cca cgc cgt ggc gtc tac ggt   691
Ile Arg His Glu Ala Ala Ser Lys Ala Pro Arg Arg Gly Val Tyr Gly
            185                 190                 195

gcc cgc ttg gtg ccg atg ctt gac gcc cca ggc atc gct gcg gtc atc   739
Ala Arg Leu Val Pro Met Leu Asp Ala Pro Gly Ile Ala Ala Val Ile
        200                 205                 210

atg gac act ccc ctg ccc ggc gag gtg ccc tcc cgc agc ctg ttc cct   787
Met Asp Thr Pro Leu Pro Gly Glu Val Pro Ser Arg Ser Leu Phe Pro
    215                 220                 225

cgc ccc tcg ggc tcg gtt att cca gag agc ttt tcg acg ggc cgt gcc   835
Arg Pro Ser Gly Ser Val Ile Pro Glu Ser Phe Ser Thr Gly Arg Ala
230                 235                 240                 245

atg caa gcc ggc ggc ccc tcg cta caa atc cgg gtt gac gga att tcc   883
Met Gln Ala Gly Gly Pro Ser Leu Gln Ile Arg Val Asp Gly Ile Ser
                250                 255                 260

cgc aaa cgt aaa gtg gag cgc gtt acc ttc tat cga cat ttg cgc gat   931
Arg Lys Arg Lys Val Glu Arg Val Thr Phe Tyr Arg His Leu Arg Asp
            265                 270                 275

ctc caa atc gtg cgg ccg taaaacaagg agccagcatg gca                 972
Leu Gln Ile Val Arg Pro
        280
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Application Filed with the USPTO as a PCT International Application

<210> 2242
<211> 283
<212> PRT
<213> Corynebacterium glutamicum

<400> 2242

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Met Arg Leu Leu Val Leu Arg Cys Asp Ala Pro His Ile Asn Glu Phe
  1               5                  10                  15

Pro Ala Leu Ser Thr Ser Val Glu Ile His Asp Leu Pro Ala Val Pro
             20                  25                  30
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Thr Arg Lys Asp Leu Lys Ile Leu Asp Asp Val Ala Phe Asp Val Leu
         35                  40                  45

Pro Gln Asp Pro Thr Pro Ser Leu Asp Glu Ile Ala Lys Gln Pro Asp
     50                  55                  60

Val Glu His Leu Ser Ser Pro Lys Phe Ala Pro Gln Gln Pro Glu Thr
 65                  70                  75                  80

Arg Leu Arg Ile Val Val Ile Gly Ser Asp Ala Ala Leu Ser Ala Val
                 85                  90                  95

Leu Thr Arg Leu Met Arg Ala Asp Asn Leu Trp Ala Glu Ile Gly Phe
            100                 105                 110

Val Pro Val Gly Pro Ser Thr Ala Ala Lys Asn Trp Gly Leu Pro Ala
        115                 120                 125

Asp Glu Ala Ala Ala Leu Glu Leu Ala Leu Thr Gly Leu Val Asn Pro
    130                 135                 140

Ala Pro Leu Ile Arg Asp Asp Val Ala Val Ala Val Ala Gly Ser Ala
145                 150                 155                 160

Thr Ile Thr Asn Trp Glu Pro Gly Glu Ile Thr Gly Glu Val Ile Val
                165                 170                 175

Asp Asp His Val Leu Ile Arg His Glu Ala Ala Ser Lys Ala Pro Arg
            180                 185                 190

Arg Gly Val Tyr Gly Ala Arg Leu Val Pro Met Leu Asp Ala Pro Gly
        195                 200                 205

Ile Ala Ala Val Ile Met Asp Thr Pro Leu Pro Gly Glu Val Pro Ser
    210                 215                 220

Arg Ser Leu Phe Pro Arg Pro Ser Gly Ser Val Ile Pro Glu Ser Phe
225                 230                 235                 240

Ser Thr Gly Arg Ala Met Gln Ala Gly Gly Pro Ser Leu Gln Ile Arg
                245                 250                 255

Val Asp Gly Ile Ser Arg Lys Arg Lys Val Glu Arg Val Thr Phe Tyr
            260                 265                 270

Arg His Leu Arg Asp Leu Gln Ile Val Arg Pro
        275                 280
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<210> 2243
<211> 402
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(379)
<223> RXA01452

<400> 2243
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cgtctagcgt tattgacgct cctcgttata cgctggtctc gtg atc aga tcg ttc   115
                                            Val Ile Arg Ser Phe
                                              1               5

gcc gac cgc gac acc gag ttg gtc tgg ttg cgt gaa ggt gcg aaa cgc   163
Ala Asp Arg Asp Thr Glu Leu Val Trp Leu Arg Glu Gly Ala Lys Arg
                 10                  15                  20

gtc gat ccg cga ata cac aaa gtg gcg aat cgg aag ctg cat ctg ctg   211
Val Asp Pro Arg Ile His Lys Val Ala Asn Arg Lys Leu His Leu Leu
             25                  30                  35

gac gcg gcg acg acc ctc gat gct ctg cgt gtg act ccg ggg aat cgc   259
Asp Ala Ala Thr Thr Leu Asp Ala Leu Arg Val Thr Pro Gly Asn Arg
         40                  45                  50

ctg gaa acg ctc gag ggt gat cga gtc ggt cag tac agc att cga gtc   307
Leu Glu Thr Leu Glu Gly Asp Arg Val Gly Gln Tyr Ser Ile Arg Val
     55                  60                  65

aac gac cag tgg cgg atc tgc ttc cgt tgg aac gac tcg ggc ccc gaa   355
Asn Asp Gln Trp Arg Ile Cys Phe Arg Trp Asn Asp Ser Gly Pro Glu
 70                  75                  80                  85

aac gtc gag atc gtg gat tat cac tgaggaggag acgatggctc aga         402
Asn Val Glu Ile Val Asp Tyr His
                 90
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<210> 2244
<211> 93
<212> PRT
<213> Corynebacterium glutamicum

<400> 2244

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Val Ile Arg Ser Phe Ala Asp Arg Asp Thr Glu Leu Val Trp Leu Arg
  1               5                  10                  15

Glu Gly Ala Lys Arg Val Asp Pro Arg Ile His Lys Val Ala Asn Arg
             20                  25                  30

Lys Leu His Leu Leu Asp Ala Ala Thr Thr Leu Asp Ala Leu Arg Val
         35                  40                  45

Thr Pro Gly Asn Arg Leu Glu Thr Leu Glu Gly Asp Arg Val Gly Gln
     50                  55                  60

Tyr Ser Ile Arg Val Asn Asp Gln Trp Arg Ile Cys Phe Arg Trp Asn
 65                  70                  75                  80

Asp Ser Gly Pro Glu Asn Val Glu Ile Val Asp Tyr His
                 85                  90
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<210> 2245
<211> 645
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(622)
<223> RXA01456

<400> 2245
aagacaatat ccttatatgt acgtgattat gcgtttctcc cccactctac ggtttaatca 60

cctataaagg ccaacaagta gttcacaaaa ggaaaaaatt atg aac gat tcc att 115
Met Asn Asp Ser Ile
1 5

ttt agt ccc caa gca ctg aat aaa gcg atg ctc gaa gcc gtc gag ttt 163
Phe Ser Pro Gln Ala Leu Asn Lys Ala Met Leu Glu Ala Val Glu Phe
10 15 20

atc cac gcc gaa ggt tgg gac gcc ggc cct acc ctg ttc gca ttg gtc 211
Ile His Ala Glu Gly Trp Asp Ala Gly Pro Thr Leu Phe Ala Leu Val
25 30 35

ccc act gaa atg ctg gtg gat act ctt gat gag gca gct gac gac tcc 259
Pro Thr Glu Met Leu Val Asp Thr Leu Asp Glu Ala Ala Asp Asp Ser
40 45 50

cca cta acc ctt gtt gta cag gac aac ctc cct gac aac ttg ctg cca 307
Pro Leu Thr Leu Val Val Gln Asp Asn Leu Pro Asp Asn Leu Leu Pro
55 60 65

ggt tcc gaa gcg tta ggt gac tat gtg tcc cgt ttg gcg tgg cca gca 355
Gly Ser Glu Ala Leu Gly Asp Tyr Val Ser Arg Leu Ala Trp Pro Ala
70 75 80 85

gag att gcc ggc gcg gtg ttg gct cag gaa att atg ttc acc gat gct 403
Glu Ile Ala Gly Ala Val Leu Ala Gln Glu Ile Met Phe Thr Asp Ala
90 95 100

gcc gtt gca ggc tca gaa cca cga ccc gct cgt ctt ttt tcc ggc gtt 451
Ala Val Ala Gly Ser Glu Pro Arg Pro Ala Arg Leu Phe Ser Gly Val
105 110 115

ttg cgc ggc gaa gca gaa ctc acc ctt ctg cag ctt cgc ccc acc gaa 499
Leu Arg Gly Glu Ala Glu Leu Thr Leu Leu Gln Leu Arg Pro Thr Glu
120 125 130

gag gaa ttg gca gaa cgc gga ccg ttt gct gaa gat gaa atc gaa ctg 547
Glu Glu Leu Ala Glu Arg Gly Pro Phe Ala Glu Asp Glu Ile Glu Leu
135 140 145

cgc ggc ggc cca ggg gtt gca ccg ggt gta atc gca gca ctg cgc tac 595
Arg Gly Gly Pro Gly Val Ala Pro Gly Val Ile Ala Ala Leu Arg Tyr
150 155 160 165

acc ctc gaa gcg gac cca gac gaa atc taaaaactga cttttcgtcc 642
Thr Leu Glu Ala Asp Pro Asp Glu Ile
170

agg 645

<210> 2246
<211> 174
<212> PRT

<213> Corynebacterium glutamicum

<400> 2246
Met Asn Asp Ser Ile Phe Ser Pro Gln Ala Leu Asn Lys Ala Met Leu
1 5 10 15

Glu Ala Val Glu Phe Ile His Ala Glu Gly Trp Asp Ala Gly Pro Thr
20 25 30

Leu Phe Ala Leu Val Pro Thr Glu Met Leu Val Asp Thr Leu Asp Glu
35 40 45

Ala Ala Asp Asp Ser Pro Leu Thr Leu Val Val Gln Asp Asn Leu Pro
50 55 60

Asp Asn Leu Leu Pro Gly Ser Glu Ala Leu Gly Asp Tyr Val Ser Arg
65 70 75 80

Leu Ala Trp Pro Ala Glu Ile Ala Gly Ala Val Leu Ala Gln Glu Ile
85 90 95

Met Phe Thr Asp Ala Ala Val Ala Gly Ser Glu Pro Arg Pro Ala Arg
100 105 110

Leu Phe Ser Gly Val Leu Arg Gly Glu Ala Glu Leu Thr Leu Leu Gln
115 120 125

Leu Arg Pro Thr Glu Glu Glu Leu Ala Glu Arg Gly Pro Phe Ala Glu
130 135 140

Asp Glu Ile Glu Leu Arg Gly Gly Pro Gly Val Ala Pro Gly Val Ile
145 150 155 160

Ala Ala Leu Arg Tyr Thr Leu Glu Ala Asp Pro Asp Glu Ile
165 170

<210> 2247
<211> 798
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(775)
<223> RXA01457

<400> 2247
gaagcggacc cagacgaaat ctaaaaactg acttttcgtc caggttcgct aggataaatt 60

aagttaaccc cgcccacaat ttatttgagg agttcacact gtg gcg tcc acc ccg 115
Val Ala Ser Thr Pro
1 5

cac aag cat gtc cgc gtt gca ctg gga tta gtg gcg ctc att cct ctt 163
His Lys His Val Arg Val Ala Leu Gly Leu Val Ala Leu Ile Pro Leu
10 15 20

tta gct gca tgt acg ggc ggc gga tcc acc gaa act tcc act gaa tcc 211
Leu Ala Ala Cys Thr Gly Gly Gly Ser Thr Glu Thr Ser Thr Glu Ser
25 30 35

```
acg gca gaa aca act cct gcg aca aca acg gaa gca acg aca act cct   259
Thr Ala Glu Thr Thr Pro Ala Thr Thr Thr Glu Ala Thr Thr Thr Pro
         40                  45                  50

gct acc act gct tcg tct tca gta att gaa acg aca gag tca agc act   307
Ala Thr Thr Ala Ser Ser Ser Val Ile Glu Thr Thr Glu Ser Ser Thr
     55                  60                  65

gcc gaa acg tcg acg aaa gag agt ggg gag acg tcg aca agc aaa cct   355
Ala Glu Thr Ser Thr Lys Glu Ser Gly Glu Thr Ser Thr Ser Lys Pro
 70                  75                  80                  85

cgt atg acc aag gac gtt gaa gtc gcc tat aaa gct ttc tcc tcg ctc   403
Arg Met Thr Lys Asp Val Glu Val Ala Tyr Lys Ala Phe Ser Ser Leu
                 90                  95                 100

gcg ccc gtc gag ctt ttt gag caa ttc gaa acc tgc gac ccg tca ggg   451
Ala Pro Val Glu Leu Phe Glu Gln Phe Glu Thr Cys Asp Pro Ser Gly
            105                 110                 115

gtc gag gat tcc ttc gcg tgc aac ggg ccg gaa gtt ggc caa ttc caa   499
Val Glu Asp Ser Phe Ala Cys Asn Gly Pro Glu Val Gly Gln Phe Gln
        120                 125                 130

ttc ttt gac aat gcg tcg aag gcc acg agc acg acg cag ctg ctc acg   547
Phe Phe Asp Asn Ala Ser Lys Ala Thr Ser Thr Thr Gln Leu Leu Thr
    135                 140                 145

gaa ctg cgc agc tca cgc gtg gtt gag gat tcc gga tcc aag gtt gtg   595
Glu Leu Arg Ser Ser Arg Val Val Glu Asp Ser Gly Ser Lys Val Val
150                 155                 160                 165

ggc tgg acc acg att ggc acg atg tcg att atc acg gtc gtt gat aat   643
Gly Trp Thr Thr Ile Gly Thr Met Ser Ile Ile Thr Val Val Asp Asn
                170                 175                 180

gac caa ggc cta gtg ctg cag caa atg gtg tcc tcc gac aaa atc gat   691
Asp Gln Gly Leu Val Leu Gln Gln Met Val Ser Ser Asp Lys Ile Asp
            185                 190                 195

ccg gag gaa cgc atc tac gaa ctt ggg ctg tcg aca ccg aag gac act   739
Pro Glu Glu Arg Ile Tyr Glu Leu Gly Leu Ser Thr Pro Lys Asp Thr
        200                 205                 210

gaa gag tcc tcg gaa gaa acc tca gcg tct aaa aac tagccacacg        785
Glu Glu Ser Ser Glu Glu Thr Ser Ala Ser Lys Asn
    215                 220                 225

tctggaaatc aga                                                   798
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<210> 2248
<211> 225
<212> PRT
<213> Corynebacterium glutamicum

<400> 2248

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Val Ala Ser Thr Pro His Lys His Val Arg Val Ala Leu Gly Leu Val
  1               5                  10                  15
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Ala Leu Ile Pro Leu Leu Ala Ala Cys Thr Gly Gly Gly Ser Thr Glu
            20                  25                  30

Thr Ser Thr Glu Ser Thr Ala Glu Thr Thr Pro Ala Thr Thr Thr Glu
        35                  40                  45

Ala Thr Thr Thr Pro Ala Thr Thr Ala Ser Ser Ser Val Ile Glu Thr
    50                  55                  60

Thr Glu Ser Ser Thr Ala Glu Thr Ser Thr Lys Glu Ser Gly Glu Thr
65                  70                  75                  80

Ser Thr Ser Lys Pro Arg Met Thr Lys Asp Val Glu Val Ala Tyr Lys
                85                  90                  95

Ala Phe Ser Ser Leu Ala Pro Val Glu Leu Phe Glu Gln Phe Glu Thr
            100                 105                 110

Cys Asp Pro Ser Gly Val Glu Asp Ser Phe Ala Cys Asn Gly Pro Glu
        115                 120                 125

Val Gly Gln Phe Gln Phe Phe Asp Asn Ala Ser Lys Ala Thr Ser Thr
    130                 135                 140

Thr Gln Leu Leu Thr Glu Leu Arg Ser Ser Arg Val Val Glu Asp Ser
145                 150                 155                 160

Gly Ser Lys Val Val Gly Trp Thr Thr Ile Gly Thr Met Ser Ile Ile
                165                 170                 175

Thr Val Val Asp Asn Asp Gln Gly Leu Val Leu Gln Gln Met Val Ser
            180                 185                 190

Ser Asp Lys Ile Asp Pro Glu Glu Arg Ile Tyr Glu Leu Gly Leu Ser
        195                 200                 205

Thr Pro Lys Asp Thr Glu Glu Ser Ser Glu Glu Thr Ser Ala Ser Lys
    210                 215                 220

Asn
225
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<210> 2249
<211> 1287
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1264)
<223> RXA01463

<400> 2249
attagaacaa atattcgtta gaacacttgt ttgttttgat ttgtgtggtt agggtgggtg 60

ctaatgagtt aaaaagggga aatttaaacc attaggggc atg gaa atg tca tac 115
                                        Met Glu Met Ser Tyr
                                          1   5

ttc agc cat cag gac cca aat aat cca gag agt cac atc aac ttc acc 163

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Phe Ser His Gln Asp Pro Asn Asn Pro Glu Ser His Ile Asn Phe Thr
                10                  15                  20

atg gcg caa atg gag atc cag cgc tgg act ttg ctg atc tca aac cca   211
Met Ala Gln Met Glu Ile Gln Arg Trp Thr Leu Leu Ile Ser Asn Pro
            25                  30                  35

gag gcg gac gct agc act ctt gtc atg gag ttg aaa acc gtc acg ggg   259
Glu Ala Asp Ala Ser Thr Leu Val Met Glu Leu Lys Thr Val Thr Gly
        40                  45                  50

gaa tcc aag cat ttt atc aac cag gct att aac gcc atg tgg gct tta   307
Glu Ser Lys His Phe Ile Asn Gln Ala Ile Asn Ala Met Trp Ala Leu
    55                  60                  65

atg aag ctg ccc att tta aga gtg gtg gta gaa act cac ttc cac gtt   355
Met Lys Leu Pro Ile Leu Arg Val Val Val Glu Thr His Phe His Val
70                  75                  80                  85

cgg att ccg tac ctg gcc cgc att atg cag gca gtc aag cag gct aaa   403
Arg Ile Pro Tyr Leu Ala Arg Ile Met Gln Ala Val Lys Gln Ala Lys
                90                  95                  100

ccg gag ttg tgg gat gag ttg gac cat cgc att gcc gaa aag ctg aca   451
Pro Glu Leu Trp Asp Glu Leu Asp His Arg Ile Ala Glu Lys Leu Thr
            105                 110                 115

ccg cgc att gct ggc cag gca ctg atg gaa gcc tcc gca ctt gca ggg   499
Pro Arg Ile Ala Gly Gln Ala Leu Met Glu Ala Ser Ala Leu Ala Gly
        120                 125                 130

ctg att act cgc tgg atc aag gaa ctg gat cca acc ttc aca gga aag   547
Leu Ile Thr Arg Trp Ile Lys Glu Leu Asp Pro Thr Phe Thr Gly Lys
    135                 140                 145

aag cgt ggg cca aag ggg agt gat ggc acc ttg act ttc cgc cac gtg   595
Lys Arg Gly Pro Lys Gly Ser Asp Gly Thr Leu Thr Phe Arg His Val
150                 155                 160                 165

gac ggg cgt acg tac atc agt gga aat att gac ggt gtc acc ggc aag   643
Asp Gly Arg Thr Tyr Ile Ser Gly Asn Ile Asp Gly Val Thr Gly Lys
                170                 175                 180

ctg ttc caa aaa gct ctg gaa aaa gtg aaa cag aag ggc gag gac ctc   691
Leu Phe Gln Lys Ala Leu Glu Lys Val Lys Gln Lys Gly Glu Asp Leu
            185                 190                 195

gcg cgg gcc ctg gtc acc ttc ctg gcg ggg cgg acc aaa gtg aaa atc   739
Ala Arg Ala Leu Val Thr Phe Leu Ala Gly Arg Thr Lys Val Lys Ile
        200                 205                 210

gtc agc gcg gta tac acg ccc ctg gtg ggt ggc gtg tcc tgg att ccg   787
Val Ser Ala Val Tyr Thr Pro Leu Val Gly Gly Val Ser Trp Ile Pro
    215                 220                 225

ggg gtg gga ttc ctg agt caa gag gag tcc cgg aag ctg ggt aag act   835
Gly Val Gly Phe Leu Ser Gln Glu Glu Ser Arg Lys Leu Gly Lys Thr
230                 235                 240                 245

gcc tcg aag gtc att gac ctg gat acg atc gcc act cgt gtg gaa aat   883
Ala Ser Lys Val Ile Asp Leu Asp Thr Ile Ala Thr Arg Val Glu Asn
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                250                 255                 260

ggc tac acc cca agt ccc gag cta cgc ctt tat gtg atg ggg cgg gac   931
Gly Tyr Thr Pro Ser Pro Glu Leu Arg Leu Tyr Val Met Gly Arg Asp
            265                 270                 275

ggc acc tgt agg cat ccg ggc tgc acg gtg tct gcc gac aac tgc cag   979
Gly Thr Cys Arg His Pro Gly Cys Thr Val Ser Ala Asp Asn Cys Gln
        280                 285                 290

atc gat cac gtg atc ccg ttc ggt gag ggt ggg ttg act gtg gcc tgg   1027
Ile Asp His Val Ile Pro Phe Gly Glu Gly Gly Leu Thr Val Ala Trp
    295                 300                 305

aac ttg cag tgc ctc tgc gcg cat cat cac aat atg aag act gat ggg   1075
Asn Leu Gln Cys Leu Cys Ala His His His Asn Met Lys Thr Asp Gly
310                 315                 320                 325

cgc atc cag gcg gcg att gat tcc atg ggt cgg gtc gcc tgg att ggg   1123
Arg Ile Gln Ala Ala Ile Asp Ser Met Gly Arg Val Ala Trp Ile Gly
                330                 335                 340

ccg tgc aat cgc aca gtg gta acc gaa cct gtc gga ccg ttg gcg caa   1171
Pro Cys Asn Arg Thr Val Val Thr Glu Pro Val Gly Pro Leu Ala Gln
            345                 350                 355

gag atg ccc acg ggg cag tgg ggg cag act ctg gaa gca cgg atg gag   1219
Glu Met Pro Thr Gly Gln Trp Gly Gln Thr Leu Glu Ala Arg Met Glu
        360                 365                 370

aag act ttt gaa aag ctc cgc agt tca ctc gag gta ttg gat gac       1264
Lys Thr Phe Glu Lys Leu Arg Ser Ser Leu Glu Val Leu Asp Asp
    375                 380                 385

taaaccctta tgcacacccc tag                                        1287


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<213> Corynebacterium glutamicum

<400> 2250
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His Ile Asn Phe Thr Met Ala Gln Met Glu Ile Gln Arg Trp Thr Leu
             20                  25                  30

Leu Ile Ser Asn Pro Glu Ala Asp Ala Ser Thr Leu Val Met Glu Leu
         35                  40                  45

Lys Thr Val Thr Gly Glu Ser Lys His Phe Ile Asn Gln Ala Ile Asn
     50                  55                  60

Ala Met Trp Ala Leu Met Lys Leu Pro Ile Leu Arg Val Val Val Glu
 65                  70                  75                  80

Thr His Phe His Val Arg Ile Pro Tyr Leu Ala Arg Ile Met Gln Ala
                 85                  90                  95
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Val Lys Gln Ala Lys Pro Glu Leu Trp Asp Glu Leu Asp His Arg Ile
            100                 105                 110

Ala Glu Lys Leu Thr Pro Arg Ile Ala Gly Gln Ala Leu Met Glu Ala
        115                 120                 125

Ser Ala Leu Ala Gly Leu Ile Thr Arg Trp Ile Lys Glu Leu Asp Pro
    130                 135                 140

Thr Phe Thr Gly Lys Lys Arg Gly Pro Lys Gly Ser Asp Gly Thr Leu
145                 150                 155                 160

Thr Phe Arg His Val Asp Gly Arg Thr Tyr Ile Ser Gly Asn Ile Asp
                165                 170                 175

Gly Val Thr Gly Lys Leu Phe Gln Lys Ala Leu Glu Lys Val Lys Gln
            180                 185                 190

Lys Gly Glu Asp Leu Ala Arg Ala Leu Val Thr Phe Leu Ala Gly Arg
        195                 200                 205

Thr Lys Val Lys Ile Val Ser Ala Val Tyr Thr Pro Leu Val Gly Gly
    210                 215                 220

Val Ser Trp Ile Pro Gly Val Gly Phe Leu Ser Gln Glu Glu Ser Arg
225                 230                 235                 240

Lys Leu Gly Lys Thr Ala Ser Lys Val Ile Asp Leu Asp Thr Ile Ala
                245                 250                 255

Thr Arg Val Glu Asn Gly Tyr Thr Pro Ser Pro Glu Leu Arg Leu Tyr
            260                 265                 270

Val Met Gly Arg Asp Gly Thr Cys Arg His Pro Gly Cys Thr Val Ser
        275                 280                 285

Ala Asp Asn Cys Gln Ile Asp His Val Ile Pro Phe Gly Glu Gly Gly
    290                 295                 300

Leu Thr Val Ala Trp Asn Leu Gln Cys Leu Cys Ala His His His Asn
305                 310                 315                 320

Met Lys Thr Asp Gly Arg Ile Gln Ala Ala Ile Asp Ser Met Gly Arg
                325                 330                 335

Val Ala Trp Ile Gly Pro Cys Asn Arg Thr Val Val Thr Glu Pro Val
            340                 345                 350

Gly Pro Leu Ala Gln Glu Met Pro Thr Gly Gln Trp Gly Gln Thr Leu
        355                 360                 365

Glu Ala Arg Met Glu Lys Thr Phe Glu Lys Leu Arg Ser Ser Leu Glu
    370                 375                 380

Val Leu Asp Asp
385
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<210> 2251
<211> 1155
<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1132)
<223> RXA01469

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ccagatgagc agcagttcac tgactagtat tctgtaggtc atg gca ttt gca gac 115
Met Ala Phe Ala Asp
1 5

att gtg cgc agc gtc gaa aac cgc acc aac gca gcg acc ctc aac tgg 163
Ile Val Arg Ser Val Glu Asn Arg Thr Asn Ala Ala Thr Leu Asn Trp
10 15 20

tcc atc aaa aat ggc tgg aag ccc gaa gtc acc gga ttt tcc ggg tac 211
Ser Ile Lys Asn Gly Trp Lys Pro Glu Val Thr Gly Phe Ser Gly Tyr
25 30 35

ggc tcc ggg cgt cga gtg cgc gtc ctt gcg cgc gtg ctc atg tcc aac 259
Gly Ser Gly Arg Arg Val Arg Val Leu Ala Arg Val Leu Met Ser Asn
40 45 50

ccc gaa aat ttg ctt gtc gac gcc ccc tcc caa tca att acc caa caa 307
Pro Glu Asn Leu Leu Val Asp Ala Pro Ser Gln Ser Ile Thr Gln Gln
55 60 65

gca cag cgc ggt tgg cgc cag ttc ttc acc atc caa gtg ccc aac ctg 355
Ala Gln Arg Gly Trp Arg Gln Phe Phe Thr Ile Gln Val Pro Asn Leu
70 75 80 85

cca gta act gtc acc gtt ggt ggg aaa aca gtt acc tca tcc acc aac 403
Pro Val Thr Val Thr Val Gly Gly Lys Thr Val Thr Ser Ser Thr Asn
90 95 100

gac aac ggc tac gtt gac ctc ctg gtg gaa gac cac aac ctt gac ccc 451
Asp Asn Gly Tyr Val Asp Leu Leu Val Glu Asp His Asn Leu Asp Pro
105 110 115

ggc tgg cac acc atc cag atc caa gcc gaa ggt tcc acc ccc gcc gaa 499
Gly Trp His Thr Ile Gln Ile Gln Ala Glu Gly Ser Thr Pro Ala Glu
120 125 130

gcc cgc gtc ctc atc gtg gaa aac acc gcc cga atc gga ctc atc tcc 547
Ala Arg Val Leu Ile Val Glu Asn Thr Ala Arg Ile Gly Leu Ile Ser
135 140 145

gac atc gac gac acc atc atg gtc acc tgg ctt ccc cga gca ctc ctc 595
Asp Ile Asp Asp Thr Ile Met Val Thr Trp Leu Pro Arg Ala Leu Leu
150 155 160 165

gcc gca tgg aac tcg tgg gtt ttg cac acc aac acc cgc aaa cca gtc 643
Ala Ala Trp Asn Ser Trp Val Leu His Thr Asn Thr Arg Lys Pro Val
170 175 180

ccc gga atg aac cgc ttc tac gaa gaa ctc ctc aaa gac cac ccc gac 691
Pro Gly Met Asn Arg Phe Tyr Glu Glu Leu Leu Lys Asp His Pro Asp
185 190 195

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gca ccc gtg ttc tac ctc tcc acc ggc gca tgg aac acc ttt gaa acc   739
Ala Pro Val Phe Tyr Leu Ser Thr Gly Ala Trp Asn Thr Phe Glu Thr
        200                 205                 210

ctc caa gag ttc atc aac aaa cac gca ctc ccc gac ggc ccc atg ctg   787
Leu Gln Glu Phe Ile Asn Lys His Ala Leu Pro Asp Gly Pro Met Leu
    215                 220                 225

ctc acc gac tgg gga cca acc ccc aca gga cta ttc cgc tca ggt caa   835
Leu Thr Asp Trp Gly Pro Thr Pro Thr Gly Leu Phe Arg Ser Gly Gln
230                 235                 240                 245

gag cac aag aaa gtc caa ctg cgc aac ctg ttt atc gaa tac ccc gac   883
Glu His Lys Lys Val Gln Leu Arg Asn Leu Phe Ile Glu Tyr Pro Asp
                250                 255                 260

atg aaa tgg atc ctc gtc ggc gac gat ggc caa cac gat ccc ctc atc   931
Met Lys Trp Ile Leu Val Gly Asp Asp Gly Gln His Asp Pro Leu Ile
            265                 270                 275

tac ggc gaa gca gtc gaa gaa cac ccc aac cgc atc gca ggc gtt gca   979
Tyr Gly Glu Ala Val Glu Glu His Pro Asn Arg Ile Ala Gly Val Ala
        280                 285                 290

atc cgt gag ctc tcc ccc ggc gaa cat gtg ctc tcc cac gga aca act  1027
Ile Arg Glu Leu Ser Pro Gly Glu His Val Leu Ser His Gly Thr Thr
    295                 300                 305

gcg tca ctg tcc acc atc acg acc aac ggg ggc caa gga gtc cca gta  1075
Ala Ser Leu Ser Thr Ile Thr Thr Asn Gly Gly Gln Gly Val Pro Val
310                 315                 320                 325

gtt cac ggc cgc gat gga tat gag ttg ctg cag cgc tac gag acg aag  1123
Val His Gly Arg Asp Gly Tyr Glu Leu Leu Gln Arg Tyr Glu Thr Lys
                330                 335                 340

ccg ttc gcc tgagtcctac tgggtgtctc atg                           1155
Pro Phe Ala
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<210> 2252
<211> 344
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<213> Corynebacterium glutamicum

<400> 2252

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Ala Thr Leu Asn Trp Ser Ile Lys Asn Gly Trp Lys Pro Glu Val Thr
             20                  25                  30

Gly Phe Ser Gly Tyr Gly Ser Gly Arg Arg Val Arg Val Leu Ala Arg
         35                  40                  45

Val Leu Met Ser Asn Pro Glu Asn Leu Leu Val Asp Ala Pro Ser Gln
     50                  55                  60

Ser Ile Thr Gln Gln Ala Gln Arg Gly Trp Arg Gln Phe Phe Thr Ile
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 65                  70                  75                  80

Gln Val Pro Asn Leu Pro Val Thr Val Thr Val Gly Gly Lys Thr Val
                 85                  90                  95

Thr Ser Ser Thr Asn Asp Asn Gly Tyr Val Asp Leu Leu Val Glu Asp
            100                 105                 110

His Asn Leu Asp Pro Gly Trp His Thr Ile Gln Ile Gln Ala Glu Gly
        115                 120                 125

Ser Thr Pro Ala Glu Ala Arg Val Leu Ile Val Glu Asn Thr Ala Arg
    130                 135                 140

Ile Gly Leu Ile Ser Asp Ile Asp Asp Thr Ile Met Val Thr Trp Leu
145                 150                 155                 160

Pro Arg Ala Leu Leu Ala Ala Trp Asn Ser Trp Val Leu His Thr Asn
                165                 170                 175

Thr Arg Lys Pro Val Pro Gly Met Asn Arg Phe Tyr Glu Glu Leu Leu
            180                 185                 190

Lys Asp His Pro Asp Ala Pro Val Phe Tyr Leu Ser Thr Gly Ala Trp
        195                 200                 205

Asn Thr Phe Glu Thr Leu Gln Glu Phe Ile Asn Lys His Ala Leu Pro
    210                 215                 220

Asp Gly Pro Met Leu Leu Thr Asp Trp Gly Pro Thr Pro Thr Gly Leu
225                 230                 235                 240

Phe Arg Ser Gly Gln Glu His Lys Lys Val Gln Leu Arg Asn Leu Phe
                245                 250                 255

Ile Glu Tyr Pro Asp Met Lys Trp Ile Leu Val Gly Asp Asp Gly Gln
            260                 265                 270

His Asp Pro Leu Ile Tyr Gly Glu Ala Val Glu Glu His Pro Asn Arg
        275                 280                 285

Ile Ala Gly Val Ala Ile Arg Glu Leu Ser Pro Gly Glu His Val Leu
    290                 295                 300

Ser His Gly Thr Thr Ala Ser Leu Ser Thr Ile Thr Thr Asn Gly Gly
305                 310                 315                 320

Gln Gly Val Pro Val Val His Gly Arg Asp Gly Tyr Glu Leu Leu Gln
                325                 330                 335

Arg Tyr Glu Thr Lys Pro Phe Ala
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<211> 549
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(526)
<223> RXA01470

<400> 2253
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ggaattgaag gcagttaagt gttgccgaag gaaaccgaac atg acg aac aat gca 115
Met Thr Asn Asn Ala
1 5

tta acc gtg cca acc cgg acc cgt cat cag gcg gat ttg ctc acg gca 163
Leu Thr Val Pro Thr Arg Thr Arg His Gln Ala Asp Leu Leu Thr Ala
10 15 20

gac ttc tgg gaa gac atg ggg ttg ccc caa ctg aaa act acc atc gaa 211
Asp Phe Trp Glu Asp Met Gly Leu Pro Gln Leu Lys Thr Thr Ile Glu
25 30 35

gaa tcc atc gac gat gta gcc ctc cca atg cat acc gct gtt cta gaa 259
Glu Ser Ile Asp Asp Val Ala Leu Pro Met His Thr Ala Val Leu Glu
40 45 50

atc agc gga atg cca aag gaa ctg cgt cag acc gtg gaa tcc gca atg 307
Ile Ser Gly Met Pro Lys Glu Leu Arg Gln Thr Val Glu Ser Ala Met
55 60 65

gtt gtg tgt att ccg agt cct tcg gag ctg tcc ggc tcc aac agg gac 355
Val Val Cys Ile Pro Ser Pro Ser Glu Leu Ser Gly Ser Asn Arg Asp
70 75 80 85

ccg ctc acc gca cga tgg ttc act gca tgg cgc cgt gac cca ttc gaa 403
Pro Leu Thr Ala Arg Trp Phe Thr Ala Trp Arg Arg Asp Pro Phe Glu
90 95 100

ctt ggc ctc act gag tgt cga gag gtg atc acc gga act cca cgc gaa 451
Leu Gly Leu Thr Glu Cys Arg Glu Val Ile Thr Gly Thr Pro Arg Glu
105 110 115

ctc gac aaa ctt cga gga gtg ctg gaa tct ctg gct gat gaa tac cgt 499
Leu Asp Lys Leu Arg Gly Val Leu Glu Ser Leu Ala Asp Glu Tyr Arg
120 125 130

ttt gaa gtt gag ctg cga atc gtt gac tagaaagcca gtgattcttt 546
Phe Glu Val Glu Leu Arg Ile Val Asp
135 140

agc 549

<210> 2254
<211> 142
<212> PRT
<213> Corynebacterium glutamicum

<400> 2254
Met Thr Asn Asn Ala Leu Thr Val Pro Thr Arg Thr Arg His Gln Ala
1 5 10 15

Asp Leu Leu Thr Ala Asp Phe Trp Glu Asp Met Gly Leu Pro Gln Leu
20 25 30

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Lys Thr Thr Ile Glu Glu Ser Ile Asp Asp Val Ala Leu Pro Met His
         35                  40                  45

Thr Ala Val Leu Glu Ile Ser Gly Met Pro Lys Glu Leu Arg Gln Thr
     50                  55                  60

Val Glu Ser Ala Met Val Val Cys Ile Pro Ser Pro Ser Glu Leu Ser
 65                  70                  75                  80

Gly Ser Asn Arg Asp Pro Leu Thr Ala Arg Trp Phe Thr Ala Trp Arg
                85                  90                  95

Arg Asp Pro Phe Glu Leu Gly Leu Thr Glu Cys Arg Glu Val Ile Thr
            100                 105                 110

Gly Thr Pro Arg Glu Leu Asp Lys Leu Arg Gly Val Leu Glu Ser Leu
        115                 120                 125

Ala Asp Glu Tyr Arg Phe Glu Val Glu Leu Arg Ile Val Asp
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Application Filed with the Chinese Patent Office on 2007-12-29

<210> 2255
<211> 579
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> RXA01472

<400> 2255

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                                              Met Asn Gln Ala Asn
                                                1               5

ctg cct gcc gaa atc gcg gac ctc tcc gat gaa acc gca ctg tgg gaa   163
Leu Pro Ala Glu Ile Ala Asp Leu Ser Asp Glu Thr Ala Leu Trp Glu
                10                  15                  20

atc atc aac gaa tac aac tgg gac gac ggc ttc gcg gtt ccc ctt gca   211
Ile Ile Asn Glu Tyr Asn Trp Asp Asp Gly Phe Ala Val Pro Leu Ala
            25                  30                  35

gta gtc cga cac ccc aaa tgc gac cga gcg cta gcc ctt cgc ctg ttt   259
Val Val Arg His Pro Lys Cys Asp Arg Ala Leu Ala Leu Arg Leu Phe
        40                  45                  50

tgg gac atc gat gaa acc gcc caa atc cac cac tcc gac gaa gaa tca   307
Trp Asp Ile Asp Glu Thr Ala Gln Ile His His Ser Asp Glu Glu Ser
    55                  60                  65

gcg atc gcc gag ttg tac gcc agc acc gca gaa aac gac cca gca gaa   355
Ala Ile Ala Glu Leu Tyr Ala Ser Thr Ala Glu Asn Asp Pro Ala Glu
70                  75                  80                  85

ttc gac aga atc atg gac tac tgc acc aca ctg gtc gaa ggg ctc cgc   403
Phe Asp Arg Ile Met Asp Tyr Cys Thr Thr Leu Val Glu Gly Leu Arg
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                90                  95                  100

aag cag acc tat cct cgg ggc gcc aac cgt ttc gac acg gga ttt ttc   451
Lys Gln Thr Tyr Pro Arg Gly Ala Asn Arg Phe Asp Thr Gly Phe Phe
            105                 110                 115

aac ctc gag gac cct tct ttg acc gac cgt cag cgc aaa atc cgc gcc   499
Asn Leu Glu Asp Pro Ser Leu Thr Asp Arg Gln Arg Lys Ile Arg Ala
        120                 125                 130

ggg aaa acc aaa ttt gcg ctc aag aat ttc gag gaa gct ttc ctc caa   547
Gly Lys Thr Lys Phe Ala Leu Lys Asn Phe Glu Glu Ala Phe Leu Gln
    135                 140                 145

cca gag cta taaaaaaggt tgtagaagaa att                            579
Pro Glu Leu
150
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<210> 2256
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 2256

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  1               5                  10                  15

Thr Ala Leu Trp Glu Ile Ile Asn Glu Tyr Asn Trp Asp Asp Gly Phe
             20                  25                  30

Ala Val Pro Leu Ala Val Val Arg His Pro Lys Cys Asp Arg Ala Leu
         35                  40                  45

Ala Leu Arg Leu Phe Trp Asp Ile Asp Glu Thr Ala Gln Ile His His
     50                  55                  60

Ser Asp Glu Glu Ser Ala Ile Ala Glu Leu Tyr Ala Ser Thr Ala Glu
 65                  70                  75                  80

Asn Asp Pro Ala Glu Phe Asp Arg Ile Met Asp Tyr Cys Thr Thr Leu
                 85                  90                  95

Val Glu Gly Leu Arg Lys Gln Thr Tyr Pro Arg Gly Ala Asn Arg Phe
            100                 105                 110

Asp Thr Gly Phe Phe Asn Leu Glu Asp Pro Ser Leu Thr Asp Arg Gln
        115                 120                 125

Arg Lys Ile Arg Ala Gly Lys Thr Lys Phe Ala Leu Lys Asn Phe Glu
    130                 135                 140

Glu Ala Phe Leu Gln Pro Glu Leu
145                 150
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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(865)
<223> RXA01473

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Met Thr Asp Ile Gly
1 5

gat gtc gat caa ata gtc tgg gaa ttc atc cat ttc cac gat gac tcg 163
Asp Val Asp Gln Ile Val Trp Glu Phe Ile His Phe His Asp Asp Ser
10 15 20

ata aat cca ttc ttt gag ttc atc aag agt gat tgc atc aac gat gag 211
Ile Asn Pro Phe Phe Glu Phe Ile Lys Ser Asp Cys Ile Asn Asp Glu
25 30 35

gca atc gaa cgc aaa acc cag atc ctc gga atc atc ttg ggt aac gag 259
Ala Ile Glu Arg Lys Thr Gln Ile Leu Gly Ile Ile Leu Gly Asn Glu
40 45 50

cca tgc ggg agt gtt att cac gcc cgc cag aat aca ata aag ccc atg 307
Pro Cys Gly Ser Val Ile His Ala Arg Gln Asn Thr Ile Lys Pro Met
55 60 65

agc cat acg gtc tct ttt ggc gac ggc tgg atc caa gtc ctt gag gat 355
Ser His Thr Val Ser Phe Gly Asp Gly Trp Ile Gln Val Leu Glu Asp
70 75 80 85

gct gca gaa acc gtg tcg atc acc gac acg ttg gat gcc ctc cga ttt 403
Ala Ala Glu Thr Val Ser Ile Thr Asp Thr Leu Asp Ala Leu Arg Phe
90 95 100

tct ccc gag caa gcg gaa tgg gct gca gaa ttc gga cca cta ctg tgc 451
Ser Pro Glu Gln Ala Glu Trp Ala Ala Glu Phe Gly Pro Leu Leu Cys
105 110 115

ggc cca gcg aac caa ccg ccg gcg tat ctc acg gct tta gac ggg cac 499
Gly Pro Ala Asn Gln Pro Pro Ala Tyr Leu Thr Ala Leu Asp Gly His
120 125 130

aca aag cta ccg ctt agc ccg cag ctg acg gag ttc tat agc tac gcc 547
Thr Lys Leu Pro Leu Ser Pro Gln Leu Thr Glu Phe Tyr Ser Tyr Ala
135 140 145

cga tcc tgg aca aac agt gag gcc ttg gga aac gtc att gat ccc gat 595
Arg Ser Trp Thr Asn Ser Glu Ala Leu Gly Asn Val Ile Asp Pro Asp
150 155 160 165

gac tac ctc gat cat ctc acc gac cct cgc ctt cat ttg cag gat ctt 643
Asp Tyr Leu Asp His Leu Thr Asp Pro Arg Leu His Leu Gln Asp Leu
170 175 180

ctg gat aat gag ttt gaa cgg gtg ggg gtg ctc gtc gat aag caa aat 691
Leu Asp Asn Glu Phe Glu Arg Val Gly Val Leu Val Asp Lys Gln Asn
185 190 195

cgc ccg ctc gac cct gcc cgg tgc gcg ctg ttc tcg ctc gac gca ctt 739

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Arg Pro Leu Asp Pro Ala Arg Cys Ala Leu Phe Ser Leu Asp Ala Leu
        200                 205                 210

gca cgc gcg ccc tac aac cgc gcc tac ttc gtc ttc gcc gcg ccc gag   787
Ala Arg Ala Pro Tyr Asn Arg Ala Tyr Phe Val Phe Ala Ala Pro Glu
    215                 220                 225

cct gag atc tgg gcg ttt gag aac gag cac gtc cac gcg ccg gac ttg   835
Pro Glu Ile Trp Ala Phe Glu Asn Glu His Val His Ala Pro Asp Leu
230                 235                 240                 245

cgc gcc tat tta caa gca cgc tta tcg acg taattacact cggtggaaac     885
Arg Ala Tyr Leu Gln Ala Arg Leu Ser Thr
                250                 255

cgt                                                               888


<210> 2258
<211> 255
<212> PRT
<213> Corynebacterium glutamicum

<400> 2258
Met Thr Asp Ile Gly Asp Val Asp Gln Ile Val Trp Glu Phe Ile His
  1               5                  10                  15

Phe His Asp Asp Ser Ile Asn Pro Phe Phe Glu Phe Ile Lys Ser Asp
             20                  25                  30

Cys Ile Asn Asp Glu Ala Ile Glu Arg Lys Thr Gln Ile Leu Gly Ile
         35                  40                  45

Ile Leu Gly Asn Glu Pro Cys Gly Ser Val Ile His Ala Arg Gln Asn
     50                  55                  60

Thr Ile Lys Pro Met Ser His Thr Val Ser Phe Gly Asp Gly Trp Ile
 65                  70                  75                  80

Gln Val Leu Glu Asp Ala Ala Glu Thr Val Ser Ile Thr Asp Thr Leu
                 85                  90                  95

Asp Ala Leu Arg Phe Ser Pro Glu Gln Ala Glu Trp Ala Ala Glu Phe
            100                 105                 110

Gly Pro Leu Leu Cys Gly Pro Ala Asn Gln Pro Pro Ala Tyr Leu Thr
        115                 120                 125

Ala Leu Asp Gly His Thr Lys Leu Pro Leu Ser Pro Gln Leu Thr Glu
    130                 135                 140

Phe Tyr Ser Tyr Ala Arg Ser Trp Thr Asn Ser Glu Ala Leu Gly Asn
145                 150                 155                 160

Val Ile Asp Pro Asp Asp Tyr Leu Asp His Leu Thr Asp Pro Arg Leu
                165                 170                 175

His Leu Gln Asp Leu Leu Asp Asn Glu Phe Glu Arg Val Gly Val Leu
            180                 185                 190

Val Asp Lys Gln Asn Arg Pro Leu Asp Pro Ala Arg Cys Ala Leu Phe
```

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        195                 200                 205

Ser Leu Asp Ala Leu Ala Arg Ala Pro Tyr Asn Arg Ala Tyr Phe Val
    210                 215                 220

Phe Ala Ala Pro Glu Pro Glu Ile Trp Ala Phe Glu Asn Glu His Val
225                 230                 235                 240

His Ala Pro Asp Leu Arg Ala Tyr Leu Gln Ala Arg Leu Ser Thr
                245                 250                 255


<210> 2259
<211> 669
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(646)
<223> RXA01474

<400> 2259
catcaccgat gtcagtcata agcacgatct tattcttggc taccaggata ttgttggttt 60

ttggccctac tcgacactat aacgcaccga ggaaactgca ttg gtg gga att gct   115
                                              Leu Val Gly Ile Ala
                                                1               5

tac gcc cgt ttc cct gat acc cgc gac gat tcc atc agc cgc ggc aaa   163
Tyr Ala Arg Phe Pro Asp Thr Arg Asp Asp Ser Ile Ser Arg Gly Lys
                10                  15                  20

gca cga tca gcg ttg gag aaa tcc acg ggc ctt aaa gag cgt ttc gcg   211
Ala Arg Ser Ala Leu Glu Lys Ser Thr Gly Leu Lys Glu Arg Phe Ala
            25                  30                  35

cgt cat ttt cct gca att tcc ata cct gtc gat acg ggt gat gct gca   259
Arg His Phe Pro Ala Ile Ser Ile Pro Val Asp Thr Gly Asp Ala Ala
        40                  45                  50

gat att ctc gta tcg ggt tgg tgg ctt tca ggt tct aaa aag aag atc   307
Asp Ile Leu Val Ser Gly Trp Trp Leu Ser Gly Ser Lys Lys Lys Ile
    55                  60                  65

ctg act gca gcg gaa atc cag acc tta ttt atc aac cga ttg gcc aca   355
Leu Thr Ala Ala Glu Ile Gln Thr Leu Phe Ile Asn Arg Leu Ala Thr
70                  75                  80                  85

ggt cca ttg agc act caa ttg gaa act gct acc ggg ttg aaa ctg cag   403
Gly Pro Leu Ser Thr Gln Leu Glu Thr Ala Thr Gly Leu Lys Leu Gln
                90                  95                  100

gtg gtg acc aat cga gag cgt atg aag atc act ctc att gaa ccc aaa   451
Val Val Thr Asn Arg Glu Arg Met Lys Ile Thr Leu Ile Glu Pro Lys
            105                 110                 115

ggc aca tca gga cat gcc atc gac ccc caa gct ggc aag ggt tca agg   499
Gly Thr Ser Gly His Ala Ile Asp Pro Gln Ala Gly Lys Gly Ser Arg
        120                 125                 130
```

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ggt ggc ttc ctc ctg gac aat ggc caa gaa gat gaa tac gac gat gtc   547
Gly Gly Phe Leu Leu Asp Asn Gly Gln Glu Asp Glu Tyr Asp Asp Val
    135                 140                 145

gac acc gtc aca atc ccc gat gca ctc aat gtc atc ggt tac att ctt   595
Asp Thr Val Thr Ile Pro Asp Ala Leu Asn Val Ile Gly Tyr Ile Leu
150                 155                 160                 165

acc cat gga act cca cct caa gaa ggc tgg aag gta gac gtg ttg gag   643
Thr His Gly Thr Pro Pro Gln Glu Gly Trp Lys Val Asp Val Leu Glu
                170                 175                 180

cgt tagtcctcga tgaattcttc tcc                                    669
Arg
```

<210> 2260
<211> 182
<212> PRT
<213> Corynebacterium glutamicum

<400> 2260

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Leu Val Gly Ile Ala Tyr Ala Arg Phe Pro Asp Thr Arg Asp Asp Ser
  1               5                  10                  15

Ile Ser Arg Gly Lys Ala Arg Ser Ala Leu Glu Lys Ser Thr Gly Leu
             20                  25                  30

Lys Glu Arg Phe Ala Arg His Phe Pro Ala Ile Ser Ile Pro Val Asp
         35                  40                  45

Thr Gly Asp Ala Ala Asp Ile Leu Val Ser Gly Trp Trp Leu Ser Gly
     50                  55                  60

Ser Lys Lys Lys Ile Leu Thr Ala Ala Glu Ile Gln Thr Leu Phe Ile
 65                  70                  75                  80

Asn Arg Leu Ala Thr Gly Pro Leu Ser Thr Gln Leu Glu Thr Ala Thr
                 85                  90                  95

Gly Leu Lys Leu Gln Val Val Thr Asn Arg Glu Arg Met Lys Ile Thr
            100                 105                 110

Leu Ile Glu Pro Lys Gly Thr Ser Gly His Ala Ile Asp Pro Gln Ala
        115                 120                 125

Gly Lys Gly Ser Arg Gly Gly Phe Leu Leu Asp Asn Gly Gln Glu Asp
    130                 135                 140

Glu Tyr Asp Asp Val Asp Thr Val Thr Ile Pro Asp Ala Leu Asn Val
145                 150                 155                 160

Ile Gly Tyr Ile Leu Thr His Gly Thr Pro Pro Gln Glu Gly Trp Lys
                165                 170                 175

Val Asp Val Leu Glu Arg
            180
```

<210> 2261

<211> 549
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(526)
<223> RXA01475

<400> 2261
tggatctcaa tgtagtcgca atacggcttt tattcgtcag gcagttctgc gaatagtatt 60

cgtgcacatt ggattcacac ccgtagtagt ttttgggggga atg agc atc caa ggg 115
Met Ser Ile Gln Gly
1 5

ttt tcc gca ggt gac tat tct gca tgt ttt gaa ccg cgc atc gat gcg 163
Phe Ser Ala Gly Asp Tyr Ser Ala Cys Phe Glu Pro Arg Ile Asp Ala
10 15 20

tgg gtt gat att cgc ggt ccg cgg aag ccc gag tgg ttg gcg gaa aat 211
Trp Val Asp Ile Arg Gly Pro Arg Lys Pro Glu Trp Leu Ala Glu Asn
25 30 35

atc gat aat ccg ctg aga cac tgg ggc gat aat cct cat atc ccg gtg 259
Ile Asp Asn Pro Leu Arg His Trp Gly Asp Asn Pro His Ile Pro Val
40 45 50

tct gct gcg aaa aag gct gga aat att tac aaa gag acc ctt cga acc 307
Ser Ala Ala Lys Lys Ala Gly Asn Ile Tyr Lys Glu Thr Leu Arg Thr
55 60 65

atg aga gcc tca aca aag acc cca gac cag gat ccc tta aaa gaa acc 355
Met Arg Ala Ser Thr Lys Thr Pro Asp Gln Asp Pro Leu Lys Glu Thr
70 75 80 85

ctg cgc agc ttc atc gca agc atc aac cag ctc gcc gca aag aag aat 403
Leu Arg Ser Phe Ile Ala Ser Ile Asn Gln Leu Ala Ala Lys Lys Asn
90 95 100

ttc att gat gcc ggg gtg cgc gaa gat atc gtt gtt gcg ctg gaa aaa 451
Phe Ile Asp Ala Gly Val Arg Glu Asp Ile Val Val Ala Leu Glu Lys
105 110 115

cta tgc gaa gca gca gaa gct agc cca gaa gaa att cag cag gcg atc 499
Leu Cys Glu Ala Ala Glu Ala Ser Pro Glu Glu Ile Gln Gln Ala Ile
120 125 130

gtg atg gga gaa gaa ttc atc gag gac taacgctcca acacgtctac 546
Val Met Gly Glu Glu Phe Ile Glu Asp
135 140

ctt 549

<210> 2262
<211> 142
<212> PRT
<213> Corynebacterium glutamicum

<400> 2262

```
Met Ser Ile Gln Gly Phe Ser Ala Gly Asp Tyr Ser Ala Cys Phe Glu
  1               5                  10                  15

Pro Arg Ile Asp Ala Trp Val Asp Ile Arg Gly Pro Arg Lys Pro Glu
             20                  25                  30

Trp Leu Ala Glu Asn Ile Asp Asn Pro Leu Arg His Trp Gly Asp Asn
         35                  40                  45

Pro His Ile Pro Val Ser Ala Ala Lys Lys Ala Gly Asn Ile Tyr Lys
     50                  55                  60

Glu Thr Leu Arg Thr Met Arg Ala Ser Thr Lys Thr Pro Asp Gln Asp
 65                  70                  75                  80

Pro Leu Lys Glu Thr Leu Arg Ser Phe Ile Ala Ser Ile Asn Gln Leu
                 85                  90                  95

Ala Ala Lys Lys Asn Phe Ile Asp Ala Gly Val Arg Glu Asp Ile Val
            100                 105                 110

Val Ala Leu Glu Lys Leu Cys Glu Ala Ala Glu Ala Ser Pro Glu Glu
        115                 120                 125

Ile Gln Gln Ala Ile Val Met Gly Glu Glu Phe Ile Glu Asp
    130                 135                 140


<210> 2263
<211> 465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(442)
<223> RXA01476

<400> 2263
atccaagaaa tttcgcacct caggagtagc gatacttcgt aaatttggga agaaggagta 60

gccacatgac gttgatcgac ctcactgctg gagtgagcgc atg agc gat tca ccg   115
                                            Met Ser Asp Ser Pro
                                              1               5

tgc acc gtc gtc atc ctg aac cgc aca gct act gcg act tcc atc ctg   163
Cys Thr Val Val Ile Leu Asn Arg Thr Ala Thr Ala Thr Ser Ile Leu
                 10                  15                  20

aga gat att aaa gcc ctc acc ggt tac ggc ctg tct gag atc agg tcg   211
Arg Asp Ile Lys Ala Leu Thr Gly Tyr Gly Leu Ser Glu Ile Arg Ser
             25                  30                  35

cgc atc gtt gcg gga ctt ccc gtc gtg atc gag gag atg ttc tca aac   259
Arg Ile Val Ala Gly Leu Pro Val Val Ile Glu Glu Met Phe Ser Asn
         40                  45                  50

gcc tgg tac gac gaa cgc gca caa ctg ttg ctg gca ctg ctg acc aaa   307
Ala Trp Tyr Asp Glu Arg Ala Gln Leu Leu Leu Ala Leu Leu Thr Lys
     55                  60                  65
```

```
tgg cag aac gaa gga atc aca ttc gag att cgg gaa gtc gct gag gat   355
Trp Gln Asn Glu Gly Ile Thr Phe Glu Ile Arg Glu Val Ala Glu Asp
 70                  75                  80                  85

gat ccc atc gaa gca ggg gca ttg atc tct cta gaa gtg ctg cga aac   403
Asp Pro Ile Glu Ala Gly Ala Leu Ile Ser Leu Glu Val Leu Arg Asn
                90                  95                 100

atc att gag cca gac gat aat gaa tcg agg gac ggt atc tagtggtgaa    452
Ile Ile Glu Pro Asp Asp Asn Glu Ser Arg Asp Gly Ile
            105                 110

cgtaaacccc cgg                                                   465


<210> 2264
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 2264
Met Ser Asp Ser Pro Cys Thr Val Val Ile Leu Asn Arg Thr Ala Thr
  1               5                  10                  15

Ala Thr Ser Ile Leu Arg Asp Ile Lys Ala Leu Thr Gly Tyr Gly Leu
             20                  25                  30

Ser Glu Ile Arg Ser Arg Ile Val Ala Gly Leu Pro Val Val Ile Glu
         35                  40                  45

Glu Met Phe Ser Asn Ala Trp Tyr Asp Glu Arg Ala Gln Leu Leu Leu
     50                  55                  60

Ala Leu Leu Thr Lys Trp Gln Asn Glu Gly Ile Thr Phe Glu Ile Arg
 65                  70                  75                  80

Glu Val Ala Glu Asp Asp Pro Ile Glu Ala Gly Ala Leu Ile Ser Leu
                 85                  90                  95

Glu Val Leu Arg Asn Ile Ile Glu Pro Asp Asp Asn Glu Ser Arg Asp
            100                 105                 110

Gly Ile



<210> 2265
<211> 954
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(931)
<223> RXA01488

<400> 2265
ccttgatatc gccaccggca tcgatgatgc cctcgcactt gcctacgcac tgggctcacc 60

tgaactagag ctcattggtg tcaccaccac ctacggtaac gtg cta ctc gaa acc   115
                                              Val Leu Leu Glu Thr
```

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                                                    1               5

ggt gca gtc aat gac ctg gca ctg ctt gat ctg ttc ggt gca cca gaa   163
Gly Ala Val Asn Asp Leu Ala Leu Leu Asp Leu Phe Gly Ala Pro Glu
                10                  15                  20

gta cct gtg tac ttg ggt gag cca cac gca cag acc aag gat ggc ttt   211
Val Pro Val Tyr Leu Gly Glu Pro His Ala Gln Thr Lys Asp Gly Phe
            25                  30                  35

gaa gtt ctt gag atc tcc gcg ttc att cac gga caa aac ggc atc ggc   259
Glu Val Leu Glu Ile Ser Ala Phe Ile His Gly Gln Asn Gly Ile Gly
        40                  45                  50

gaa gtc gag ctg cca gca agc gag tca aag gca ctc ccc ggc gca gtg   307
Glu Val Glu Leu Pro Ala Ser Glu Ser Lys Ala Leu Pro Gly Ala Val
    55                  60                  65

gat ttc ctc att gat tcc gtc aac acc cac ggc gat gac ctg gtg atc   355
Asp Phe Leu Ile Asp Ser Val Asn Thr His Gly Asp Asp Leu Val Ile
70                  75                  80                  85

atc gca act ggt ccc atg acc aac ctg tct gcg gca atc gca aag gat   403
Ile Ala Thr Gly Pro Met Thr Asn Leu Ser Ala Ala Ile Ala Lys Asp
                90                  95                  100

cca agc ttt gct tcc aag gct cac gtg gtc atc atg ggt ggc gcc ttg   451
Pro Ser Phe Ala Ser Lys Ala His Val Val Ile Met Gly Gly Ala Leu
            105                 110                 115

act gtc cca ggc aac gtc agc aca tgg gca gaa gca aac atc aac cag   499
Thr Val Pro Gly Asn Val Ser Thr Trp Ala Glu Ala Asn Ile Asn Gln
        120                 125                 130

gac cca gat gca gca aac gat ctg ttc cgt tcc ggt gca gat gtc acc   547
Asp Pro Asp Ala Ala Asn Asp Leu Phe Arg Ser Gly Ala Asp Val Thr
    135                 140                 145

atg atc ggt ctt gat gtc acc ctg cag acc ctt ctt acc aag aag cac   595
Met Ile Gly Leu Asp Val Thr Leu Gln Thr Leu Leu Thr Lys Lys His
150                 155                 160                 165

act gcg cag tgg cgc gaa ctg ggc act cca gct gct atc gca ctg gcc   643
Thr Ala Gln Trp Arg Glu Leu Gly Thr Pro Ala Ala Ile Ala Leu Ala
                170                 175                 180

gac atg act gat tac tac atc aag gca tat gag acc acc gca cca cac   691
Asp Met Thr Asp Tyr Tyr Ile Lys Ala Tyr Glu Thr Thr Ala Pro His
            185                 190                 195

ctg ggc ggt tgc ggc ctg cac gac cca ctg gca gta ggc gtt gca gtg   739
Leu Gly Gly Cys Gly Leu His Asp Pro Leu Ala Val Gly Val Ala Val
        200                 205                 210

gac cca agc ctg gtc act ttg ctc ccc atc aac ctc aag gta gac att   787
Asp Pro Ser Leu Val Thr Leu Leu Pro Ile Asn Leu Lys Val Asp Ile
    215                 220                 225

gag ggc gag acc cgt gga cgc acc att ggc gat gaa gtc cgc ctc aac   835
Glu Gly Glu Thr Arg Gly Arg Thr Ile Gly Asp Glu Val Arg Leu Asn
230                 235                 240                 245
```

```
gat cca gtg cgc acc tcc cgc gca gct gtc gcc gta gac gtg gat cgt   883
Asp Pro Val Arg Thr Ser Arg Ala Ala Val Ala Val Asp Val Asp Arg
                250                 255                 260

ttc ctt tct gaa ttc atg acc cgc atc ggc cga gtc gca gca cag cag   931
Phe Leu Ser Glu Phe Met Thr Arg Ile Gly Arg Val Ala Ala Gln Gln
            265                 270                 275

taaaagcagc tctggtgaag gtt                                        954


<210> 2266
<211> 277
<212> PRT
<213> Corynebacterium glutamicum

<400> 2266
Val Leu Leu Glu Thr Gly Ala Val Asn Asp Leu Ala Leu Leu Asp Leu
  1               5                  10                  15

Phe Gly Ala Pro Glu Val Pro Val Tyr Leu Gly Glu Pro His Ala Gln
             20                  25                  30

Thr Lys Asp Gly Phe Glu Val Leu Glu Ile Ser Ala Phe Ile His Gly
         35                  40                  45

Gln Asn Gly Ile Gly Glu Val Glu Leu Pro Ala Ser Glu Ser Lys Ala
     50                  55                  60

Leu Pro Gly Ala Val Asp Phe Leu Ile Asp Ser Val Asn Thr His Gly
 65                  70                  75                  80

Asp Asp Leu Val Ile Ile Ala Thr Gly Pro Met Thr Asn Leu Ser Ala
                 85                  90                  95

Ala Ile Ala Lys Asp Pro Ser Phe Ala Ser Lys Ala His Val Val Ile
            100                 105                 110

Met Gly Gly Ala Leu Thr Val Pro Gly Asn Val Ser Thr Trp Ala Glu
        115                 120                 125

Ala Asn Ile Asn Gln Asp Pro Asp Ala Ala Asn Asp Leu Phe Arg Ser
    130                 135                 140

Gly Ala Asp Val Thr Met Ile Gly Leu Asp Val Thr Leu Gln Thr Leu
145                 150                 155                 160

Leu Thr Lys Lys His Thr Ala Gln Trp Arg Glu Leu Gly Thr Pro Ala
                165                 170                 175

Ala Ile Ala Leu Ala Asp Met Thr Asp Tyr Tyr Ile Lys Ala Tyr Glu
            180                 185                 190

Thr Thr Ala Pro His Leu Gly Gly Cys Gly Leu His Asp Pro Leu Ala
        195                 200                 205

Val Gly Val Ala Val Asp Pro Ser Leu Val Thr Leu Leu Pro Ile Asn
    210                 215                 220

Leu Lys Val Asp Ile Glu Gly Glu Thr Arg Gly Arg Thr Ile Gly Asp
```

```
225                 230                 235                 240

Glu Val Arg Leu Asn Asp Pro Val Arg Thr Ser Arg Ala Ala Val Ala
                245                 250                 255

Val Asp Val Asp Arg Phe Leu Ser Glu Phe Met Thr Arg Ile Gly Arg
            260                 265                 270

Val Ala Ala Gln Gln
        275


<210> 2267
<211> 1119
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1096)
<223> RXA01494

<400> 2267
gcgatgagga gctggctaaa ttgcgcgaag gtgcagcgcc tgcaggtgat gcagatcctt 60

acaagacttc atccaagtct gaatctgagg aataacacca gtg acg gat aat agt   115
                                            Val Thr Asp Asn Ser
                                              1               5

cag ttt cat gct gct tca gca tta gtc cag gca gct cac acg gtt agc   163
Gln Phe His Ala Ala Ser Ala Leu Val Gln Ala Ala His Thr Val Ser
                10                  15                  20

gtt gtg ggg cat ctg cga ccc gat gct gat gca atc ggc agt gta gct   211
Val Val Gly His Leu Arg Pro Asp Ala Asp Ala Ile Gly Ser Val Ala
            25                  30                  35

gcc aca gtg gcg gca cta cag caa ctt ggt aaa gac gcc gta ggt gca   259
Ala Thr Val Ala Ala Leu Gln Gln Leu Gly Lys Asp Ala Val Gly Ala
        40                  45                  50

atc ggc cag cta gat tcg atg ccc gag aac ttg tac acc att cct ggg   307
Ile Gly Gln Leu Asp Ser Met Pro Glu Asn Leu Tyr Thr Ile Pro Gly
    55                  60                  65

gca tca aac att aag ttt ggc gat tca ctg ccg gaa tct gac ctc atc   355
Ala Ser Asn Ile Lys Phe Gly Asp Ser Leu Pro Glu Ser Asp Leu Ile
70                  75                  80                  85

att gtt gtt gat tgt ggg tca atc gaa cgc acc ggt gcg ttt gaa agc   403
Ile Val Val Asp Cys Gly Ser Ile Glu Arg Thr Gly Ala Phe Glu Ser
                90                  95                  100

atc atc gtc aac aat cct gac aaa gta ttg gtg gtt gat cac cac gcc   451
Ile Ile Val Asn Asn Pro Asp Lys Val Leu Val Val Asp His His Ala
            105                 110                 115

acc aat cct ggg ttt ggt gcc gtc aac tta atc gat gtg gag gca gaa   499
Thr Asn Pro Gly Phe Gly Ala Val Asn Leu Ile Asp Val Glu Ala Glu
        120                 125                 130
```

```
tcc acc acc acg att tta tat gac tgg ttt gat gcg atg tcg gtg caa   547
Ser Thr Thr Thr Ile Leu Tyr Asp Trp Phe Asp Ala Met Ser Val Gln
    135                 140                 145

att act ccc gat atc gcc cac ggc ctt tat gct gga ctg ctc acc gat   595
Ile Thr Pro Asp Ile Ala His Gly Leu Tyr Ala Gly Leu Leu Thr Asp
150                 155                 160                 165

acc ggg tgc ttc agg tgg ggt cga cca gtc atg cat gac atg gct aaa   643
Thr Gly Cys Phe Arg Trp Gly Arg Pro Val Met His Asp Met Ala Lys
                170                 175                 180

gaa ctc atg gag ttc ggt cta gac att cgt gcc att tca tca gca ttg   691
Glu Leu Met Glu Phe Gly Leu Asp Ile Arg Ala Ile Ser Ser Ala Leu
            185                 190                 195

ctt gat caa acc tcc gtg gat gat ttg cgt ctt gtt ggc cag att gtc   739
Leu Asp Gln Thr Ser Val Asp Asp Leu Arg Leu Val Gly Gln Ile Val
        200                 205                 210

tct cgg atc gag ctg cgg gaa gca ggg cca tat act ctt gct gtt ctc   787
Ser Arg Ile Glu Leu Arg Glu Ala Gly Pro Tyr Thr Leu Ala Val Leu
    215                 220                 225

gtg gca gac ttc gat acc atc aac ggc cgt tca cgc gcc gtt gtg gaa   835
Val Ala Asp Phe Asp Thr Ile Asn Gly Arg Ser Arg Ala Val Val Glu
230                 235                 240                 245

ggc ttg atc gaa atg gtt cgc gct gtg gaa ggc gca gac ttc gga gca   883
Gly Leu Ile Glu Met Val Arg Ala Val Glu Gly Ala Asp Phe Gly Ala
                250                 255                 260

gta ttc aaa gaa tat gaa cgt ggc gtc tat acc gtg tca ctg cgt tcc   931
Val Phe Lys Glu Tyr Glu Arg Gly Val Tyr Thr Val Ser Leu Arg Ser
            265                 270                 275

tcc aat ttg agt gtc gct tcc ttg gca gtg cat ctt ggc ggt ggc gga   979
Ser Asn Leu Ser Val Ala Ser Leu Ala Val His Leu Gly Gly Gly Gly
        280                 285                 290

cac att cct gct gca ggc tat acc gct cgt ggt acg gaa atc gaa gcc   1027
His Ile Pro Ala Ala Gly Tyr Thr Ala Arg Gly Thr Glu Ile Glu Ala
    295                 300                 305

ctc gat acg ttg att gaa gca acc gtt acc ttg ggg gag tct ttg cga   1075
Leu Asp Thr Leu Ile Glu Ala Thr Val Thr Leu Gly Glu Ser Leu Arg
310                 315                 320                 325

agc tcg gcg cat gtc gat gtc taacaacgac tttgagcatg agt             1119
Ser Ser Ala His Val Asp Val
                330
```

<210> 2268
<211> 332
<212> PRT
<213> Corynebacterium glutamicum

<400> 2268

```
Val Thr Asp Asn Ser Gln Phe His Ala Ala Ser Ala Leu Val Gln Ala
  1               5                  10                  15
```

```
Ala His Thr Val Ser Val Val Gly His Leu Arg Pro Asp Ala Asp Ala
            20                  25                  30

Ile Gly Ser Val Ala Ala Thr Val Ala Ala Leu Gln Gln Leu Gly Lys
        35                  40                  45

Asp Ala Val Gly Ala Ile Gly Gln Leu Asp Ser Met Pro Glu Asn Leu
    50                  55                  60

Tyr Thr Ile Pro Gly Ala Ser Asn Ile Lys Phe Gly Asp Ser Leu Pro
65                  70                  75                  80

Glu Ser Asp Leu Ile Ile Val Val Asp Cys Gly Ser Ile Glu Arg Thr
                85                  90                  95

Gly Ala Phe Glu Ser Ile Ile Val Asn Asn Pro Asp Lys Val Leu Val
            100                 105                 110

Val Asp His His Ala Thr Asn Pro Gly Phe Gly Ala Val Asn Leu Ile
        115                 120                 125

Asp Val Glu Ala Glu Ser Thr Thr Thr Ile Leu Tyr Asp Trp Phe Asp
    130                 135                 140

Ala Met Ser Val Gln Ile Thr Pro Asp Ile Ala His Gly Leu Tyr Ala
145                 150                 155                 160

Gly Leu Leu Thr Asp Thr Gly Cys Phe Arg Trp Gly Arg Pro Val Met
                165                 170                 175

His Asp Met Ala Lys Glu Leu Met Glu Phe Gly Leu Asp Ile Arg Ala
            180                 185                 190

Ile Ser Ser Ala Leu Leu Asp Gln Thr Ser Val Asp Asp Leu Arg Leu
        195                 200                 205

Val Gly Gln Ile Val Ser Arg Ile Glu Leu Arg Glu Ala Gly Pro Tyr
    210                 215                 220

Thr Leu Ala Val Leu Val Ala Asp Phe Asp Thr Ile Asn Gly Arg Ser
225                 230                 235                 240

Arg Ala Val Val Glu Gly Leu Ile Glu Met Val Arg Ala Val Glu Gly
                245                 250                 255

Ala Asp Phe Gly Ala Val Phe Lys Glu Tyr Glu Arg Gly Val Tyr Thr
            260                 265                 270

Val Ser Leu Arg Ser Ser Asn Leu Ser Val Ala Ser Leu Ala Val His
        275                 280                 285

Leu Gly Gly Gly Gly His Ile Pro Ala Ala Gly Tyr Thr Ala Arg Gly
    290                 295                 300

Thr Glu Ile Glu Ala Leu Asp Thr Leu Ile Glu Ala Thr Val Thr Leu
305                 310                 315                 320

Gly Glu Ser Leu Arg Ser Ser Ala His Val Asp Val
                325                 330
```

<210> 2269
<211> 1041
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1018)
<223> RXA01497

<400> 2269
cgcccacggg caaagttttc aaaaactctg atccatatgg atcagagttt tttcgtatct 60

gccaccagaa agacgcccct ttggcacgcc gaattagtca atg gtg ggt aaa ctt 115
Met Val Gly Lys Leu
1 5

ccc atc atg gct gaa acc aac gaa aat gat ctt cca gtt atc gac ctt 163
Pro Ile Met Ala Glu Thr Asn Glu Asn Asp Leu Pro Val Ile Asp Leu
10 15 20

gcc caa atc gaa ggc tat gtt gta gat gac tcg gat gaa gat gat cca 211
Ala Gln Ile Glu Gly Tyr Val Val Asp Asp Ser Asp Glu Asp Asp Pro
25 30 35

gta ctt ctg cgt cca gat gga acc ccc att gaa acc tgg cgc gaa gac 259
Val Leu Leu Arg Pro Asp Gly Thr Pro Ile Glu Thr Trp Arg Glu Asp
40 45 50

ttc cct tat gaa gag cgc gtc acc cgc gaa gac tat gag aag gtc aag 307
Phe Pro Tyr Glu Glu Arg Val Thr Arg Glu Asp Tyr Glu Lys Val Lys
55 60 65

cgc tcc ctc cag atc gag ctg ctg aag tgg cag aac tgg acc aag gaa 355
Arg Ser Leu Gln Ile Glu Leu Leu Lys Trp Gln Asn Trp Thr Lys Glu
70 75 80 85

act ggc cag cgc cac atc att ttg ttc gaa ggg cgt gac gcc gct ggt 403
Thr Gly Gln Arg His Ile Ile Leu Phe Glu Gly Arg Asp Ala Ala Gly
90 95 100

aag ggt ggc acc att aag cgc ttc aac gaa cac ctg aac cct cgt ggt 451
Lys Gly Gly Thr Ile Lys Arg Phe Asn Glu His Leu Asn Pro Arg Gly
105 110 115

gcc cgt act gtt gcg ttg gag aag cca tca cca cgc gaa tcc acc tca 499
Ala Arg Thr Val Ala Leu Glu Lys Pro Ser Pro Arg Glu Ser Thr Ser
120 125 130

tgg tac ttc cag cgc tat att cag cac ttc cca gct gct ggc gag atc 547
Trp Tyr Phe Gln Arg Tyr Ile Gln His Phe Pro Ala Ala Gly Glu Ile
135 140 145

gtt ttc ttt gac cgc tct tgg tac aac cgt tcc ggc gtg gag cgc gtc 595
Val Phe Phe Asp Arg Ser Trp Tyr Asn Arg Ser Gly Val Glu Arg Val
150 155 160 165

atg ggt ttc tgc acc gaa tca cag cat gca gag ttc ctg cgt gag gtt 643
Met Gly Phe Cys Thr Glu Ser Gln His Ala Glu Phe Leu Arg Glu Val
170 175 180

```
cca atg ctg gaa aac atg atc ctg ggc tct ggt atc agc ttg acc aag   691
Pro Met Leu Glu Asn Met Ile Leu Gly Ser Gly Ile Ser Leu Thr Lys
            185                 190                 195

ttc tgg ttc tcg gtg acc cgt aaa gag cag cgc acc cgt ttt gct atc   739
Phe Trp Phe Ser Val Thr Arg Lys Glu Gln Arg Thr Arg Phe Ala Ile
        200                 205                 210

cgc cag gtt gat cct gtg cgt cag tgg aag ctt tcc cca atg gac ttg   787
Arg Gln Val Asp Pro Val Arg Gln Trp Lys Leu Ser Pro Met Asp Leu
    215                 220                 225

gct tca ctt gat cgc tgg gat gat tac acc cgc gct aag gaa gag cag   835
Ala Ser Leu Asp Arg Trp Asp Asp Tyr Thr Arg Ala Lys Glu Glu Gln
230                 235                 240                 245

ttc cgt tac acc gac act gat gag tcc ccg tgg atc acc atc aag tcg   883
Phe Arg Tyr Thr Asp Thr Asp Glu Ser Pro Trp Ile Thr Ile Lys Ser
                250                 255                 260

aat gac aag aag cgt gcg cgt atc aac gcg atg cgt tat gta ttg tcc   931
Asn Asp Lys Lys Arg Ala Arg Ile Asn Ala Met Arg Tyr Val Leu Ser
            265                 270                 275

aag ttt gat tac acc gac aag gat tac gag ctc gtt ggt gag cct gac   979
Lys Phe Asp Tyr Thr Asp Lys Asp Tyr Glu Leu Val Gly Glu Pro Asp
        280                 285                 290

cct aag gtt gtg ctt cgt ggg cgc gac cag atc ggt gac tagtcactag   1028
Pro Lys Val Val Leu Arg Gly Arg Asp Gln Ile Gly Asp
    295                 300                 305

gcgggcatga aaa                                                  1041
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Sequence Listing

<210> 2270
<211> 306
<212> PRT
<213> Corynebacterium glutamicum

<400> 2270

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Met Val Gly Lys Leu Pro Ile Met Ala Glu Thr Asn Glu Asn Asp Leu
  1               5                  10                  15

Pro Val Ile Asp Leu Ala Gln Ile Glu Gly Tyr Val Val Asp Asp Ser
             20                  25                  30

Asp Glu Asp Asp Pro Val Leu Leu Arg Pro Asp Gly Thr Pro Ile Glu
         35                  40                  45

Thr Trp Arg Glu Asp Phe Pro Tyr Glu Glu Arg Val Thr Arg Glu Asp
     50                  55                  60

Tyr Glu Lys Val Lys Arg Ser Leu Gln Ile Glu Leu Leu Lys Trp Gln
 65                  70                  75                  80

Asn Trp Thr Lys Glu Thr Gly Gln Arg His Ile Ile Leu Phe Glu Gly
                 85                  90                  95

Arg Asp Ala Ala Gly Lys Gly Gly Thr Ile Lys Arg Phe Asn Glu His
```

```
            100                 105                 110

Leu Asn Pro Arg Gly Ala Arg Thr Val Ala Leu Glu Lys Pro Ser Pro
        115                 120                 125

Arg Glu Ser Thr Ser Trp Tyr Phe Gln Arg Tyr Ile Gln His Phe Pro
    130                 135                 140

Ala Ala Gly Glu Ile Val Phe Phe Asp Arg Ser Trp Tyr Asn Arg Ser
145                 150                 155                 160

Gly Val Glu Arg Val Met Gly Phe Cys Thr Glu Ser Gln His Ala Glu
                165                 170                 175

Phe Leu Arg Glu Val Pro Met Leu Glu Asn Met Ile Leu Gly Ser Gly
            180                 185                 190

Ile Ser Leu Thr Lys Phe Trp Phe Ser Val Thr Arg Lys Glu Gln Arg
        195                 200                 205

Thr Arg Phe Ala Ile Arg Gln Val Asp Pro Val Arg Gln Trp Lys Leu
    210                 215                 220

Ser Pro Met Asp Leu Ala Ser Leu Asp Arg Trp Asp Asp Tyr Thr Arg
225                 230                 235                 240

Ala Lys Glu Glu Gln Phe Arg Tyr Thr Asp Thr Asp Glu Ser Pro Trp
                245                 250                 255

Ile Thr Ile Lys Ser Asn Asp Lys Lys Arg Ala Arg Ile Asn Ala Met
            260                 265                 270

Arg Tyr Val Leu Ser Lys Phe Asp Tyr Thr Asp Lys Asp Tyr Glu Leu
        275                 280                 285

Val Gly Glu Pro Asp Pro Lys Val Val Leu Arg Gly Arg Asp Gln Ile
    290                 295                 300

Gly Asp
305
```

Sequence Listing.txt 05/05/2010 10:40:00 AM

<210> 2271
<211> 411
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(388)
<223> RXA01501

<400> 2271
ctaacgaaat cgccggactc ctcgcaatca caagaagcga cgactagcct gtggggacaa 60

actatttcaa gaatttattc aacaaaggag ttcttcacaa atg aag gaa gta gca 115
Met Lys Glu Val Ala
1 5

gtc aac gaa gtc cca gca ggc gca cag ttg atc gat gtc cgc gag acc 163
Val Asn Glu Val Pro Ala Gly Ala Gln Leu Ile Asp Val Arg Glu Thr

```
                10                  15                  20

gat gaa tac gca gag gtt cga gca cag ggt gcc gtc aac att cct atg   211
Asp Glu Tyr Ala Glu Val Arg Ala Gln Gly Ala Val Asn Ile Pro Met
            25                  30                  35

agc gag ttc gtt ggc cgc atc gat gag atc gat ctg gac cgc gac att   259
Ser Glu Phe Val Gly Arg Ile Asp Glu Ile Asp Leu Asp Arg Asp Ile
        40                  45                  50

tat gtc att tgc aag ctg ggt gga cgc tca gct cag gtt gcc gaa tac   307
Tyr Val Ile Cys Lys Leu Gly Gly Arg Ser Ala Gln Val Ala Glu Tyr
    55                  60                  65

ctt gag cag cgc gga att gaa gcc atc aac gta aac ggt ggc acc gac   355
Leu Glu Gln Arg Gly Ile Glu Ala Ile Asn Val Asn Gly Gly Thr Asp
70                  75                  80                  85

ggc tgg gtt gct gca gga ttg cca acc gag gca taagaacccg ccgcaaaaga 408
Gly Trp Val Ala Ala Gly Leu Pro Thr Glu Ala
                90                  95

tcc                                                               411
```

<210> 2272
<211> 96
<212> PRT
<213> Corynebacterium glutamicum

<400> 2272

```
Met Lys Glu Val Ala Val Asn Glu Val Pro Ala Gly Ala Gln Leu Ile
  1               5                  10                  15

Asp Val Arg Glu Thr Asp Glu Tyr Ala Glu Val Arg Ala Gln Gly Ala
            20                  25                  30

Val Asn Ile Pro Met Ser Glu Phe Val Gly Arg Ile Asp Glu Ile Asp
        35                  40                  45

Leu Asp Arg Asp Ile Tyr Val Ile Cys Lys Leu Gly Gly Arg Ser Ala
    50                  55                  60

Gln Val Ala Glu Tyr Leu Glu Gln Arg Gly Ile Glu Ala Ile Asn Val
65                  70                  75                  80

Asn Gly Gly Thr Asp Gly Trp Val Ala Ala Gly Leu Pro Thr Glu Ala
                85                  90                  95
```

<210> 2273
<211> 732
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(709)

<223> RXA01504

<400> 2273

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gcatgtagcg agtttgatga agttgtcgcg ataagaggag gggcgtgtcg gtctgtagga 60

ttggctcgta ccgaacttag aaaactcatg ggagtttcgc atg aat atc acg tgg   115
                                          Met Asn Ile Thr Trp
                                            1               5

ctt atc ctg gcc ggt gtt tta gcc atc atc gct gtc gtg ttc ttt tat   163
Leu Ile Leu Ala Gly Val Leu Ala Ile Ile Ala Val Val Phe Phe Tyr
                10                  15                  20

ctt tca gca cag aag aaa aag agc gaa ccg cag cct cct cgt cag cgt   211
Leu Ser Ala Gln Lys Lys Lys Ser Glu Pro Gln Pro Pro Arg Gln Arg
            25                  30                  35

caa gat cct ctg aaa ttt gcc gac gga tcc gac act ttt aat gcc cgc   259
Gln Asp Pro Leu Lys Phe Ala Asp Gly Ser Asp Thr Phe Asn Ala Arg
        40                  45                  50

att ttg ggt cct gga gca att att tcc cgc ggt ggc gtg gat tat gtc   307
Ile Leu Gly Pro Gly Ala Ile Ile Ser Arg Gly Gly Val Asp Tyr Val
    55                  60                  65

tgc cgc gga gcc atc cag ttc cgt caa ggc caa tac att tgg cac gag   355
Cys Arg Gly Ala Ile Gln Phe Arg Gln Gly Gln Tyr Ile Trp His Glu
70                  75                  80                  85

tat cta ctc gac ggt ggc aaa ggc agt gag tac ctg agc gtg gaa tac   403
Tyr Leu Leu Asp Gly Gly Lys Gly Ser Glu Tyr Leu Ser Val Glu Tyr
                90                  95                  100

gat gag ggc caa ctc aac ctc gga tgg tgg att acc cgc cct gac ctg   451
Asp Glu Gly Gln Leu Asn Leu Gly Trp Trp Ile Thr Arg Pro Asp Leu
            105                 110                 115

gca caa cag ccc gca cat gat gtc acc gtg gag ggc gtt cgc tac cgt   499
Ala Gln Gln Pro Ala His Asp Val Thr Val Glu Gly Val Arg Tyr Arg
        120                 125                 130

aaa acc gaa tct ggc gtg ggc acc ttc acc tcc gaa ggc acc acc ggc   547
Lys Thr Glu Ser Gly Val Gly Thr Phe Thr Ser Glu Gly Thr Thr Gly
    135                 140                 145

gtg gct gat caa ggt gaa ttt gaa tac tgg gat ctc gcc gaa gtt ggc   595
Val Ala Asp Gln Gly Glu Phe Glu Tyr Trp Asp Leu Ala Glu Val Gly
150                 155                 160                 165

gga aac agg ttg ctc agt ttt gaa cgc tac ggc aaa gac agt cca ttt   643
Gly Asn Arg Leu Leu Ser Phe Glu Arg Tyr Gly Lys Asp Ser Pro Phe
                170                 175                 180

gaa gta tcg ctc ggg tgg acg gtg ctg ccc ggc gaa ctc acc gtt tac   691
Glu Val Ser Leu Gly Trp Thr Val Leu Pro Gly Glu Leu Thr Val Tyr
            185                 190                 195

cca gca cca gag gcc tca tgattcatca catcgattgc atg                732
Pro Ala Pro Glu Ala Ser
        200
```

<210> 2274
<211> 203
<212> PRT
<213> Corynebacterium glutamicum

<400> 2274
Met Asn Ile Thr Trp Leu Ile Leu Ala Gly Val Leu Ala Ile Ile Ala
1 5 10 15

Val Val Phe Phe Tyr Leu Ser Ala Gln Lys Lys Lys Ser Glu Pro Gln
20 25 30

Pro Pro Arg Gln Arg Gln Asp Pro Leu Lys Phe Ala Asp Gly Ser Asp
35 40 45

Thr Phe Asn Ala Arg Ile Leu Gly Pro Gly Ala Ile Ile Ser Arg Gly
50 55 60

Gly Val Asp Tyr Val Cys Arg Gly Ala Ile Gln Phe Arg Gln Gly Gln
65 70 75 80

Tyr Ile Trp His Glu Tyr Leu Leu Asp Gly Gly Lys Gly Ser Glu Tyr
85 90 95

Leu Ser Val Glu Tyr Asp Glu Gly Gln Leu Asn Leu Gly Trp Trp Ile
100 105 110

Thr Arg Pro Asp Leu Ala Gln Gln Pro Ala His Asp Val Thr Val Glu
115 120 125

Gly Val Arg Tyr Arg Lys Thr Glu Ser Gly Val Gly Thr Phe Thr Ser
130 135 140

Glu Gly Thr Thr Gly Val Ala Asp Gln Gly Glu Phe Glu Tyr Trp Asp
145 150 155 160

Leu Ala Glu Val Gly Gly Asn Arg Leu Leu Ser Phe Glu Arg Tyr Gly
165 170 175

Lys Asp Ser Pro Phe Glu Val Ser Leu Gly Trp Thr Val Leu Pro Gly
180 185 190

Glu Leu Thr Val Tyr Pro Ala Pro Glu Ala Ser
195 200

<210> 2275
<211> 621
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(598)
<223> RXA01505

<400> 2275
tcagttttga acgctacggc aaagacagtc catttgaagt atcgctcggg tggacggtgc 60

tgcccggcga actcaccgtt tacccagcac cagaggcctc atg att cat cac atc 115

```
                                                    Met Ile His His Ile
                                                      1               5

gat tgc atg cct aca gat gtc tcc gcc gaa gcg ctc ggc gtg agc tgg   163
Asp Cys Met Pro Thr Asp Val Ser Ala Glu Ala Leu Gly Val Ser Trp
                 10                  15                  20

aat ggg gaa tcg ccg gag gtg ctc gtc gat aag ctt atc gac gca tcc   211
Asn Gly Glu Ser Pro Glu Val Leu Val Asp Lys Leu Ile Asp Ala Ser
             25                  30                  35

cca cac ccc agc acc tgc cat tta gcg gtg att ggc ggc tcg cat gtg   259
Pro His Pro Ser Thr Cys His Leu Ala Val Ile Gly Gly Ser His Val
         40                  45                  50

gtt acc gtt gaa acg ccc gat ggg cgt ttc cgg gaa gaa att tcc tgc   307
Val Thr Val Glu Thr Pro Asp Gly Arg Phe Arg Glu Glu Ile Ser Cys
     55                  60                  65

cat gca caa gaa gcg gaa gat tcc cgc tgg ccg ctg ccc gac agc atc   355
His Ala Gln Glu Ala Glu Asp Ser Arg Trp Pro Leu Pro Asp Ser Ile
 70                  75                  80                  85

acg cgg gaa aac tac ctg ctg caa acc aac gtc gcc gtg ctg tct gag   403
Thr Arg Glu Asn Tyr Leu Leu Gln Thr Asn Val Ala Val Leu Ser Glu
                 90                  95                 100

gaa gat ttt gcc cgc gca gcc gaa gaa atc tcc aac ggc gac gac gac   451
Glu Asp Phe Ala Arg Ala Ala Glu Glu Ile Ser Asn Gly Asp Asp Asp
             105                 110                 115

tgg ttg atc gcc agt ttc ccc ggc gcc ggc gaa cac cac ctc acc gcg   499
Trp Leu Ile Ala Ser Phe Pro Gly Ala Gly Glu His His Leu Thr Ala
         120                 125                 130

ctg acc gca gaa ttt ctg gaa gac gta tgg gaa tgg ttt agc cac cac   547
Leu Thr Ala Glu Phe Leu Glu Asp Val Trp Glu Trp Phe Ser His His
     135                 140                 145

ctc tac cca gaa gag ctc acc atc gtg agc acg agg agc att tac aaa   595
Leu Tyr Pro Glu Glu Leu Thr Ile Val Ser Thr Arg Ser Ile Tyr Lys
150                 155                 160                 165

cca tgagctcccg aaactaccga agc                                    621
Pro
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<210> 2276
<211> 166
<212> PRT
<213> Corynebacterium glutamicum

<400> 2276

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Met Ile His His Ile Asp Cys Met Pro Thr Asp Val Ser Ala Glu Ala
  1               5                  10                  15

Leu Gly Val Ser Trp Asn Gly Glu Ser Pro Glu Val Leu Val Asp Lys
             20                  25                  30

Leu Ile Asp Ala Ser Pro His Pro Ser Thr Cys His Leu Ala Val Ile
```

```
         35                  40                  45

Gly Gly Ser His Val Val Thr Val Glu Thr Pro Asp Gly Arg Phe Arg
     50                  55                  60

Glu Glu Ile Ser Cys His Ala Gln Glu Ala Glu Asp Ser Arg Trp Pro
 65                  70                  75                  80

Leu Pro Asp Ser Ile Thr Arg Glu Asn Tyr Leu Leu Gln Thr Asn Val
                 85                  90                  95

Ala Val Leu Ser Glu Glu Asp Phe Ala Arg Ala Ala Glu Glu Ile Ser
            100                 105                 110

Asn Gly Asp Asp Asp Trp Leu Ile Ala Ser Phe Pro Gly Ala Gly Glu
        115                 120                 125

His His Leu Thr Ala Leu Thr Ala Glu Phe Leu Glu Asp Val Trp Glu
    130                 135                 140

Trp Phe Ser His His Leu Tyr Pro Glu Glu Leu Thr Ile Val Ser Thr
145                 150                 155                 160

Arg Ser Ile Tyr Lys Pro
                165
```

Application as filed

<210> 2277
<211> 534
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(511)
<223> RXA01506

<400> 2277

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cgctgaccgc agaatttctg gaagacgtat gggaatggtt tagccaccac ctctacccag 60

aagagctcac catcgtgagc acgaggagca tttacaaacc atg agc tcc cga aac   115
                                            Met Ser Ser Arg Asn
                                              1               5

tac cga agc ata gga ttc atc ctg ctg ttt tta gca gtg ttg tgc ctg   163
Tyr Arg Ser Ile Gly Phe Ile Leu Leu Phe Leu Ala Val Leu Cys Leu
                 10                  15                  20

ttc gct gcg gtt ttt gcc aag cct gcg gtg gga agc caa gtc tcc gac   211
Phe Ala Ala Val Phe Ala Lys Pro Ala Val Gly Ser Gln Val Ser Asp
             25                  30                  35

cgc tgg ccc gga aac aac ggc acc tac tca tgc gct ggc gaa agt ggg   259
Arg Trp Pro Gly Asn Asn Gly Thr Tyr Ser Cys Ala Gly Glu Ser Gly
         40                  45                  50

gtg gtg gat gaa atc gtg aac atg tcc acc cca acc gac cgc gcc acc   307
Val Val Asp Glu Ile Val Asn Met Ser Thr Pro Thr Asp Arg Ala Thr
     55                  60                  65

gac ccc gca act ggc gat act tac ctg cga tac agc aaa aac ctg atc   355
```

```
Asp Pro Ala Thr Gly Asp Thr Tyr Leu Arg Tyr Ser Lys Asn Leu Ile
 70                  75                  80                  85

atc atc tca ggt gaa ggc acg ccg gaa tgc acc atc acc gtc gaa ggc   403
Ile Ile Ser Gly Glu Gly Thr Pro Glu Cys Thr Ile Thr Val Glu Gly
                90                  95                 100

ctt gac cgc gtc aac agt ggt gcg ttc atc tgg ctc ggc ggc ggt ttc   451
Leu Asp Arg Val Asn Ser Gly Ala Phe Ile Trp Leu Gly Gly Gly Phe
            105                 110                 115

ggc cca tcc tca cca agc agt tcc agc ggc gga tcc tcc ggt tcc ggc   499
Gly Pro Ser Ser Pro Ser Ser Ser Ser Gly Gly Ser Ser Gly Ser Gly
        120                 125                 130

ggt ggc gtg aaa tagaaagaac actatgagtc aat                         534
Gly Gly Val Lys
    135
```

<210> 2278
<211> 137
<212> PRT
<213> Corynebacterium glutamicum

<400> 2278

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Met Ser Ser Arg Asn Tyr Arg Ser Ile Gly Phe Ile Leu Leu Phe Leu
  1               5                  10                  15

Ala Val Leu Cys Leu Phe Ala Ala Val Phe Ala Lys Pro Ala Val Gly
             20                  25                  30

Ser Gln Val Ser Asp Arg Trp Pro Gly Asn Asn Gly Thr Tyr Ser Cys
         35                  40                  45

Ala Gly Glu Ser Gly Val Val Asp Glu Ile Val Asn Met Ser Thr Pro
     50                  55                  60

Thr Asp Arg Ala Thr Asp Pro Ala Thr Gly Asp Thr Tyr Leu Arg Tyr
 65                  70                  75                  80

Ser Lys Asn Leu Ile Ile Ile Ser Gly Glu Gly Thr Pro Glu Cys Thr
                 85                  90                  95

Ile Thr Val Glu Gly Leu Asp Arg Val Asn Ser Gly Ala Phe Ile Trp
            100                 105                 110

Leu Gly Gly Gly Phe Gly Pro Ser Ser Pro Ser Ser Ser Ser Gly Gly
        115                 120                 125

Ser Ser Gly Ser Gly Gly Gly Val Lys
    130                 135
```

<210> 2279
<211> 546
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(523)
<223> RXA01507

<400> 2279
gcgttcatct ggctcggcgg cggtttcggc ccatcctcac caagcagttc cagcggcgga 60

tcctccggtt ccggcggtgg cgtgaaatag aaagaacact atg agt caa tat ctt 115
Met Ser Gln Tyr Leu
1 5

gtc gac gga gtg ctc ggc acc ctt tca tat ttc gtg ttg gcc gca gtg 163
Val Asp Gly Val Leu Gly Thr Leu Ser Tyr Phe Val Leu Ala Ala Val
10 15 20

atc ctc gtg gtc ggt ttt gtg att ttg gac ttg atc acc cca ggt aaa 211
Ile Leu Val Val Gly Phe Val Ile Leu Asp Leu Ile Thr Pro Gly Lys
25 30 35

ctg cat gaa ctc gtg ttt gtg cac cat ctg ccc aac gcc gct gtg atc 259
Leu His Glu Leu Val Phe Val His His Leu Pro Asn Ala Ala Val Ile
40 45 50

acc gtg gcg cag cag gtt tcc atc gga atc atc gtg gtc act gct gtg 307
Thr Val Ala Gln Gln Val Ser Ile Gly Ile Ile Val Val Thr Ala Val
55 60 65

ctg acc tcc tca gat att ttg agt gaa ggt ttg ctg gag act gca gtg 355
Leu Thr Ser Ser Asp Ile Leu Ser Glu Gly Leu Leu Glu Thr Ala Val
70 75 80 85

ttc ggt gcc ctt ggt ctg gtt atc caa gtg gtg gtc atg gcg gtg ttg 403
Phe Gly Ala Leu Gly Leu Val Ile Gln Val Val Val Met Ala Val Leu
90 95 100

gaa gct gtc att ccg gga cgt ttc cgt gat ctc gtg gaa gat ccc aaa 451
Glu Ala Val Ile Pro Gly Arg Phe Arg Asp Leu Val Glu Asp Pro Lys
105 110 115

ctc cgt tcc ggt gcc gtc gtg gcc gcc gtc atc ttg atc gtg gtg gga 499
Leu Arg Ser Gly Ala Val Val Ala Ala Val Ile Leu Ile Val Val Gly
120 125 130

acc gta aac gct gca tgt ctg att taggacccat ctggcgctgg ctg 546
Thr Val Asn Ala Ala Cys Leu Ile
135 140

<210> 2280
<211> 141
<212> PRT
<213> Corynebacterium glutamicum

<400> 2280
Met Ser Gln Tyr Leu Val Asp Gly Val Leu Gly Thr Leu Ser Tyr Phe
1 5 10 15

Val Leu Ala Ala Val Ile Leu Val Val Gly Phe Val Ile Leu Asp Leu
20 25 30

Ile Thr Pro Gly Lys Leu His Glu Leu Val Phe Val His His Leu Pro
35 40 45

```
Asn Ala Ala Val Ile Thr Val Ala Gln Gln Val Ser Ile Gly Ile Ile
     50                  55                  60

Val Val Thr Ala Val Leu Thr Ser Ser Asp Ile Leu Ser Glu Gly Leu
 65                  70                  75                  80

Leu Glu Thr Ala Val Phe Gly Ala Leu Gly Leu Val Ile Gln Val Val
                 85                  90                  95

Val Met Ala Val Leu Glu Ala Val Ile Pro Gly Arg Phe Arg Asp Leu
            100                 105                 110

Val Glu Asp Pro Lys Leu Arg Ser Gly Ala Val Val Ala Ala Val Ile
        115                 120                 125

Leu Ile Val Val Gly Thr Val Asn Ala Ala Cys Leu Ile
    130                 135                 140
```

<210> 2281
<211> 870
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(847)
<223> RXA01519

<400> 2281

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ctgggcggaa tcgcactctc agctgccgga ctttatttag agcgaagctg tgaggctccg 60

cctccccaat ctggcgaagc gatcagctag attggaattc atg aat caa gac ctg   115
                                           Met Asn Gln Asp Leu
                                             1               5

tca cac gag gat tcc ggc gac ggc aat tct gtc gac cgt gga cag att   163
Ser His Glu Asp Ser Gly Asp Gly Asn Ser Val Asp Arg Gly Gln Ile
                 10                  15                  20

ctg cta gca gta ctc att gga ctt gcc ctg att gcc agc gtc atc atg   211
Leu Leu Ala Val Leu Ile Gly Leu Ala Leu Ile Ala Ser Val Ile Met
             25                  30                  35

ctg ctg gcc aac agt gac ggc gcc atg aaa ata gca ctt ctt gca gcg   259
Leu Leu Ala Asn Ser Asp Gly Ala Met Lys Ile Ala Leu Leu Ala Ala
         40                  45                  50

ctg tgg gcg gca atc atc gga ttc ttc ctt gtt tat cgg tcc cgc aaa   307
Leu Trp Ala Ala Ile Ile Gly Phe Phe Leu Val Tyr Arg Ser Arg Lys
     55                  60                  65

caa gtc gaa gct gct gcg cgg gag aag gaa acc ctc gaa tac gca cac   355
Gln Val Glu Ala Ala Ala Arg Glu Lys Glu Thr Leu Glu Tyr Ala His
 70                  75                  80                  85

caa tct gaa ctc aac cga cta gaa gct gaa ctc gtc caa gaa aaa atg   403
Gln Ser Glu Leu Asn Arg Leu Glu Ala Glu Leu Val Gln Glu Lys Met
                 90                  95                 100
```

```
gag att tct gaa tcc cgt cgt gca cgc gat cag gaa acc ctt gag gaa   451
Glu Ile Ser Glu Ser Arg Arg Ala Arg Asp Gln Glu Thr Leu Glu Glu
            105                 110                 115

atc aaa ctt caa ctg gag gaa atg cgc acc cag ctg tct gag ctt tct   499
Ile Lys Leu Gln Leu Glu Glu Met Arg Thr Gln Leu Ser Glu Leu Ser
        120                 125                 130

ggc cgt gaa tgg ggc tat gag cca acc atg ctg cgt gcc gaa gcc cga   547
Gly Arg Glu Trp Gly Tyr Glu Pro Thr Met Leu Arg Ala Glu Ala Arg
    135                 140                 145

cga atc ctt gag ttg gaa tcc cag cag ctt tcc cag cag ttc cag gca   595
Arg Ile Leu Glu Leu Glu Ser Gln Gln Leu Ser Gln Gln Phe Gln Ala
150                 155                 160                 165

ccg cag cca gaa gtc ccg gag cct gtt gca gtt cca gag cca atg ccg   643
Pro Gln Pro Glu Val Pro Glu Pro Val Ala Val Pro Glu Pro Met Pro
                170                 175                 180

gaa cct gca ccg gtg ccg gaa cca gta cca gaa cct gag cca gtt gaa   691
Glu Pro Ala Pro Val Pro Glu Pro Val Pro Glu Pro Glu Pro Val Glu
            185                 190                 195

gtt gct gtc gaa gct gag gaa gaa cca gca cca ggt cgc aga agg cgt   739
Val Ala Val Glu Ala Glu Glu Glu Pro Ala Pro Gly Arg Arg Arg Arg
        200                 205                 210

agg cac gca gct ccc gaa gaa act ggc gga cgc cga cgc aaa gat gaa   787
Arg His Ala Ala Pro Glu Glu Thr Gly Gly Arg Arg Arg Lys Asp Glu
    215                 220                 225

cgc caa ggc ggt ttg agc gtg gct gat ctt ctg gca gca gca agg aaa   835
Arg Gln Gly Gly Leu Ser Val Ala Asp Leu Leu Ala Ala Ala Arg Lys
230                 235                 240                 245

aag gaa aac aac taatgcaggc tcctcgcctt cgc                        870
Lys Glu Asn Asn
```

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<210> 2282
<211> 249
<212> PRT
<213> Corynebacterium glutamicum

<400> 2282

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Met Asn Gln Asp Leu Ser His Glu Asp Ser Gly Asp Gly Asn Ser Val
  1               5                  10                  15

Asp Arg Gly Gln Ile Leu Leu Ala Val Leu Ile Gly Leu Ala Leu Ile
             20                  25                  30

Ala Ser Val Ile Met Leu Leu Ala Asn Ser Asp Gly Ala Met Lys Ile
         35                  40                  45

Ala Leu Leu Ala Ala Leu Trp Ala Ala Ile Ile Gly Phe Phe Leu Val
     50                  55                  60

Tyr Arg Ser Arg Lys Gln Val Glu Ala Ala Ala Arg Glu Lys Glu Thr
 65                  70                  75                  80
```

Leu Glu Tyr Ala His Gln Ser Glu Leu Asn Arg Leu Glu Ala Glu Leu
85 90 95

Val Gln Glu Lys Met Glu Ile Ser Glu Ser Arg Arg Ala Arg Asp Gln
100 105 110

Glu Thr Leu Glu Glu Ile Lys Leu Gln Leu Glu Glu Met Arg Thr Gln
115 120 125

Leu Ser Glu Leu Ser Gly Arg Glu Trp Gly Tyr Glu Pro Thr Met Leu
130 135 140

Arg Ala Glu Ala Arg Arg Ile Leu Glu Leu Glu Ser Gln Gln Leu Ser
145 150 155 160

Gln Gln Phe Gln Ala Pro Gln Pro Glu Val Pro Glu Pro Val Ala Val
165 170 175

Pro Glu Pro Met Pro Glu Pro Ala Pro Val Pro Glu Pro Val Pro Glu
180 185 190

Pro Glu Pro Val Glu Val Ala Val Glu Ala Glu Glu Glu Pro Ala Pro
195 200 205

Gly Arg Arg Arg Arg Arg His Ala Ala Pro Glu Glu Thr Gly Gly Arg
210 215 220

Arg Arg Lys Asp Glu Arg Gln Gly Gly Leu Ser Val Ala Asp Leu Leu
225 230 235 240

Ala Ala Ala Arg Lys Lys Glu Asn Asn
245

<210> 2283
<211> 507
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(484)
<223> RXA01520

<400> 2283
ctgcatacct cgctcacgca cggcatcact gtgatggatc cgctgcagac gtccggcagg 60

catcgtgatg tctgcgcacc cgattggtca ggaccggtgg gtg gcg tcc gcg ttg 115
Val Ala Ser Ala Leu
1 5

gat gag ttg ggg gag acc atc gtg ggg ctt ttg gtg ggg gag ctc ggt 163
Asp Glu Leu Gly Glu Thr Ile Val Gly Leu Leu Val Gly Glu Leu Gly
10 15 20

ggc tcg att gtc gag atc gcc gat gac aag cgc gca cag ttg gct gca 211
Gly Ser Ile Val Glu Ile Ala Asp Asp Lys Arg Ala Gln Leu Ala Ala
25 30 35

gcg ctg acc tat gcc gga ttt tta agc acc ttg cag cgc gat gcg tcg 259

```
Ala Leu Thr Tyr Ala Gly Phe Leu Ser Thr Leu Gln Arg Asp Ala Ser
         40                  45                  50

tat ttc ctg gat gaa ttt ctt ggc gat ccc gat gtg acc tct gac atc   307
Tyr Phe Leu Asp Glu Phe Leu Gly Asp Pro Asp Val Thr Ser Asp Ile
     55                  60                  65

gtt atg gat tcc gca cag caa ttc cag gca ctg cct tcg ttg gat gag   355
Val Met Asp Ser Ala Gln Gln Phe Gln Ala Leu Pro Ser Leu Asp Glu
 70                  75                  80                  85

gtc att gcc cag tac gat tcg att aac aac ccc ggc agg caa cgc ctt   403
Val Ile Ala Gln Tyr Asp Ser Ile Asn Asn Pro Gly Arg Gln Arg Leu
                 90                  95                 100

ttc cgg gat ttg gcg cgc agg cag gca gag att tcc cgc gcg caa gat   451
Phe Arg Asp Leu Ala Arg Arg Gln Ala Glu Ile Ser Arg Ala Gln Asp
            105                 110                 115

att gag ctg tgg gca att cag aag gag gac cgt tgagtttcac gcatggtcag 504
Ile Glu Leu Trp Ala Ile Gln Lys Glu Asp Arg
        120                 125

ggc                                                               507


<210> 2284
<211> 128
<212> PRT
<213> Corynebacterium glutamicum

<400> 2284
Val Ala Ser Ala Leu Asp Glu Leu Gly Glu Thr Ile Val Gly Leu Leu
  1               5                  10                  15

Val Gly Glu Leu Gly Gly Ser Ile Val Glu Ile Ala Asp Asp Lys Arg
             20                  25                  30

Ala Gln Leu Ala Ala Ala Leu Thr Tyr Ala Gly Phe Leu Ser Thr Leu
         35                  40                  45

Gln Arg Asp Ala Ser Tyr Phe Leu Asp Glu Phe Leu Gly Asp Pro Asp
     50                  55                  60

Val Thr Ser Asp Ile Val Met Asp Ser Ala Gln Gln Phe Gln Ala Leu
 65                  70                  75                  80

Pro Ser Leu Asp Glu Val Ile Ala Gln Tyr Asp Ser Ile Asn Asn Pro
                 85                  90                  95

Gly Arg Gln Arg Leu Phe Arg Asp Leu Ala Arg Arg Gln Ala Glu Ile
            100                 105                 110

Ser Arg Ala Gln Asp Ile Glu Leu Trp Ala Ile Gln Lys Glu Asp Arg
        115                 120                 125


<210> 2285
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<211> 1074
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1051)
<223> RXA01523

<400> 2285
aatcctccaa acctgtggat agaacaatct atccacaggt tttcagtttt ctgcaaagtt 60

catccttggc ttcttatgcc ttcggatcca tagtggggtc atg aaa aac tgg caa 115
Met Lys Asn Trp Gln
1 5

gaa gaa ttc caa cta gtc aat ctc acg aaa ctt ctg cat agc gat acc 163
Glu Glu Phe Gln Leu Val Asn Leu Thr Lys Leu Leu His Ser Asp Thr
10 15 20

gag act tct gcg gca atc agt aat ggt caa atg att aaa ctc act cat 211
Glu Thr Ser Ala Ala Ile Ser Asn Gly Gln Met Ile Lys Leu Thr His
25 30 35

gaa gtc gca atc aat gct gaa aag tac cga agc ctt cct gca tgg gat 259
Glu Val Ala Ile Asn Ala Glu Lys Tyr Arg Ser Leu Pro Ala Trp Asp
40 45 50

aaa gca gcc gcc cga gct ttt gca gtg ggt atg act gtg gac aaa gca 307
Lys Ala Ala Ala Arg Ala Phe Ala Val Gly Met Thr Val Asp Lys Ala
55 60 65

gtg gta gcg ggg cag tct gcg gcg agg tta tgg gga tac caa act ttg 355
Val Val Ala Gly Gln Ser Ala Ala Arg Leu Trp Gly Tyr Gln Thr Leu
70 75 80 85

act gtt gag aaa acc gtg ttg tgt ctg ttg ccg gaa agg cta cgt tca 403
Thr Val Glu Lys Thr Val Leu Cys Leu Leu Pro Glu Arg Leu Arg Ser
90 95 100

aaa tcc tcc aag cat tgg ccg tcc ggg atg cga tat aaa gat cgt tac 451
Lys Ser Ser Lys His Trp Pro Ser Gly Met Arg Tyr Lys Asp Arg Tyr
105 110 115

ctc tcg tcg cgt gat att cga gag gtt cat ggg atc cga gtt acg gga 499
Leu Ser Ser Arg Asp Ile Arg Glu Val His Gly Ile Arg Val Thr Gly
120 125 130

gcg ttc cgc aca ttt ttg gac atc gct ttg gat gat ggg gtg gtg gcg 547
Ala Phe Arg Thr Phe Leu Asp Ile Ala Leu Asp Asp Gly Val Val Ala
135 140 145

gct gtg gtc act att gat tca gct cga aga cag aat cca tcg ctt acg 595
Ala Val Val Thr Ile Asp Ser Ala Arg Arg Gln Asn Pro Ser Leu Thr
150 155 160 165

cgt gag aag tta atg cac agt gcg gaa agt ttc ccg agg cat cgg ggt 643
Arg Glu Lys Leu Met His Ser Ala Glu Ser Phe Pro Arg His Arg Gly
170 175 180

gtg aag gcg tat cgg cag gcg att gag ttg tcg att ccc aat tcg gat 691

```
Val Lys Ala Tyr Arg Gln Ala Ile Glu Leu Ser Ile Pro Asn Ser Asp
            185                 190                 195

agt gct cag gag acg agg gct cgg tta atc ctt cgg gag gcc aag ctc   739
Ser Ala Gln Glu Thr Arg Ala Arg Leu Ile Leu Arg Glu Ala Lys Leu
        200                 205                 210

ccg gaa atc cag tca gtg aag gtg cag gcc cgt ttc gat caa tcg cac   787
Pro Glu Ile Gln Ser Val Lys Val Gln Ala Arg Phe Asp Gln Ser His
    215                 220                 225

aac aag tat ttc ctc gtc gat ttc ttg atc aat gag tgg atc atc gtg   835
Asn Lys Tyr Phe Leu Val Asp Phe Leu Ile Asn Glu Trp Ile Ile Val
230                 235                 240                 245

gag att gat gga cgt tcg aaa tat gat tcc ccg gag ctc aat gag gtg   883
Glu Ile Asp Gly Arg Ser Lys Tyr Asp Ser Pro Glu Leu Asn Glu Val
                250                 255                 260

ctc atg gct gaa cgc gat cgg gag aaa ttc ttc ctc aat cag ggc tat   931
Leu Met Ala Glu Arg Asp Arg Glu Lys Phe Phe Leu Asn Gln Gly Tyr
            265                 270                 275

gcg gtc tta aga atc gat ccg aaa cag tta gac ctc aac caa gat ggg   979
Ala Val Leu Arg Ile Asp Pro Lys Gln Leu Asp Leu Asn Gln Asp Gly
        280                 285                 290

gag tgt gag ttc atc gga atc ctc aaa aac act ttg cag aag acc cca   1027
Glu Cys Glu Phe Ile Gly Ile Leu Lys Asn Thr Leu Gln Lys Thr Pro
    295                 300                 305

cct gag cac ctc aag caa gcc gcc taaacactcc aagaaccacc att         1074
Pro Glu His Leu Lys Gln Ala Ala
310                 315
```

<210> 2286
<211> 317
<212> PRT
<213> Corynebacterium glutamicum

<400> 2286

```
Met Lys Asn Trp Gln Glu Glu Phe Gln Leu Val Asn Leu Thr Lys Leu
  1               5                  10                  15

Leu His Ser Asp Thr Glu Thr Ser Ala Ala Ile Ser Asn Gly Gln Met
             20                  25                  30

Ile Lys Leu Thr His Glu Val Ala Ile Asn Ala Glu Lys Tyr Arg Ser
         35                  40                  45

Leu Pro Ala Trp Asp Lys Ala Ala Ala Arg Ala Phe Ala Val Gly Met
     50                  55                  60

Thr Val Asp Lys Ala Val Val Ala Gly Gln Ser Ala Ala Arg Leu Trp
 65                  70                  75                  80

Gly Tyr Gln Thr Leu Thr Val Glu Lys Thr Val Leu Cys Leu Leu Pro
                 85                  90                  95

Glu Arg Leu Arg Ser Lys Ser Ser Lys His Trp Pro Ser Gly Met Arg
```

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            100                 105                 110

Tyr Lys Asp Arg Tyr Leu Ser Ser Arg Asp Ile Arg Glu Val His Gly
        115                 120                 125

Ile Arg Val Thr Gly Ala Phe Arg Thr Phe Leu Asp Ile Ala Leu Asp
    130                 135                 140

Asp Gly Val Val Ala Ala Val Val Thr Ile Asp Ser Ala Arg Arg Gln
145                 150                 155                 160

Asn Pro Ser Leu Thr Arg Glu Lys Leu Met His Ser Ala Glu Ser Phe
                165                 170                 175

Pro Arg His Arg Gly Val Lys Ala Tyr Arg Gln Ala Ile Glu Leu Ser
            180                 185                 190

Ile Pro Asn Ser Asp Ser Ala Gln Glu Thr Arg Ala Arg Leu Ile Leu
        195                 200                 205

Arg Glu Ala Lys Leu Pro Glu Ile Gln Ser Val Lys Val Gln Ala Arg
    210                 215                 220

Phe Asp Gln Ser His Asn Lys Tyr Phe Leu Val Asp Phe Leu Ile Asn
225                 230                 235                 240

Glu Trp Ile Ile Val Glu Ile Asp Gly Arg Ser Lys Tyr Asp Ser Pro
                245                 250                 255

Glu Leu Asn Glu Val Leu Met Ala Glu Arg Asp Arg Glu Lys Phe Phe
            260                 265                 270

Leu Asn Gln Gly Tyr Ala Val Leu Arg Ile Asp Pro Lys Gln Leu Asp
        275                 280                 285

Leu Asn Gln Asp Gly Glu Cys Glu Phe Ile Gly Ile Leu Lys Asn Thr
    290                 295                 300

Leu Gln Lys Thr Pro Pro Glu His Leu Lys Gln Ala Ala
305                 310                 315
```

<210> 2287
<211> 1845
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1822)
<223> RXA01525

<400> 2287
gtctctgtag aaatctaggg ctttcgacgc ttgagccccg cgcacctgca aggtgcgctg 60

```
tagggaggcg tcgacaagca tctttaagta gctttgaagc atg cgt tcc ttt caa   115
                                            Met Arg Ser Phe Gln
                                              1               5

tcg atc ctt gac ctg gta aat tca gca tcc gag gtg gct acc aaa att   163
Ser Ile Leu Asp Leu Val Asn Ser Ala Ser Glu Val Ala Thr Lys Ile
```

```
                  10                  15                  20

gtg ttg aag cgc ttc gaa aaa cgg ata acc agc gaa act gac tgg gta   211
Val Leu Lys Arg Phe Glu Lys Arg Ile Thr Ser Glu Thr Asp Trp Val
            25                  30                  35

ccg tat cag cgg ttt agt ctt tgg tcg gtt ggt tct ccg cta acg atc   259
Pro Tyr Gln Arg Phe Ser Leu Trp Ser Val Gly Ser Pro Leu Thr Ile
        40                  45                  50

gaa cgc aaa ggc ccc gat gtg cgt gtg agc aag gac aac act gcc gtt   307
Glu Arg Lys Gly Pro Asp Val Arg Val Ser Lys Asp Asn Thr Ala Val
    55                  60                  65

ctt cag cgc tat caa aga ccg gaa gca gaa gga ctg atc agc tac ttc   355
Leu Gln Arg Tyr Gln Arg Pro Glu Ala Glu Gly Leu Ile Ser Tyr Phe
70                  75                  80                  85

atg gat cca aag cca tgg ata act gaa ttg gca ggc ctg aat ctg gac   403
Met Asp Pro Lys Pro Trp Ile Thr Glu Leu Ala Gly Leu Asn Leu Asp
                90                  95                 100

gat gtt tcc gaa gat aca gtt gca ggt cgg aca gta tta gtg gtt ccc   451
Asp Val Ser Glu Asp Thr Val Ala Gly Arg Thr Val Leu Val Val Pro
            105                 110                 115

cta tcc aat gtc att ctc agc atc gat gcg gaa ttt ggg atg att cta   499
Leu Ser Asn Val Ile Leu Ser Ile Asp Ala Glu Phe Gly Met Ile Leu
        120                 125                 130

act gcg gaa aac gac ata gaa aag atc cac gca ata tct gtc gaa ctc   547
Thr Ala Glu Asn Asp Ile Glu Lys Ile His Ala Ile Ser Val Glu Leu
    135                 140                 145

tta gaa aaa tgg aga tca tcc cat tac cct gag ccg cat ttt cct gca   595
Leu Glu Lys Trp Arg Ser Ser His Tyr Pro Glu Pro His Phe Pro Ala
150                 155                 160                 165

gcg gtt ctc cca cct gcg tcg act gga aac cgc aac ctc cga gtt cta   643
Ala Val Leu Pro Pro Ala Ser Thr Gly Asn Arg Asn Leu Arg Val Leu
                170                 175                 180

tgc cct gag ttt tcc att cca agt gtc aac gtt ggt gat cag gtt tta   691
Cys Pro Glu Phe Ser Ile Pro Ser Val Asn Val Gly Asp Gln Val Leu
            185                 190                 195

cta ttt tta aca ttt gat caa acc ctg cca cca gta gat cag ctt gaa   739
Leu Phe Leu Thr Phe Asp Gln Thr Leu Pro Pro Val Asp Gln Leu Glu
        200                 205                 210

act act cgc cgc gga tac act gat cca atc cag ctt gac tac gac cac   787
Thr Thr Arg Arg Gly Tyr Thr Asp Pro Ile Gln Leu Asp Tyr Asp His
    215                 220                 225

cgc caa tac agg ttt cac gcc gac ggt tgg gat gcc atc atc tcc acg   835
Arg Gln Tyr Arg Phe His Ala Asp Gly Trp Asp Ala Ile Ile Ser Thr
230                 235                 240                 245

gtg gag cca cta cac gac gaa gaa gaa ctc aca ggt tac ttc ctg cac   883
Val Glu Pro Leu His Asp Glu Glu Glu Leu Thr Gly Tyr Phe Leu His
                250                 255                 260
```

```
cgc ctt gac cca gat agc gcg tac cca acc att gca gtc gtt aca gca   931
Arg Leu Asp Pro Asp Ser Ala Tyr Pro Thr Ile Ala Val Val Thr Ala
            265                 270                 275

gcg cac tac cac ggt acg gac gca att atc gac gtg acc cta gat ggt   979
Ala His Tyr His Gly Thr Asp Ala Ile Ile Asp Val Thr Leu Asp Gly
        280                 285                 290

gtg cat cca ccc aaa aac caa gaa act ctt gaa ggc atc agc act agt   1027
Val His Pro Pro Lys Asn Gln Glu Thr Leu Glu Gly Ile Ser Thr Ser
    295                 300                 305

acc agt gac ggt gac ata ttt tgg ctc tcc gat gaa agc ttg cct ttc   1075
Thr Ser Asp Gly Asp Ile Phe Trp Leu Ser Asp Glu Ser Leu Pro Phe
310                 315                 320                 325

gtc cgt gga ttc agc gtg tca aca ggc gaa cta tta cac gag atc tcc   1123
Val Arg Gly Phe Ser Val Ser Thr Gly Glu Leu Leu His Glu Ile Ser
                330                 335                 340

atc ccc acg ttc caa gag atc gtc ctc gat tcc gct aat aga gcc cgc   1171
Ile Pro Thr Phe Gln Glu Ile Val Leu Asp Ser Ala Asn Arg Ala Arg
            345                 350                 355

gta aaa caa aag caa tgg cct cac gat ttc agt gat tgc aag gga aaa   1219
Val Lys Gln Lys Gln Trp Pro His Asp Phe Ser Asp Cys Lys Gly Lys
        360                 365                 370

aca tgg gag ctt ccg gat ctt aaa gaa gta ttc gaa gct gtc cct tcg   1267
Thr Trp Glu Leu Pro Asp Leu Lys Glu Val Phe Glu Ala Val Pro Ser
    375                 380                 385

att cca gca ggt tgg aga ttg tta gac agc ttc ggg aaa aac ttg cac   1315
Ile Pro Ala Gly Trp Arg Leu Leu Asp Ser Phe Gly Lys Asn Leu His
390                 395                 400                 405

aat gtc aca cgc gaa aac cct cgt ctt aat gac aac ttt tgg ctt caa   1363
Asn Val Thr Arg Glu Asn Pro Arg Leu Asn Asp Asn Phe Trp Leu Gln
                410                 415                 420

aca atc ctt agg ctt aaa cca ttt aaa gca gta gat ctt gat atc ggc   1411
Thr Ile Leu Arg Leu Lys Pro Phe Lys Ala Val Asp Leu Asp Ile Gly
            425                 430                 435

cga tcg ata atc aca gca att tac cca tac ggt gat cga att tac tta   1459
Arg Ser Ile Ile Thr Ala Ile Tyr Pro Tyr Gly Asp Arg Ile Tyr Leu
        440                 445                 450

cgc gct agt aac cac cac atc acg ttt aac cag gac ctc gag att ctc   1507
Arg Ala Ser Asn His His Ile Thr Phe Asn Gln Asp Leu Glu Ile Leu
    455                 460                 465

aac gta gaa gtc ttt ggc gac cct gag gtt ccc gaa tct ggt cta att   1555
Asn Val Glu Val Phe Gly Asp Pro Glu Val Pro Glu Ser Gly Leu Ile
470                 475                 480                 485

tat ctt cca cct ggg gat tct cca aca ctc ggt ttt ccc acc gga aca   1603
Tyr Leu Pro Pro Gly Asp Ser Pro Thr Leu Gly Phe Pro Thr Gly Thr
                490                 495                 500
```

```
ctc atg atg ttt cat gag caa gaa ggc aca tat gct ttc cac gac cct   1651
Leu Met Met Phe His Glu Gln Glu Gly Thr Tyr Ala Phe His Asp Pro
            505                 510                 515

gaa aca aca gaa caa ata aca act gtg aac tta gac agg aat agt ttt   1699
Glu Thr Thr Glu Gln Ile Thr Thr Val Asn Leu Asp Arg Asn Ser Phe
        520                 525                 530

tca gtg gca tat tct tcc cga acc aaa att gtt att tca ctg aaa aac   1747
Ser Val Ala Tyr Ser Ser Arg Thr Lys Ile Val Ile Ser Leu Lys Asn
    535                 540                 545

cca gaa agc cga cct acc aac aag ctg ttg gtg tgg gaa cca caa acc   1795
Pro Glu Ser Arg Pro Thr Asn Lys Leu Leu Val Trp Glu Pro Gln Thr
550                 555                 560                 565

ggg tgg cga gaa cag aac ctg gag cgc tgagcacgct taaggtgagg         1842
Gly Trp Arg Glu Gln Asn Leu Glu Arg
                570

tgg                                                              1845
```

<210> 2288
<211> 574
<212> PRT
<213> Corynebacterium glutamicum

<400> 2288

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Met Arg Ser Phe Gln Ser Ile Leu Asp Leu Val Asn Ser Ala Ser Glu
  1               5                  10                  15

Val Ala Thr Lys Ile Val Leu Lys Arg Phe Glu Lys Arg Ile Thr Ser
             20                  25                  30

Glu Thr Asp Trp Val Pro Tyr Gln Arg Phe Ser Leu Trp Ser Val Gly
         35                  40                  45

Ser Pro Leu Thr Ile Glu Arg Lys Gly Pro Asp Val Arg Val Ser Lys
     50                  55                  60

Asp Asn Thr Ala Val Leu Gln Arg Tyr Gln Arg Pro Glu Ala Glu Gly
 65                  70                  75                  80

Leu Ile Ser Tyr Phe Met Asp Pro Lys Pro Trp Ile Thr Glu Leu Ala
                 85                  90                  95

Gly Leu Asn Leu Asp Asp Val Ser Glu Asp Thr Val Ala Gly Arg Thr
            100                 105                 110

Val Leu Val Val Pro Leu Ser Asn Val Ile Leu Ser Ile Asp Ala Glu
        115                 120                 125

Phe Gly Met Ile Leu Thr Ala Glu Asn Asp Ile Glu Lys Ile His Ala
    130                 135                 140

Ile Ser Val Glu Leu Leu Glu Lys Trp Arg Ser Ser His Tyr Pro Glu
145                 150                 155                 160

Pro His Phe Pro Ala Ala Val Leu Pro Pro Ala Ser Thr Gly Asn Arg
                165                 170                 175
```

Asn Leu Arg Val Leu Cys Pro Glu Phe Ser Ile Pro Ser Val Asn Val
180 185 190

Gly Asp Gln Val Leu Leu Phe Leu Thr Phe Asp Gln Thr Leu Pro Pro
195 200 205

Val Asp Gln Leu Glu Thr Thr Arg Arg Gly Tyr Thr Asp Pro Ile Gln
210 215 220

Leu Asp Tyr Asp His Arg Gln Tyr Arg Phe His Ala Asp Gly Trp Asp
225 230 235 240

Ala Ile Ile Ser Thr Val Glu Pro Leu His Asp Glu Glu Glu Leu Thr
245 250 255

Gly Tyr Phe Leu His Arg Leu Asp Pro Asp Ser Ala Tyr Pro Thr Ile
260 265 270

Ala Val Val Thr Ala Ala His Tyr His Gly Thr Asp Ala Ile Ile Asp
275 280 285

Val Thr Leu Asp Gly Val His Pro Pro Lys Asn Gln Glu Thr Leu Glu
290 295 300

Gly Ile Ser Thr Ser Thr Ser Asp Gly Asp Ile Phe Trp Leu Ser Asp
305 310 315 320

Glu Ser Leu Pro Phe Val Arg Gly Phe Ser Val Ser Thr Gly Glu Leu
325 330 335

Leu His Glu Ile Ser Ile Pro Thr Phe Gln Glu Ile Val Leu Asp Ser
340 345 350

Ala Asn Arg Ala Arg Val Lys Gln Lys Gln Trp Pro His Asp Phe Ser
355 360 365

Asp Cys Lys Gly Lys Thr Trp Glu Leu Pro Asp Leu Lys Glu Val Phe
370 375 380

Glu Ala Val Pro Ser Ile Pro Ala Gly Trp Arg Leu Leu Asp Ser Phe
385 390 395 400

Gly Lys Asn Leu His Asn Val Thr Arg Glu Asn Pro Arg Leu Asn Asp
405 410 415

Asn Phe Trp Leu Gln Thr Ile Leu Arg Leu Lys Pro Phe Lys Ala Val
420 425 430

Asp Leu Asp Ile Gly Arg Ser Ile Ile Thr Ala Ile Tyr Pro Tyr Gly
435 440 445

Asp Arg Ile Tyr Leu Arg Ala Ser Asn His His Ile Thr Phe Asn Gln
450 455 460

Asp Leu Glu Ile Leu Asn Val Glu Val Phe Gly Asp Pro Glu Val Pro
465 470 475 480

Glu Ser Gly Leu Ile Tyr Leu Pro Pro Gly Asp Ser Pro Thr Leu Gly
485 490 495

```
Phe Pro Thr Gly Thr Leu Met Met Phe His Glu Gln Glu Gly Thr Tyr
            500                 505                 510

Ala Phe His Asp Pro Glu Thr Thr Glu Gln Ile Thr Thr Val Asn Leu
        515                 520                 525

Asp Arg Asn Ser Phe Ser Val Ala Tyr Ser Ser Arg Thr Lys Ile Val
    530                 535                 540

Ile Ser Leu Lys Asn Pro Glu Ser Arg Pro Thr Asn Lys Leu Leu Val
545                 550                 555                 560

Trp Glu Pro Gln Thr Gly Trp Arg Glu Gln Asn Leu Glu Arg
                565                 570


<210> 2289
<211> 2634
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2611)
<223> RXA01527

<400> 2289
atttggcttt tgcggatgag cggaagttgg ctaggcaggc gcatgatttg ttgcctgagt 60

ttgctttgaa ggaaaaggcg gagggaaggt ccaccccaag gtg att ccg aac ccc   115
                                            Val Ile Pro Asn Pro
                                              1               5

aac ccg aac ccc aaa gcc aaa act ctt cgc ctc gtt tca gcg ctg acc   163
Asn Pro Asn Pro Lys Ala Lys Thr Leu Arg Leu Val Ser Ala Leu Thr
                 10                  15                  20

gcc atc act gtg gtg ggt ttt agc gct tca cct gtt cat gcg ttg ccg   211
Ala Ile Thr Val Val Gly Phe Ser Ala Ser Pro Val His Ala Leu Pro
             25                  30                  35

att ccg ttg gat cct tct gat ccg gcg gtg tcg gag ttg tgg gtg aat   259
Ile Pro Leu Asp Pro Ser Asp Pro Ala Val Ser Glu Leu Trp Val Asn
         40                  45                  50

ccg aat gcg cgg gct gat gat gag ctt tct ggt gtg gat gta gag atc   307
Pro Asn Ala Arg Ala Asp Asp Glu Leu Ser Gly Val Asp Val Glu Ile
     55                  60                  65

tcg gat ttt gtc atg ccg aat agc aat cta act gtg cag gtg ggg gag   355
Ser Asp Phe Val Met Pro Asn Ser Asn Leu Thr Val Gln Val Gly Glu
 70                  75                  80                  85

tct ttt aag gcg cag gtt cgg gtg act aat cgt tcg tcg gag acg ttg   403
Ser Phe Lys Ala Gln Val Arg Val Thr Asn Arg Ser Ser Glu Thr Leu
                 90                  95                 100

agc aat att acg ttg cag gcg cgt cgt gcg gag gcg tcg ttt gat atg   451
Ser Asn Ile Thr Leu Gln Ala Arg Arg Ala Glu Ala Ser Phe Asp Met
            105                 110                 115
```

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gcg agt gct cgg gtg gcg gcg acg gat aat aat tat ggc tac ttc ggc   499
Ala Ser Ala Arg Val Ala Ala Thr Asp Asn Asn Tyr Gly Tyr Phe Gly
        120                 125                 130

gcg atg gtg act ctt gat gat gag ttg gag ccg ggg gag agt gtt gag   547
Ala Met Val Thr Leu Asp Asp Glu Leu Glu Pro Gly Glu Ser Val Glu
    135                 140                 145

act gag gtg gag att tct acc gat agt ttg tcg att tct cag ccg ggt   595
Thr Glu Val Glu Ile Ser Thr Asp Ser Leu Ser Ile Ser Gln Pro Gly
150                 155                 160                 165

tct tat ccg acg atg ttg gcg ttg tcg ggg cag ctt gat ggg gtg gcg   643
Ser Tyr Pro Thr Met Leu Ala Leu Ser Gly Gln Leu Asp Gly Val Ala
                170                 175                 180

cag cat ttg gat tcg cag cgt ttc ctt ctg cca gtc ctc agc gat aca   691
Gln His Leu Asp Ser Gln Arg Phe Leu Leu Pro Val Leu Ser Asp Thr
            185                 190                 195

act gat aca gaa gac acc gcc acc ccc acg acg atg att tac ccg ata   739
Thr Asp Thr Glu Asp Thr Ala Thr Pro Thr Thr Met Ile Tyr Pro Ile
        200                 205                 210

tca gcc cag acg aat gtg ttg ggt ggt gag acc ggc gag gcg ccg gaa   787
Ser Ala Gln Thr Asn Val Leu Gly Gly Glu Thr Gly Glu Ala Pro Glu
    215                 220                 225

gag ccg cct ttg ctg gtc agt tcc gac gcg ctt gcg ggc gag ttg gat   835
Glu Pro Pro Leu Leu Val Ser Ser Asp Ala Leu Ala Gly Glu Leu Asp
230                 235                 240                 245

gag ggc ggt cgt ttg caa aag ctt atc gac gcc tac ctc cag tct tca   883
Glu Gly Gly Arg Leu Gln Lys Leu Ile Asp Ala Tyr Leu Gln Ser Ser
                250                 255                 260

ccc gcc gtg cag caa gcc acg tgc ctt gct att gat ccg cag ctt ctt   931
Pro Ala Val Gln Gln Ala Thr Cys Leu Ala Ile Asp Pro Gln Leu Leu
            265                 270                 275

gat gtg gtg gat cgc atg acc ggc ggt tac acc gtg acc gat act cgt   979
Asp Val Val Asp Arg Met Thr Gly Gly Tyr Thr Val Thr Asp Thr Arg
        280                 285                 290

ccc agt acg gtg cgg cag aat cag cgg ctt cgt gag ttg tgg act gcc   1027
Pro Ser Thr Val Arg Gln Asn Gln Arg Leu Arg Glu Leu Trp Thr Ala
    295                 300                 305

gat aat caa ccc acc aat ggt gtc gcg ggc acg ggt gcg gaa aac gct   1075
Asp Asn Gln Pro Thr Asn Gly Val Ala Gly Thr Gly Ala Glu Asn Ala
310                 315                 320                 325

gcc att ttc ttg gag aaa ctc cga cag gcc aca gcc acc tcg tgc acc   1123
Ala Ile Phe Leu Glu Lys Leu Arg Gln Ala Thr Ala Thr Ser Cys Thr
                330                 335                 340

gtg gcg ttg ccg tgg gcg aat gct gat cta aat gca gtg agc caa acc   1171
Val Ala Leu Pro Trp Ala Asn Ala Asp Leu Asn Ala Val Ser Gln Thr
            345                 350                 355

ggt aat cag tgg ttg atg cgc gag gcg cta cag cga ggt gtc acc acc   1219
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```
Gly Asn Gln Trp Leu Met Arg Glu Ala Leu Gln Arg Gly Val Thr Thr
        360                 365                 370

ttt gaa gaa gtg ttg ggt gtt att ccg gaa tcc aat gtg gtg att cct   1267
Phe Glu Glu Val Leu Gly Val Ile Pro Glu Ser Asn Val Val Ile Pro
    375                 380                 385

gga aat ggt ttt gtg gag ccc tcc acc gtg ggt gat ctc gga tgg gcg   1315
Gly Asn Gly Phe Val Glu Pro Ser Thr Val Gly Asp Leu Gly Trp Ala
390                 395                 400                 405

gaa gta acg ctt aat ccg gat cag gcg tgg gag gtg cag tca gag gag   1363
Glu Val Thr Leu Asn Pro Asp Gln Ala Trp Glu Val Gln Ser Glu Glu
                410                 415                 420

ttg gtt gct gcc cct gat gcc aca gag caa agc gca ttg gat aac cct   1411
Leu Val Ala Ala Pro Asp Ala Thr Glu Gln Ser Ala Leu Asp Asn Pro
            425                 430                 435

aag cca acg cca ggc acg gtg acg ccg cca acc cct atg tca acg gtg   1459
Lys Pro Thr Pro Gly Thr Val Thr Pro Pro Thr Pro Met Ser Thr Val
        440                 445                 450

tcc gtg ttg gtt tct gat aac acg gtg tgg cgc aca acg agc gcg gat   1507
Ser Val Leu Val Ser Asp Asn Thr Val Trp Arg Thr Thr Ser Ala Asp
    455                 460                 465

cgg ttc cac tct ttg gct ccg gga ata act ggg gtg tcg tat cag gga   1555
Arg Phe His Ser Leu Ala Pro Gly Ile Thr Gly Val Ser Tyr Gln Gly
470                 475                 480                 485

tcg tta tcg gca acc ttg gct acc ttg gga caa aac cct gag act gtg   1603
Ser Leu Ser Ala Thr Leu Ala Thr Leu Gly Gln Asn Pro Glu Thr Val
                490                 495                 500

ggc tat tcc aat ccg gat tcg cgt tat gac tac gcc atg gat tct gag   1651
Gly Tyr Ser Asn Pro Asp Ser Arg Tyr Asp Tyr Ala Met Asp Ser Glu
            505                 510                 515

agc gcc cgc aat ctc acc ggc cag gcg gcg ctg cgc ttg acg gtg gac   1699
Ser Ala Arg Asn Leu Thr Gly Gln Ala Ala Leu Arg Leu Thr Val Asp
        520                 525                 530

aac ggc gat gaa gac tct ccc gtg ttg atc atg ccg agc gcg gtg ctg   1747
Asn Gly Asp Glu Asp Ser Pro Val Leu Ile Met Pro Ser Ala Val Leu
    535                 540                 545

ggc gcc gaa gac ggc gcg atg ttg ctt gag acc acc ggg gct ttg ctt   1795
Gly Ala Glu Asp Gly Ala Met Leu Leu Glu Thr Thr Gly Ala Leu Leu
550                 555                 560                 565

gcc gac ggc tcc gcc cga cct ttt tcc ctg cag caa tat gtc act gcc   1843
Ala Asp Gly Ser Ala Arg Pro Phe Ser Leu Gln Gln Tyr Val Thr Ala
                570                 575                 580

aat gcg gaa caa aga aat act ttg gcc aca gca aca act cca ccg gat   1891
Asn Ala Glu Gln Arg Asn Thr Leu Ala Thr Ala Thr Thr Pro Pro Asp
            585                 590                 595

gac act gct ttt ggt gca ccc tac gac gat cct gcg tca ttg acg gaa   1939
Asp Thr Ala Phe Gly Ala Pro Tyr Asp Asp Pro Ala Ser Leu Thr Glu
```

```
        600                 605                 610

acc gaa att ctg cga acc act cag cag gcg gag tac atc gat gat ctc   1987
Thr Glu Ile Leu Arg Thr Thr Gln Gln Ala Glu Tyr Ile Asp Asp Leu
    615                 620                 625

act ggc atc atg tcc aat gat ccc agc att gca ctg acc cgt tat ggg   2035
Thr Gly Ile Met Ser Asn Asp Pro Ser Ile Ala Leu Thr Arg Tyr Gly
630                 635                 640                 645

ttt aca gca ccg ctg cgg caa gat ctg ctg cgc gcg ttg agt atc agt   2083
Phe Thr Ala Pro Leu Arg Gln Asp Leu Leu Arg Ala Leu Ser Ile Ser
                650                 655                 660

gag cgt cgt tcg tta gct cgc cac acc cag gca acc tct gct gcc gat   2131
Glu Arg Arg Ser Leu Ala Arg His Thr Gln Ala Thr Ser Ala Ala Asp
            665                 670                 675

aaa tta ctt aat cgc aac cgc gat act ctg cag aag ctg cgt agc tct   2179
Lys Leu Leu Asn Arg Asn Arg Asp Thr Leu Gln Lys Leu Arg Ser Ser
        680                 685                 690

gtg gcg ttg ttg ccg ccg gga aat gtg tat acc cga acc tcg gaa tcg   2227
Val Ala Leu Leu Pro Pro Gly Asn Val Tyr Thr Arg Thr Ser Glu Ser
    695                 700                 705

tct ccg ttg ttg att gtg gcg caa aac ggt ttg cca ttg ccc gcg gag   2275
Ser Pro Leu Leu Ile Val Ala Gln Asn Gly Leu Pro Leu Pro Ala Glu
710                 715                 720                 725

act cag att ttg tat tcc gga aat cag gat gcg cac atc aat act ccg   2323
Thr Gln Ile Leu Tyr Ser Gly Asn Gln Asp Ala His Ile Asn Thr Pro
                730                 735                 740

ggt gtg gtt cgt att ccg gcg cag ggt tcc atc acc ttg cag atg act   2371
Gly Val Val Arg Ile Pro Ala Gln Gly Ser Ile Thr Leu Gln Met Thr
            745                 750                 755

gcg gat ttg ccc gat gac aat ctg cgc act gat ctc acg ttg tgg ttg   2419
Ala Asp Leu Pro Asp Asp Asn Leu Arg Thr Asp Leu Thr Leu Trp Leu
        760                 765                 770

gca tcc cca gat ggg gcc acc att agt gaa cct gtg gaa att act gtc   2467
Ala Ser Pro Asp Gly Ala Thr Ile Ser Glu Pro Val Glu Ile Thr Val
    775                 780                 785

cag cct cgc ccg aat ttg ggc acc acg ctg ttt ttc gtg gca gcg ggc   2515
Gln Pro Arg Pro Asn Leu Gly Thr Thr Leu Phe Phe Val Ala Ala Gly
790                 795                 800                 805

att ctg gca gta gga ggg ttg ttg ttt ata cgg aag aaa cga aac gtc   2563
Ile Leu Ala Val Gly Gly Leu Leu Phe Ile Arg Lys Lys Arg Asn Val
                810                 815                 820

gaa aag cgc tcg ccc ggt acg gga tcg ccc aaa ccg cca cca acc cac   2611
Glu Lys Arg Ser Pro Gly Thr Gly Ser Pro Lys Pro Pro Pro Thr His
            825                 830                 835

taacgtatcg catagttatt ttc                                        2634
```

<210> 2290
<211> 837
<212> PRT
<213> Corynebacterium glutamicum

<400> 2290
Val Ile Pro Asn Pro Asn Pro Asn Pro Lys Ala Lys Thr Leu Arg Leu
1 5 10 15

Val Ser Ala Leu Thr Ala Ile Thr Val Val Gly Phe Ser Ala Ser Pro
20 25 30

Val His Ala Leu Pro Ile Pro Leu Asp Pro Ser Asp Pro Ala Val Ser
35 40 45

Glu Leu Trp Val Asn Pro Asn Ala Arg Ala Asp Asp Glu Leu Ser Gly
50 55 60

Val Asp Val Glu Ile Ser Asp Phe Val Met Pro Asn Ser Asn Leu Thr
65 70 75 80

Val Gln Val Gly Glu Ser Phe Lys Ala Gln Val Arg Val Thr Asn Arg
85 90 95

Ser Ser Glu Thr Leu Ser Asn Ile Thr Leu Gln Ala Arg Arg Ala Glu
100 105 110

Ala Ser Phe Asp Met Ala Ser Ala Arg Val Ala Ala Thr Asp Asn Asn
115 120 125

Tyr Gly Tyr Phe Gly Ala Met Val Thr Leu Asp Asp Glu Leu Glu Pro
130 135 140

Gly Glu Ser Val Glu Thr Glu Val Glu Ile Ser Thr Asp Ser Leu Ser
145 150 155 160

Ile Ser Gln Pro Gly Ser Tyr Pro Thr Met Leu Ala Leu Ser Gly Gln
165 170 175

Leu Asp Gly Val Ala Gln His Leu Asp Ser Gln Arg Phe Leu Leu Pro
180 185 190

Val Leu Ser Asp Thr Thr Asp Thr Glu Asp Thr Ala Thr Pro Thr Thr
195 200 205

Met Ile Tyr Pro Ile Ser Ala Gln Thr Asn Val Leu Gly Gly Glu Thr
210 215 220

Gly Glu Ala Pro Glu Glu Pro Pro Leu Leu Val Ser Ser Asp Ala Leu
225 230 235 240

Ala Gly Glu Leu Asp Glu Gly Gly Arg Leu Gln Lys Leu Ile Asp Ala
245 250 255

Tyr Leu Gln Ser Ser Pro Ala Val Gln Gln Ala Thr Cys Leu Ala Ile
260 265 270

Asp Pro Gln Leu Leu Asp Val Val Asp Arg Met Thr Gly Gly Tyr Thr
275 280 285

Val Thr Asp Thr Arg Pro Ser Thr Val Arg Gln Asn Gln Arg Leu Arg

```
    290                 295                 300

Glu Leu Trp Thr Ala Asp Asn Gln Pro Thr Asn Gly Val Ala Gly Thr
305                 310                 315                 320

Gly Ala Glu Asn Ala Ala Ile Phe Leu Glu Lys Leu Arg Gln Ala Thr
                325                 330                 335

Ala Thr Ser Cys Thr Val Ala Leu Pro Trp Ala Asn Ala Asp Leu Asn
            340                 345                 350

Ala Val Ser Gln Thr Gly Asn Gln Trp Leu Met Arg Glu Ala Leu Gln
        355                 360                 365

Arg Gly Val Thr Thr Phe Glu Glu Val Leu Gly Val Ile Pro Glu Ser
    370                 375                 380

Asn Val Val Ile Pro Gly Asn Gly Phe Val Glu Pro Ser Thr Val Gly
385                 390                 395                 400

Asp Leu Gly Trp Ala Glu Val Thr Leu Asn Pro Asp Gln Ala Trp Glu
                405                 410                 415

Val Gln Ser Glu Glu Leu Val Ala Ala Pro Asp Ala Thr Glu Gln Ser
            420                 425                 430

Ala Leu Asp Asn Pro Lys Pro Thr Pro Gly Thr Val Thr Pro Pro Thr
        435                 440                 445

Pro Met Ser Thr Val Ser Val Leu Val Ser Asp Asn Thr Val Trp Arg
    450                 455                 460

Thr Thr Ser Ala Asp Arg Phe His Ser Leu Ala Pro Gly Ile Thr Gly
465                 470                 475                 480

Val Ser Tyr Gln Gly Ser Leu Ser Ala Thr Leu Ala Thr Leu Gly Gln
                485                 490                 495

Asn Pro Glu Thr Val Gly Tyr Ser Asn Pro Asp Ser Arg Tyr Asp Tyr
            500                 505                 510

Ala Met Asp Ser Glu Ser Ala Arg Asn Leu Thr Gly Gln Ala Ala Leu
        515                 520                 525

Arg Leu Thr Val Asp Asn Gly Asp Glu Asp Ser Pro Val Leu Ile Met
    530                 535                 540

Pro Ser Ala Val Leu Gly Ala Glu Asp Gly Ala Met Leu Leu Glu Thr
545                 550                 555                 560

Thr Gly Ala Leu Leu Ala Asp Gly Ser Ala Arg Pro Phe Ser Leu Gln
                565                 570                 575

Gln Tyr Val Thr Ala Asn Ala Glu Gln Arg Asn Thr Leu Ala Thr Ala
            580                 585                 590

Thr Thr Pro Pro Asp Asp Thr Ala Phe Gly Ala Pro Tyr Asp Asp Pro
        595                 600                 605

Ala Ser Leu Thr Glu Thr Glu Ile Leu Arg Thr Thr Gln Gln Ala Glu
    610                 615                 620
```

```
Tyr Ile Asp Asp Leu Thr Gly Ile Met Ser Asn Asp Pro Ser Ile Ala
625                 630                 635                 640

Leu Thr Arg Tyr Gly Phe Thr Ala Pro Leu Arg Gln Asp Leu Leu Arg
                645                 650                 655

Ala Leu Ser Ile Ser Glu Arg Arg Ser Leu Ala Arg His Thr Gln Ala
            660                 665                 670

Thr Ser Ala Ala Asp Lys Leu Leu Asn Arg Asn Arg Asp Thr Leu Gln
        675                 680                 685

Lys Leu Arg Ser Ser Val Ala Leu Leu Pro Pro Gly Asn Val Tyr Thr
    690                 695                 700

Arg Thr Ser Glu Ser Ser Pro Leu Leu Ile Val Ala Gln Asn Gly Leu
705                 710                 715                 720

Pro Leu Pro Ala Glu Thr Gln Ile Leu Tyr Ser Gly Asn Gln Asp Ala
                725                 730                 735

His Ile Asn Thr Pro Gly Val Val Arg Ile Pro Ala Gln Gly Ser Ile
            740                 745                 750

Thr Leu Gln Met Thr Ala Asp Leu Pro Asp Asp Asn Leu Arg Thr Asp
        755                 760                 765

Leu Thr Leu Trp Leu Ala Ser Pro Asp Gly Ala Thr Ile Ser Glu Pro
    770                 775                 780

Val Glu Ile Thr Val Gln Pro Arg Pro Asn Leu Gly Thr Thr Leu Phe
785                 790                 795                 800

Phe Val Ala Ala Gly Ile Leu Ala Val Gly Gly Leu Leu Phe Ile Arg
                805                 810                 815

Lys Lys Arg Asn Val Glu Lys Arg Ser Pro Gly Thr Gly Ser Pro Lys
            820                 825                 830

Pro Pro Pro Thr His
        835
```

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<210> 2291
<211> 1365
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1342)
<223> RXA01536

<400> 2291
agcatagatg acttgacact gttgcagcag gcggttttca cctggcctct taggatttgg 60

tcaaatggtt gcaacgacgc cagggaagga ggcgcacccc atg gca ttt gga ttt 115
                                              Met Ala Phe Gly Phe
                                                1   5

```
ttt agt aga cgt aag aaa aag aac aaa gac aaa aac ccg aat gaa aat   163
Phe Ser Arg Arg Lys Lys Lys Asn Lys Asp Lys Asn Pro Asn Glu Asn
                 10                  15                  20

tca gca gtg ccc gca cac tct gaa gat tca cct cag gag gtt ttt gag   211
Ser Ala Val Pro Ala His Ser Glu Asp Ser Pro Gln Glu Val Phe Glu
             25                  30                  35

ggt aat ggt cgt cag gta ggc gac ccc att gaa cag cag gtt gat cga   259
Gly Asn Gly Arg Gln Val Gly Asp Pro Ile Glu Gln Gln Val Asp Arg
         40                  45                  50

gat gct aaa ggt cgt ctc aca gcg gcg gat ttc ttg ccg gac gct gat   307
Asp Ala Lys Gly Arg Leu Thr Ala Ala Asp Phe Leu Pro Asp Ala Asp
     55                  60                  65

ctg cca cag ctg aat cgt tcg cgt gca aat atg ctg cgc cgt gaa ttg   355
Leu Pro Gln Leu Asn Arg Ser Arg Ala Asn Met Leu Arg Arg Glu Leu
 70                  75                  80                  85

gag tac cgt ttt tca ctc cag aat gcc cac att aat atc gat gga aac   403
Glu Tyr Arg Phe Ser Leu Gln Asn Ala His Ile Asn Ile Asp Gly Asn
                 90                  95                 100

acg gcc atg att cag cgt tca gat ggc ggg gca gca cat gtc tcg ttg   451
Thr Ala Met Ile Gln Arg Ser Asp Gly Gly Ala Ala His Val Ser Leu
            105                 110                 115

cgc acc ctc gcg atg aat gca gct ggc ctt gat aac ttt gat caa ctc   499
Arg Thr Leu Ala Met Asn Ala Ala Gly Leu Asp Asn Phe Asp Gln Leu
        120                 125                 130

cct gaa ctg gtg gaa agc ttc gtt cac ggc acg ctg gcc gat gca aca   547
Pro Glu Leu Val Glu Ser Phe Val His Gly Thr Leu Ala Asp Ala Thr
    135                 140                 145

tta aac gat ctt tct act gct gac ctg tat aaa gca ctg cgc ctt cgc   595
Leu Asn Asp Leu Ser Thr Ala Asp Leu Tyr Lys Ala Leu Arg Leu Arg
150                 155                 160                 165

ctg ctg cca aca cct ggc gaa ggc gac gat cta gtt gag cat gga ctc   643
Leu Leu Pro Thr Pro Gly Glu Gly Asp Asp Leu Val Glu His Gly Leu
                170                 175                 180

gac cgg gaa agc cag atc cgc gac gat tca atc ctg cgc acc ttc acc   691
Asp Arg Glu Ser Gln Ile Arg Asp Asp Ser Ile Leu Arg Thr Phe Thr
            185                 190                 195

tct gac atg tcg atc gcg ctg gtg ctc gat acc gag cat gcc atc cgc   739
Ser Asp Met Ser Ile Ala Leu Val Leu Asp Thr Glu His Ala Ile Arg
        200                 205                 210

atc cag cca ctc aaa gag ctc gag gag ttc gat gac ctc agc gcc cta   787
Ile Gln Pro Leu Lys Glu Leu Glu Glu Phe Asp Asp Leu Ser Ala Leu
    215                 220                 225

gag cgg gct gcg gac cgc aat acc tgg caa gag ctt tac gac gca aac   835
Glu Arg Ala Ala Asp Arg Asn Thr Trp Gln Glu Leu Tyr Asp Ala Asn
230                 235                 240                 245

gtt gac gct tcc ttc gtc gac gct gaa tca gac agc gaa ggg tca tca   883
```

```
Val Asp Ala Ser Phe Val Asp Ala Glu Ser Asp Ser Glu Gly Ser Ser
                250                 255                 260

ttt tgg gct ttc gaa tct aac tcg tac tac ttg ggt agt gca cca ctg   931
Phe Trp Ala Phe Glu Ser Asn Ser Tyr Tyr Leu Gly Ser Ala Pro Leu
            265                 270                 275

ttc ctc aac gat ctg ttg gca aag tgg gca cct gac ctg gac caa agt   979
Phe Leu Asn Asp Leu Leu Ala Lys Trp Ala Pro Asp Leu Asp Gln Ser
        280                 285                 290

gat ggc gtc atc ttt gct gtc cct gat cgt gat ctg ttg att gcg cgt   1027
Asp Gly Val Ile Phe Ala Val Pro Asp Arg Asp Leu Leu Ile Ala Arg
    295                 300                 305

cct gtg acc acc ggc gaa gat ctg atg aac gga atc acc gcg atg gtg   1075
Pro Val Thr Thr Gly Glu Asp Leu Met Asn Gly Ile Thr Ala Met Val
310                 315                 320                 325

agg atc gcg atg cgc ttt ggc ctc ggg aac ccg acg tcg ata agc ccg   1123
Arg Ile Ala Met Arg Phe Gly Leu Gly Asn Pro Thr Ser Ile Ser Pro
                330                 335                 340

cgc ctg cac ctg ctg cgc gac aac cag gtg acc acc ttc acc gac ttc   1171
Arg Leu His Leu Leu Arg Asp Asn Gln Val Thr Thr Phe Thr Asp Phe
            345                 350                 355

cgc gtc gtc tct cct gaa atg gaa gct gaa tgg gaa gac agc gcg ttt   1219
Arg Val Val Ser Pro Glu Met Glu Ala Glu Trp Glu Asp Ser Ala Phe
        360                 365                 370

gac gcg cca ccg gcc ggc gcg atc ggc att gag gtg cgc cca gat ccg   1267
Asp Ala Pro Pro Ala Gly Ala Ile Gly Ile Glu Val Arg Pro Asp Pro
    375                 380                 385

tat ctg atg gag cgc ctc caa cag ggc ggc ttt ggt gat ttc gga gat   1315
Tyr Leu Met Glu Arg Leu Gln Gln Gly Gly Phe Gly Asp Phe Gly Asp
390                 395                 400                 405

ttc ggc aag ccc cgc gat cta gat atg tagcgaaaaa gggaccttca         1362
Phe Gly Lys Pro Arg Asp Leu Asp Met
                410

ctt                                                               1365


<210> 2292
<211> 414
<212> PRT
<213> Corynebacterium glutamicum

<400> 2292
Met Ala Phe Gly Phe Phe Ser Arg Arg Lys Lys Lys Asn Lys Asp Lys
  1               5                  10                  15

Asn Pro Asn Glu Asn Ser Ala Val Pro Ala His Ser Glu Asp Ser Pro
             20                  25                  30

Gln Glu Val Phe Glu Gly Asn Gly Arg Gln Val Gly Asp Pro Ile Glu
         35                  40                  45
```

```
Gln Gln Val Asp Arg Asp Ala Lys Gly Arg Leu Thr Ala Ala Asp Phe
     50                  55                  60

Leu Pro Asp Ala Asp Leu Pro Gln Leu Asn Arg Ser Arg Ala Asn Met
 65                  70                  75                  80

Leu Arg Arg Glu Leu Glu Tyr Arg Phe Ser Leu Gln Asn Ala His Ile
                 85                  90                  95

Asn Ile Asp Gly Asn Thr Ala Met Ile Gln Arg Ser Asp Gly Gly Ala
            100                 105                 110

Ala His Val Ser Leu Arg Thr Leu Ala Met Asn Ala Ala Gly Leu Asp
        115                 120                 125

Asn Phe Asp Gln Leu Pro Glu Leu Val Glu Ser Phe Val His Gly Thr
    130                 135                 140

Leu Ala Asp Ala Thr Leu Asn Asp Leu Ser Thr Ala Asp Leu Tyr Lys
145                 150                 155                 160

Ala Leu Arg Leu Arg Leu Leu Pro Thr Pro Gly Glu Gly Asp Asp Leu
                165                 170                 175

Val Glu His Gly Leu Asp Arg Glu Ser Gln Ile Arg Asp Asp Ser Ile
            180                 185                 190

Leu Arg Thr Phe Thr Ser Asp Met Ser Ile Ala Leu Val Leu Asp Thr
        195                 200                 205

Glu His Ala Ile Arg Ile Gln Pro Leu Lys Glu Leu Glu Glu Phe Asp
    210                 215                 220

Asp Leu Ser Ala Leu Glu Arg Ala Ala Asp Arg Asn Thr Trp Gln Glu
225                 230                 235                 240

Leu Tyr Asp Ala Asn Val Asp Ala Ser Phe Val Asp Ala Glu Ser Asp
                245                 250                 255

Ser Glu Gly Ser Ser Phe Trp Ala Phe Glu Ser Asn Ser Tyr Tyr Leu
            260                 265                 270

Gly Ser Ala Pro Leu Phe Leu Asn Asp Leu Leu Ala Lys Trp Ala Pro
        275                 280                 285

Asp Leu Asp Gln Ser Asp Gly Val Ile Phe Ala Val Pro Asp Arg Asp
    290                 295                 300

Leu Leu Ile Ala Arg Pro Val Thr Thr Gly Glu Asp Leu Met Asn Gly
305                 310                 315                 320

Ile Thr Ala Met Val Arg Ile Ala Met Arg Phe Gly Leu Gly Asn Pro
                325                 330                 335

Thr Ser Ile Ser Pro Arg Leu His Leu Leu Arg Asp Asn Gln Val Thr
            340                 345                 350

Thr Phe Thr Asp Phe Arg Val Val Ser Pro Glu Met Glu Ala Glu Trp
        355                 360                 365

Glu Asp Ser Ala Phe Asp Ala Pro Pro Ala Gly Ala Ile Gly Ile Glu
```

```
    370                 375                 380

Val Arg Pro Asp Pro Tyr Leu Met Glu Arg Leu Gln Gln Gly Gly Phe
385                 390                 395                 400

Gly Asp Phe Gly Asp Phe Gly Lys Pro Arg Asp Leu Asp Met
                405                 410
```

<210> 2293
<211> 825
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(802)
<223> RXA01540

<400> 2293

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ccatgcagca ctatgggttc cctgatcccg atgcgtactt tgaccatgcc actatcgcag 60

gaaaacacca cacactcatc acaagaaagt aggtctcacc atg act ttt gca gaa   115
                                            Met Thr Phe Ala Glu
                                              1               5

ctt agc tca ccg cgt acc atc atc gct ttt aat ggc cgt gcc gaa tct   163
Leu Ser Ser Pro Arg Thr Ile Ile Ala Phe Asn Gly Arg Ala Glu Ser
                10                  15                  20

ggc aaa gat act gca gca cag tat ctc acc cat atg cac agt ttt cac   211
Gly Lys Asp Thr Ala Ala Gln Tyr Leu Thr His Met His Ser Phe His
            25                  30                  35

cgc atc gcc ttt gcc gat ggt gtc cgt gac gca ctc tat gcg ctt aac   259
Arg Ile Ala Phe Ala Asp Gly Val Arg Asp Ala Leu Tyr Ala Leu Asn
        40                  45                  50

cca ctg gtc tgt gtg gag cag gct atc acc aca cat ggt gcc att tat   307
Pro Leu Val Cys Val Glu Gln Ala Ile Thr Thr His Gly Ala Ile Tyr
    55                  60                  65

gac cgc gtg gcc act gtt gtg gac aca ctt ggt tgg gat acc gca aag   355
Asp Arg Val Ala Thr Val Val Asp Thr Leu Gly Trp Asp Thr Ala Lys
70                  75                  80                  85

caa atc ccc gac atc cgc gca ctt atg cag cgt att ggt acc gaa gct   403
Gln Ile Pro Asp Ile Arg Ala Leu Met Gln Arg Ile Gly Thr Glu Ala
                90                  95                  100

ggt tgg cgc atc cac ggc gag cat ctg tgg gtc aat ctt gct atc aaa   451
Gly Trp Arg Ile His Gly Glu His Leu Trp Val Asn Leu Ala Ile Lys
            105                 110                 115

aag atc aat gaa ctg ccc gct gac cac gcc att gtc atc act gat ttg   499
Lys Ile Asn Glu Leu Pro Ala Asp His Ala Ile Val Ile Thr Asp Leu
        120                 125                 130

cga ttc ccc aat gag att gag tgg ttg aac agc ctc aaa gcc aac ccg   547
Arg Phe Pro Asn Glu Ile Glu Trp Leu Asn Ser Leu Lys Ala Asn Pro
    135                 140                 145
```

```
atg aac acc att cag acc gtc aaa gtc atc cga cca gat cat gaa tcg   595
Met Asn Thr Ile Gln Thr Val Lys Val Ile Arg Pro Asp His Glu Ser
150                 155                 160                 165

acc ttg act gca gga tca ttc ggt act acc tca cat att tcc gaa agc   643
Thr Leu Thr Ala Gly Ser Phe Gly Thr Thr Ser His Ile Ser Glu Ser
                170                 175                 180

ttt aat ctc act acc gac act gtg ctc cgc aac gat ggc acc att gac   691
Phe Asn Leu Thr Thr Asp Thr Val Leu Arg Asn Asp Gly Thr Ile Asp
            185                 190                 195

gat ttg cac tca aag ctg gct gat ttt ttg agc act tcc ccg cag ccc   739
Asp Leu His Ser Lys Leu Ala Asp Phe Leu Ser Thr Ser Pro Gln Pro
        200                 205                 210

gtg ctc tct cgt aac gcc cct gta cca aaa cac aac gca ccg gca cca   787
Val Leu Ser Arg Asn Ala Pro Val Pro Lys His Asn Ala Pro Ala Pro
    215                 220                 225

acc act gat gcc atg taaataaccc ccgtatcaag atc                    825
Thr Thr Asp Ala Met
230
```

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<210> 2294
<211> 234
<212> PRT
<213> Corynebacterium glutamicum

<400> 2294

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Met Thr Phe Ala Glu Leu Ser Ser Pro Arg Thr Ile Ile Ala Phe Asn
  1               5                  10                  15

Gly Arg Ala Glu Ser Gly Lys Asp Thr Ala Ala Gln Tyr Leu Thr His
             20                  25                  30

Met His Ser Phe His Arg Ile Ala Phe Ala Asp Gly Val Arg Asp Ala
         35                  40                  45

Leu Tyr Ala Leu Asn Pro Leu Val Cys Val Glu Gln Ala Ile Thr Thr
     50                  55                  60

His Gly Ala Ile Tyr Asp Arg Val Ala Thr Val Val Asp Thr Leu Gly
 65                  70                  75                  80

Trp Asp Thr Ala Lys Gln Ile Pro Asp Ile Arg Ala Leu Met Gln Arg
                 85                  90                  95

Ile Gly Thr Glu Ala Gly Trp Arg Ile His Gly Glu His Leu Trp Val
            100                 105                 110

Asn Leu Ala Ile Lys Lys Ile Asn Glu Leu Pro Ala Asp His Ala Ile
        115                 120                 125

Val Ile Thr Asp Leu Arg Phe Pro Asn Glu Ile Glu Trp Leu Asn Ser
    130                 135                 140

Leu Lys Ala Asn Pro Met Asn Thr Ile Gln Thr Val Lys Val Ile Arg
145                 150                 155                 160
```

```
Pro Asp His Glu Ser Thr Leu Thr Ala Gly Ser Phe Gly Thr Thr Ser
                165                 170                 175

His Ile Ser Glu Ser Phe Asn Leu Thr Thr Asp Thr Val Leu Arg Asn
            180                 185                 190

Asp Gly Thr Ile Asp Asp Leu His Ser Lys Leu Ala Asp Phe Leu Ser
        195                 200                 205

Thr Ser Pro Gln Pro Val Leu Ser Arg Asn Ala Pro Val Pro Lys His
    210                 215                 220

Asn Ala Pro Ala Pro Thr Thr Asp Ala Met
225                 230


<210> 2295
<211> 2889
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2866)
<223> RXA01543

<400> 2295
gtgctttagc caaggtgagg catcaagaga agcaacagcg tcgttaccgt ttttttggtg 60

ggggcgctgt tgttgtagtt aaagaaagag cggtgggaaa atg agt ttg aaa caa   115
                                            Met Ser Leu Lys Gln
                                              1               5

gcc att atc gtg cgc aat gaa tat acg att aag cag gca aat ggc aaa   163
Ala Ile Ile Val Arg Asn Glu Tyr Thr Ile Lys Gln Ala Asn Gly Lys
                10                  15                  20

ggt tca cga gga tca tcg cca ggt aaa tat atc tct ggc tat atg gca   211
Gly Ser Arg Gly Ser Ser Pro Gly Lys Tyr Ile Ser Gly Tyr Met Ala
            25                  30                  35

cgc agc gat gcg gta gaa gca gta gca cct att gtg cgc aat aaa tta   259
Arg Ser Asp Ala Val Glu Ala Val Ala Pro Ile Val Arg Asn Lys Leu
        40                  45                  50

gat gat ttc atc atg cgg tat atg gca cgt gat agt gcc gtg gag cag   307
Asp Asp Phe Ile Met Arg Tyr Met Ala Arg Asp Ser Ala Val Glu Gln
    55                  60                  65

ctc acc acg gac agt aac gca gac tat gac cag caa cct gaa atg aac   355
Leu Thr Thr Asp Ser Asn Ala Asp Tyr Asp Gln Gln Pro Glu Met Asn
70                  75                  80                  85

tct cgt cgt ggc cgg caa ggt cgc cgc gcg acc ttg aaa caa cgt cgt   403
Ser Arg Arg Gly Arg Gln Gly Arg Arg Ala Thr Leu Lys Gln Arg Arg
                90                  95                  100

gca gaa cgc agc gcc cgg cga gca gca ttg cga gcg ggc gtg aat aca   451
Ala Glu Arg Ser Ala Arg Arg Ala Ala Leu Arg Ala Gly Val Asn Thr
            105                 110                 115
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gac tcc gac acc acc aac cca tca caa cct gtg cac ccg agg gaa ctc   499
Asp Ser Asp Thr Thr Asn Pro Ser Gln Pro Val His Pro Arg Glu Leu
        120                 125                 130

gcg gaa ttt act acc cag gat ggg cag cgc gtt cat gat ctc atg ctg   547
Ala Glu Phe Thr Thr Gln Asp Gly Gln Arg Val His Asp Leu Met Leu
    135                 140                 145

agg gct cag ggt aat ggg gga gtg gcc ttt ggg tat ggc gat gtc tcg   595
Arg Ala Gln Gly Asn Gly Gly Val Ala Phe Gly Tyr Gly Asp Val Ser
150                 155                 160                 165

ctg tca cat gat gat ctt cat gca gca agt aat aac gtc caa gag ctc   643
Leu Ser His Asp Asp Leu His Ala Ala Ser Asn Asn Val Gln Glu Leu
                170                 175                 180

tat gaa aat agg cat acc gtg atg aaa gtg gtc cta tct ttt acc cag   691
Tyr Glu Asn Arg His Thr Val Met Lys Val Val Leu Ser Phe Thr Gln
            185                 190                 195

gat tac ctg acc gcg cat ggc ctt att cca gag gat ctc gat att aag   739
Asp Tyr Leu Thr Ala His Gly Leu Ile Pro Glu Asp Leu Asp Ile Lys
        200                 205                 210

cgt gct ggt gat tat cgc ggc cag gtt gac caa atg aag cta cgc atg   787
Arg Ala Gly Asp Tyr Arg Gly Gln Val Asp Gln Met Lys Leu Arg Met
    215                 220                 225

gct gtc atg cat ggt gtg gat cgt cta gcc cag cgt cat tat gat gat   835
Ala Val Met His Gly Val Asp Arg Leu Ala Gln Arg His Tyr Asp Asp
230                 235                 240                 245

ttg cgc tat gtc ggc gtg att cag gtt gat acg aag cat gtg cac gcc   883
Leu Arg Tyr Val Gly Val Ile Gln Val Asp Thr Lys His Val His Ala
                250                 255                 260

cac ttg acc atg gtg gat gct ggt tat gga cac cgg gct gct gat ggt   931
His Leu Thr Met Val Asp Ala Gly Tyr Gly His Arg Ala Ala Asp Gly
            265                 270                 275

acg caa aaa ggc aaa atc aat aag cca ggt aag gct att ttg cgg cgt   979
Thr Gln Lys Gly Lys Ile Asn Lys Pro Gly Lys Ala Ile Leu Arg Arg
        280                 285                 290

ggt att gac gcc tgg ctt gat cag cat cag cat atg gcg cac ttg tca  1027
Gly Ile Asp Ala Trp Leu Asp Gln His Gln His Met Ala His Leu Ser
    295                 300                 305

gca gca gtg ggg tat gaa aaa cgc aat gtc acc agc tac gtc aag cgc  1075
Ala Ala Val Gly Tyr Glu Lys Arg Asn Val Thr Ser Tyr Val Lys Arg
310                 315                 320                 325

tgg gcg ttt cat cag ctc acc caa gaa agt gct gcg caa ttt gtg gtc  1123
Trp Ala Phe His Gln Leu Thr Gln Glu Ser Ala Ala Gln Phe Val Val
                330                 335                 340

gct tgt ttg cca gag gat aag cga ctg tgg cgt gca tcg acc aat gcc  1171
Ala Cys Leu Pro Glu Asp Lys Arg Leu Trp Arg Ala Ser Thr Asn Ala
            345                 350                 355
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aag gaa atg gat aag ccg aat aga tta gtg cgc gag ttg gtg gag gcg   1219
Lys Glu Met Asp Lys Pro Asn Arg Leu Val Arg Glu Leu Val Glu Ala
        360                 365                 370

cga ctt ggt gag act gat tca ccg atg ccg gca gca ctg tcg cag gtc   1267
Arg Leu Gly Glu Thr Asp Ser Pro Met Pro Ala Ala Leu Ser Gln Val
    375                 380                 385

tat cag tat gcg caa aaa cgc cgc gtt aaa gaa ggt tta agc aag cag   1315
Tyr Gln Tyr Ala Gln Lys Arg Arg Val Lys Glu Gly Leu Ser Lys Gln
390                 395                 400                 405

gac acc cag cgt ttg att gat aat ggc cgc gaa aag atc att gag cag   1363
Asp Thr Gln Arg Leu Ile Asp Asn Gly Arg Glu Lys Ile Ile Glu Gln
                410                 415                 420

gcc atg aac ggt gtc tac agt gtc cta tcc gcg att tcc gat gag caa   1411
Ala Met Asn Gly Val Tyr Ser Val Leu Ser Ala Ile Ser Asp Glu Gln
            425                 430                 435

cgc gat gtc tct acg gcc atg ttg aca gtc atg cgt caa gac tat gag   1459
Arg Asp Val Ser Thr Ala Met Leu Thr Val Met Arg Gln Asp Tyr Glu
        440                 445                 450

gat ttg ctc gat ggt att gcg cgg aag aag agc aag gat cta gac gag   1507
Asp Leu Leu Asp Gly Ile Ala Arg Lys Lys Ser Lys Asp Leu Asp Glu
    455                 460                 465

cag ggt agt agt gga tca caa gag gtg ggg aaa gaa gag cct gag cca   1555
Gln Gly Ser Ser Gly Ser Gln Glu Val Gly Lys Glu Glu Pro Glu Pro
470                 475                 480                 485

agt att gag gaa ttt ggg ctg cgt ttg cgg tcg tat tca gca cgc ttg   1603
Ser Ile Glu Glu Phe Gly Leu Arg Leu Arg Ser Tyr Ser Ala Arg Leu
                490                 495                 500

aat cat cac cga gaa caa cga gaa gcc ttt gcc gtg aaa aaa cgc tcg   1651
Asn His His Arg Glu Gln Arg Glu Ala Phe Ala Val Lys Lys Arg Ser
            505                 510                 515

tgg gag gac gct aac tct caa ggt ttg gct gat ccc acc tca cag gta   1699
Trp Glu Asp Ala Asn Ser Gln Gly Leu Ala Asp Pro Thr Ser Gln Val
        520                 525                 530

atg tgg agt ttt tat gac act gag gag cag tat cat gcg atg tgc caa   1747
Met Trp Ser Phe Tyr Asp Thr Glu Glu Gln Tyr His Ala Met Cys Gln
    535                 540                 545

tcc aag tac cag cac ttt ttg acc ttt gcc cca cct gtc ggt cag tgg   1795
Ser Lys Tyr Gln His Phe Leu Thr Phe Ala Pro Pro Val Gly Gln Trp
550                 555                 560                 565

gag aag caa tgg gct gag gtt gct gat tac ggt aaa agg gtt gtg ggt   1843
Glu Lys Gln Trp Ala Glu Val Ala Asp Tyr Gly Lys Arg Val Val Gly
                570                 575                 580

ctg cgt gca ctg cgg gca gat cgt tct ttg gca cgc atg agc gat gaa   1891
Leu Arg Ala Leu Arg Ala Asp Arg Ser Leu Ala Arg Met Ser Asp Glu
            585                 590                 595

cgt gca gct gaa gct ttg ggt cgg caa ctt tat gac caa ccc ggt ggt   1939
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Arg Ala Ala Glu Ala Leu Gly Arg Gln Leu Tyr Asp Gln Pro Gly Gly
        600                 605                 610

ggg tta ttg gct cga aca ggc gct gag ggt aaa gct ggg cgt gcg gtc   1987
Gly Leu Leu Ala Arg Thr Gly Ala Glu Gly Lys Ala Gly Arg Ala Val
    615                 620                 625

ctg gat ggc cga att gag cgc atg atg gtg acc tat cag caa aaa att   2035
Leu Asp Gly Arg Ile Glu Arg Met Met Val Thr Tyr Gln Gln Lys Ile
630                 635                 640                 645

gat gat ttg cga cga gaa tgg gca cag ctc ggt gca cgt tta gag gtt   2083
Asp Asp Leu Arg Arg Glu Trp Ala Gln Leu Gly Ala Arg Leu Glu Val
                650                 655                 660

gaa ggt gat gct gta ttg atg gat gca gca gat cta cgt gaa tct ggg   2131
Glu Gly Asp Ala Val Leu Met Asp Ala Ala Asp Leu Arg Glu Ser Gly
            665                 670                 675

gga gag ggt gca gat gaa cgc cag ata cag cag caa aca att gag ttg   2179
Gly Glu Gly Ala Asp Glu Arg Gln Ile Gln Gln Gln Thr Ile Glu Leu
        680                 685                 690

ccg gtc gct gat gta tct gat tct gtg cgc aca tac ctt gac gaa gag   2227
Pro Val Ala Asp Val Ser Asp Ser Val Arg Thr Tyr Leu Asp Glu Glu
    695                 700                 705

tta cgt gat agt cgt gat gtg agc gct cat gat cca gtg cac acc ttg   2275
Leu Arg Asp Ser Arg Asp Val Ser Ala His Asp Pro Val His Thr Leu
710                 715                 720                 725

cgt ggc agg ttt cag gtc gtg ttt cga ccg gag cat gat ttt gag cag   2323
Arg Gly Arg Phe Gln Val Val Phe Arg Pro Glu His Asp Phe Glu Gln
                730                 735                 740

gtg ggt ggc cct gac ctg cgc gat ctt cac tat gcc tgg ttt agc gat   2371
Val Gly Gly Pro Asp Leu Arg Asp Leu His Tyr Ala Trp Phe Ser Asp
            745                 750                 755

cag aag gtc agt cag ccc att gtg tgt agt tac ggt gag tta gtc acc   2419
Gln Lys Val Ser Gln Pro Ile Val Cys Ser Tyr Gly Glu Leu Val Thr
        760                 765                 770

cag cga cgt tat gct ttt gaa cgc gct cgg gag tgg atg atc agt tcg   2467
Gln Arg Arg Tyr Ala Phe Glu Arg Ala Arg Glu Trp Met Ile Ser Ser
    775                 780                 785

cag cag gaa cca gaa gca gtg gca gaa gag ctt gat cat gcc ggc gcg   2515
Gln Gln Glu Pro Glu Ala Val Ala Glu Glu Leu Asp His Ala Gly Ala
790                 795                 800                 805

gac ata act cgc atg gaa gca acc agt agt gag gta tcc cgt aca ggt   2563
Asp Ile Thr Arg Met Glu Ala Thr Ser Ser Glu Val Ser Arg Thr Gly
                810                 815                 820

att ttg cgt agt gcc atg ctt gcc aga att aga gag cag gcg cga caa   2611
Ile Leu Arg Ser Ala Met Leu Ala Arg Ile Arg Glu Gln Ala Arg Gln
            825                 830                 835

cgc gct cag cgt gca gcg gaa gag cag gct cgt cgt gag cgt gag ttg   2659
Arg Ala Gln Arg Ala Ala Glu Glu Gln Ala Arg Arg Glu Arg Glu Leu
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        840                 845                 850

gta gca cag cga caa caa gaa att gat cag gag acc acg caa cca gcg   2707
Val Ala Gln Arg Gln Gln Glu Ile Asp Gln Glu Thr Thr Gln Pro Ala
    855                 860                 865

ttc gag gtg gtg caa cga cat gta caa ccg gag tcg gtg cag att aag   2755
Phe Glu Val Val Gln Arg His Val Gln Pro Glu Ser Val Gln Ile Lys
870                 875                 880                 885

cgg ggt aga aca gtt gcg cta gat aag cga gtg cag cca ctg att cgt   2803
Arg Gly Arg Thr Val Ala Leu Asp Lys Arg Val Gln Pro Leu Ile Arg
                890                 895                 900

gat gct gtg gat cga gct gtg ctg gat tca cag ctg cgg agt acc cgt   2851
Asp Ala Val Asp Arg Ala Val Leu Asp Ser Gln Leu Arg Ser Thr Arg
            905                 910                 915

gat ggt gga ttg ggg taggcggttg attaaaaaaa aag                    2889
Asp Gly Gly Leu Gly
        920
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<210> 2296
<211> 922
<212> PRT
<213> Corynebacterium glutamicum

<400> 2296

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Met Ser Leu Lys Gln Ala Ile Ile Val Arg Asn Glu Tyr Thr Ile Lys
  1               5                  10                  15

Gln Ala Asn Gly Lys Gly Ser Arg Gly Ser Ser Pro Gly Lys Tyr Ile
             20                  25                  30

Ser Gly Tyr Met Ala Arg Ser Asp Ala Val Glu Ala Val Ala Pro Ile
         35                  40                  45

Val Arg Asn Lys Leu Asp Asp Phe Ile Met Arg Tyr Met Ala Arg Asp
     50                  55                  60

Ser Ala Val Glu Gln Leu Thr Thr Asp Ser Asn Ala Asp Tyr Asp Gln
 65                  70                  75                  80

Gln Pro Glu Met Asn Ser Arg Arg Gly Arg Gln Gly Arg Arg Ala Thr
                 85                  90                  95

Leu Lys Gln Arg Arg Ala Glu Arg Ser Ala Arg Arg Ala Ala Leu Arg
            100                 105                 110

Ala Gly Val Asn Thr Asp Ser Asp Thr Thr Asn Pro Ser Gln Pro Val
        115                 120                 125

His Pro Arg Glu Leu Ala Glu Phe Thr Thr Gln Asp Gly Gln Arg Val
    130                 135                 140

His Asp Leu Met Leu Arg Ala Gln Gly Asn Gly Gly Val Ala Phe Gly
145                 150                 155                 160

Tyr Gly Asp Val Ser Leu Ser His Asp Asp Leu His Ala Ala Ser Asn
                165                 170                 175
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Asn Val Gln Glu Leu Tyr Glu Asn Arg His Thr Val Met Lys Val Val
180 185 190

Leu Ser Phe Thr Gln Asp Tyr Leu Thr Ala His Gly Leu Ile Pro Glu
195 200 205

Asp Leu Asp Ile Lys Arg Ala Gly Asp Tyr Arg Gly Gln Val Asp Gln
210 215 220

Met Lys Leu Arg Met Ala Val Met His Gly Val Asp Arg Leu Ala Gln
225 230 235 240

Arg His Tyr Asp Asp Leu Arg Tyr Val Gly Val Ile Gln Val Asp Thr
245 250 255

Lys His Val His Ala His Leu Thr Met Val Asp Ala Gly Tyr Gly His
260 265 270

Arg Ala Ala Asp Gly Thr Gln Lys Gly Lys Ile Asn Lys Pro Gly Lys
275 280 285

Ala Ile Leu Arg Arg Gly Ile Asp Ala Trp Leu Asp Gln His Gln His
290 295 300

Met Ala His Leu Ser Ala Ala Val Gly Tyr Glu Lys Arg Asn Val Thr
305 310 315 320

Ser Tyr Val Lys Arg Trp Ala Phe His Gln Leu Thr Gln Glu Ser Ala
325 330 335

Ala Gln Phe Val Val Ala Cys Leu Pro Glu Asp Lys Arg Leu Trp Arg
340 345 350

Ala Ser Thr Asn Ala Lys Glu Met Asp Lys Pro Asn Arg Leu Val Arg
355 360 365

Glu Leu Val Glu Ala Arg Leu Gly Glu Thr Asp Ser Pro Met Pro Ala
370 375 380

Ala Leu Ser Gln Val Tyr Gln Tyr Ala Gln Lys Arg Arg Val Lys Glu
385 390 395 400

Gly Leu Ser Lys Gln Asp Thr Gln Arg Leu Ile Asp Asn Gly Arg Glu
405 410 415

Lys Ile Ile Glu Gln Ala Met Asn Gly Val Tyr Ser Val Leu Ser Ala
420 425 430

Ile Ser Asp Glu Gln Arg Asp Val Ser Thr Ala Met Leu Thr Val Met
435 440 445

Arg Gln Asp Tyr Glu Asp Leu Leu Asp Gly Ile Ala Arg Lys Lys Ser
450 455 460

Lys Asp Leu Asp Glu Gln Gly Ser Ser Gly Ser Gln Glu Val Gly Lys
465 470 475 480

Glu Glu Pro Glu Pro Ser Ile Glu Glu Phe Gly Leu Arg Leu Arg Ser
485 490 495

Tyr Ser Ala Arg Leu Asn His His Arg Glu Gln Arg Glu Ala Phe Ala
500 505 510

Val Lys Lys Arg Ser Trp Glu Asp Ala Asn Ser Gln Gly Leu Ala Asp
515 520 525

Pro Thr Ser Gln Val Met Trp Ser Phe Tyr Asp Thr Glu Glu Gln Tyr
530 535 540

His Ala Met Cys Gln Ser Lys Tyr Gln His Phe Leu Thr Phe Ala Pro
545 550 555 560

Pro Val Gly Gln Trp Glu Lys Gln Trp Ala Glu Val Ala Asp Tyr Gly
565 570 575

Lys Arg Val Val Gly Leu Arg Ala Leu Arg Ala Asp Arg Ser Leu Ala
580 585 590

Arg Met Ser Asp Glu Arg Ala Ala Glu Ala Leu Gly Arg Gln Leu Tyr
595 600 605

Asp Gln Pro Gly Gly Gly Leu Leu Ala Arg Thr Gly Ala Glu Gly Lys
610 615 620

Ala Gly Arg Ala Val Leu Asp Gly Arg Ile Glu Arg Met Met Val Thr
625 630 635 640

Tyr Gln Gln Lys Ile Asp Asp Leu Arg Arg Glu Trp Ala Gln Leu Gly
645 650 655

Ala Arg Leu Glu Val Glu Gly Asp Ala Val Leu Met Asp Ala Ala Asp
660 665 670

Leu Arg Glu Ser Gly Gly Glu Gly Ala Asp Glu Arg Gln Ile Gln Gln
675 680 685

Gln Thr Ile Glu Leu Pro Val Ala Asp Val Ser Asp Ser Val Arg Thr
690 695 700

Tyr Leu Asp Glu Glu Leu Arg Asp Ser Arg Asp Val Ser Ala His Asp
705 710 715 720

Pro Val His Thr Leu Arg Gly Arg Phe Gln Val Val Phe Arg Pro Glu
725 730 735

His Asp Phe Glu Gln Val Gly Gly Pro Asp Leu Arg Asp Leu His Tyr
740 745 750

Ala Trp Phe Ser Asp Gln Lys Val Ser Gln Pro Ile Val Cys Ser Tyr
755 760 765

Gly Glu Leu Val Thr Gln Arg Arg Tyr Ala Phe Glu Arg Ala Arg Glu
770 775 780

Trp Met Ile Ser Ser Gln Gln Glu Pro Glu Ala Val Ala Glu Glu Leu
785 790 795 800

Asp His Ala Gly Ala Asp Ile Thr Arg Met Glu Ala Thr Ser Ser Glu
805 810 815

Val Ser Arg Thr Gly Ile Leu Arg Ser Ala Met Leu Ala Arg Ile Arg

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            820                 825                 830

Glu Gln Ala Arg Gln Arg Ala Gln Arg Ala Ala Glu Glu Gln Ala Arg
        835                 840                 845

Arg Glu Arg Glu Leu Val Ala Gln Arg Gln Gln Glu Ile Asp Gln Glu
    850                 855                 860

Thr Thr Gln Pro Ala Phe Glu Val Val Gln Arg His Val Gln Pro Glu
865                 870                 875                 880

Ser Val Gln Ile Lys Arg Gly Arg Thr Val Ala Leu Asp Lys Arg Val
                885                 890                 895

Gln Pro Leu Ile Arg Asp Ala Val Asp Arg Ala Val Leu Asp Ser Gln
            900                 905                 910

Leu Arg Ser Thr Arg Asp Gly Gly Leu Gly
        915                 920


<210> 2297
<211> 723
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(700)
<223> RXA01544

<400> 2297
ctagatctat aacgaggatc ggcgctactt taagcatgtt tgtgctgttg gcgccgattt 60

tttcatagct gtacacacat aaggcaacag gagaaataca gtg aaa ctt gac gac   115
                                            Val Lys Leu Asp Asp
                                              1               5

gct atg gtc atg atc gaa cag cgc ctg gtc aaa ggt cgc ggc gca acc   163
Ala Met Val Met Ile Glu Gln Arg Leu Val Lys Gly Arg Gly Ala Thr
                 10                  15                  20

aag acg caa cta gca ccc tat gag cat atc cag cgc aat att gca gcc   211
Lys Thr Gln Leu Ala Pro Tyr Glu His Ile Gln Arg Asn Ile Ala Ala
             25                  30                  35

cga ggg ttg aga gcc gat gac gga ggc tcg tgc ttc ggt tat ggg gat   259
Arg Gly Leu Arg Ala Asp Asp Gly Gly Ser Cys Phe Gly Tyr Gly Asp
         40                  45                  50

gcg tcg ctg agt aat gac gat gta gca act gct gca gaa gat att cag   307
Ala Ser Leu Ser Asn Asp Asp Val Ala Thr Ala Ala Glu Asp Ile Gln
     55                  60                  65

gat ttg ttt gcg tgc ggg cat acg gtt atc tca gcg att gtc gtt ttt   355
Asp Leu Phe Ala Cys Gly His Thr Val Ile Ser Ala Ile Val Val Phe
 70                  75                  80                  85

gat aag agc tat ctc agt gag cat gga atc atg agc ttt gat ccg aac   403
Asp Lys Ser Tyr Leu Ser Glu His Gly Ile Met Ser Phe Asp Pro Asn
                 90                  95                 100
```

```
tat ttt ggt cag gat att tat gcg gac acc cat cca gag att gat ctc   451
Tyr Phe Gly Gln Asp Ile Tyr Ala Asp Thr His Pro Glu Ile Asp Leu
            105                 110                 115

atg gaa ttg cgt tta gcc gtg atg aat ggg ctc ttg ggg ctt gag gga   499
Met Glu Leu Arg Leu Ala Val Met Asn Gly Leu Leu Gly Leu Glu Gly
        120                 125                 130

acg ttt ttt gag gat atg cgt tat gtc gca tct atc gag gtg agc cgg   547
Thr Phe Phe Glu Asp Met Arg Tyr Val Ala Ser Ile Glu Val Ser Arg
    135                 140                 145

agc tat gtc tat gcg cac ata atg atg gcg gat gca ggc gtt gac gat   595
Ser Tyr Val Tyr Ala His Ile Met Met Ala Asp Ala Gly Val Asp Asp
150                 155                 160                 165

gca cgc ggt aat gca cag gtg aag att acg gac acc gaa cga gtg ctg   643
Ala Arg Gly Asn Ala Gln Val Lys Ile Thr Asp Thr Glu Arg Val Leu
                170                 175                 180

ttt aga cgt ggt gtt gaa tcc cgg ttt gtg gag caa gag gca cgc aac   691
Phe Arg Arg Gly Val Glu Ser Arg Phe Val Glu Gln Glu Ala Arg Asn
            185                 190                 195

gtc gtg ctt tagccaaggt gaggcatcaa gag                            723
Val Val Leu
        200
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<210> 2298
<211> 200
<212> PRT
<213> Corynebacterium glutamicum

<400> 2298

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Val Lys Leu Asp Asp Ala Met Val Met Ile Glu Gln Arg Leu Val Lys
  1               5                  10                  15

Gly Arg Gly Ala Thr Lys Thr Gln Leu Ala Pro Tyr Glu His Ile Gln
             20                  25                  30

Arg Asn Ile Ala Ala Arg Gly Leu Arg Ala Asp Asp Gly Gly Ser Cys
         35                  40                  45

Phe Gly Tyr Gly Asp Ala Ser Leu Ser Asn Asp Asp Val Ala Thr Ala
     50                  55                  60

Ala Glu Asp Ile Gln Asp Leu Phe Ala Cys Gly His Thr Val Ile Ser
 65                  70                  75                  80

Ala Ile Val Val Phe Asp Lys Ser Tyr Leu Ser Glu His Gly Ile Met
                 85                  90                  95

Ser Phe Asp Pro Asn Tyr Phe Gly Gln Asp Ile Tyr Ala Asp Thr His
            100                 105                 110

Pro Glu Ile Asp Leu Met Glu Leu Arg Leu Ala Val Met Asn Gly Leu
        115                 120                 125

Leu Gly Leu Glu Gly Thr Phe Phe Glu Asp Met Arg Tyr Val Ala Ser
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    130                 135                 140

Ile Glu Val Ser Arg Ser Tyr Val Tyr Ala His Ile Met Met Ala Asp
145                 150                 155                 160

Ala Gly Val Asp Asp Ala Arg Gly Asn Ala Gln Val Lys Ile Thr Asp
                165                 170                 175

Thr Glu Arg Val Leu Phe Arg Arg Gly Val Glu Ser Arg Phe Val Glu
            180                 185                 190

Gln Glu Ala Arg Asn Val Val Leu
        195                 200


<210> 2299
<211> 1374
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1351)
<223> RXA01545

<400> 2299
ataagaaccg acacgacgcc ctcaacgacg ctgttgcagc agctcgcaac tagctagtta 60

ccacgcctga cacacgatac gtagagaaaa gagaaatgat atg aag ctt gca ggt   115
                                            Met Lys Leu Ala Gly
                                              1               5

ttt aac acc aat tca ccc gca gcg cag cgg gtt gcc gaa cag ggt gaa   163
Phe Asn Thr Asn Ser Pro Ala Ala Gln Arg Val Ala Glu Gln Gly Glu
                10                  15                  20

aag gta cag ctc gat gca ccg gtg tac gcg gtg ttt acc cca gat gtt   211
Lys Val Gln Leu Asp Ala Pro Val Tyr Ala Val Phe Thr Pro Asp Val
            25                  30                  35

gtt gaa gtt gag ttt att ggc acg cag cat gag ccg gta ttg cac gtt   259
Val Glu Val Glu Phe Ile Gly Thr Gln His Glu Pro Val Leu His Val
        40                  45                  50

gag ggt gcc atc gac agc gtg act gca ttg tcg cag cta ccg tac gac   307
Glu Gly Ala Ile Asp Ser Val Thr Ala Leu Ser Gln Leu Pro Tyr Asp
    55                  60                  65

att caa aaa att acg ttt gat tca gaa aac caa cag cgt ttt agt gga   355
Ile Gln Lys Ile Thr Phe Asp Ser Glu Asn Gln Gln Arg Phe Ser Gly
70                  75                  80                  85

ttt tat aaa ttc agt cca cag cag cat aaa gag ctc att gat aaa ggt   403
Phe Tyr Lys Phe Ser Pro Gln Gln His Lys Glu Leu Ile Asp Lys Gly
                90                  95                  100

ctg tat cta gaa ggt ttc cag cca ccg cgc gag atg atg acg agc ctg   451
Leu Tyr Leu Glu Gly Phe Gln Pro Pro Arg Glu Met Met Thr Ser Leu
            105                 110                 115

ccg tgg gaa cta ccc atg aat gcc gat gtc act gtc gtg gca cca gag   499
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Pro Trp Glu Leu Pro Met Asn Ala Asp Val Thr Val Val Ala Pro Glu
        120                 125                 130

tcg cag gat gcg cca ccg att gtg ctt gtg ggc tta tct gag att cat   547
Ser Gln Asp Ala Pro Pro Ile Val Leu Val Gly Leu Ser Glu Ile His
    135                 140                 145

ggt gtg gat ttt agt caa gaa tcc tct ggc tat gag ctc acc agc atg   595
Gly Val Asp Phe Ser Gln Glu Ser Ser Gly Tyr Glu Leu Thr Ser Met
150                 155                 160                 165

ttt gag gac tac cgt agc cag cgt gaa gcg ggc gag gcg gac aag gat   643
Phe Glu Asp Tyr Arg Ser Gln Arg Glu Ala Gly Glu Ala Asp Lys Asp
                170                 175                 180

ttc tct gag tca att tct cgt gca gag att gaa ggc aaa gat att ttc   691
Phe Ser Glu Ser Ile Ser Arg Ala Glu Ile Glu Gly Lys Asp Ile Phe
            185                 190                 195

gct gat gct aac cgc acc cgt acc ggt gtc agt gca cat gca cag cgc   739
Ala Asp Ala Asn Arg Thr Arg Thr Gly Val Ser Ala His Ala Gln Arg
        200                 205                 210

ctt gag cag gag cga gcg ctg agc gca gca cag ttg atg gcg aaa ctt   787
Leu Glu Gln Glu Arg Ala Leu Ser Ala Ala Gln Leu Met Ala Lys Leu
    215                 220                 225

gct ggc att tcc ttc cag act gaa ccc gtg ctt gtt ggt gcg gaa gag   835
Ala Gly Ile Ser Phe Gln Thr Glu Pro Val Leu Val Gly Ala Glu Glu
230                 235                 240                 245

agc ttt gat gct gag caa ttc ctc gcc cat gat ctt gat gac acc gct   883
Ser Phe Asp Ala Glu Gln Phe Leu Ala His Asp Leu Asp Asp Thr Ala
                250                 255                 260

ggt atg agt gag tgg gag cgc gag gtt acc gag ttc tac aac gag aag   931
Gly Met Ser Glu Trp Glu Arg Glu Val Thr Glu Phe Tyr Asn Glu Lys
            265                 270                 275

att cgc gcc cag gag cct gtg gtg gag cgg gag gct gag cgg gat agc   979
Ile Arg Ala Gln Glu Pro Val Val Glu Arg Glu Ala Glu Arg Asp Ser
        280                 285                 290

gat att gag act gag gtt gat gca gca cca act gtc agt gct gca gag   1027
Asp Ile Glu Thr Glu Val Asp Ala Ala Pro Thr Val Ser Ala Ala Glu
    295                 300                 305

att aac gat gtt att cat gat ctt gat gag ctt gaa ttc gat gac gtg   1075
Ile Asn Asp Val Ile His Asp Leu Asp Glu Leu Glu Phe Asp Asp Val
310                 315                 320                 325

att gat ctt gat gca gat gat gtt gtc aat acc gcc gag gta gag gcg   1123
Ile Asp Leu Asp Ala Asp Asp Val Val Asn Thr Ala Glu Val Glu Ala
                330                 335                 340

cca gca agt gtc agt gct gca gag att tct gcg aca gag ctt gat ttt   1171
Pro Ala Ser Val Ser Ala Ala Glu Ile Ser Ala Thr Glu Leu Asp Phe
            345                 350                 355

gat cgc gag tca cgg gct aag acc gcg cag cga gaa gcc agc cga cgt   1219
Asp Arg Glu Ser Arg Ala Lys Thr Ala Gln Arg Glu Ala Ser Arg Arg
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        360                 365                 370

gtt gca cag aag att cag act caa gaa tct gtg cgt gag gca tat att   1267
Val Ala Gln Lys Ile Gln Thr Gln Glu Ser Val Arg Glu Ala Tyr Ile
    375                 380                 385

cgc gag caa aag cat ggc tat gac gca tca cct gcg gag ggg cgc aag   1315
Arg Glu Gln Lys His Gly Tyr Asp Ala Ser Pro Ala Glu Gly Arg Lys
390                 395                 400                 405

ttt gat gag aaa att gca gaa cgc ggg cta gat cta taacgaggat        1361
Phe Asp Glu Lys Ile Ala Glu Arg Gly Leu Asp Leu
                410                 415

cggcgctact tta                                                   1374
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<210> 2300
<211> 417
<212> PRT
<213> Corynebacterium glutamicum

<400> 2300

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Met Lys Leu Ala Gly Phe Asn Thr Asn Ser Pro Ala Ala Gln Arg Val
  1               5                  10                  15

Ala Glu Gln Gly Glu Lys Val Gln Leu Asp Ala Pro Val Tyr Ala Val
             20                  25                  30

Phe Thr Pro Asp Val Val Glu Val Glu Phe Ile Gly Thr Gln His Glu
         35                  40                  45

Pro Val Leu His Val Glu Gly Ala Ile Asp Ser Val Thr Ala Leu Ser
     50                  55                  60

Gln Leu Pro Tyr Asp Ile Gln Lys Ile Thr Phe Asp Ser Glu Asn Gln
 65                  70                  75                  80

Gln Arg Phe Ser Gly Phe Tyr Lys Phe Ser Pro Gln Gln His Lys Glu
                 85                  90                  95

Leu Ile Asp Lys Gly Leu Tyr Leu Glu Gly Phe Gln Pro Pro Arg Glu
            100                 105                 110

Met Met Thr Ser Leu Pro Trp Glu Leu Pro Met Asn Ala Asp Val Thr
        115                 120                 125

Val Val Ala Pro Glu Ser Gln Asp Ala Pro Pro Ile Val Leu Val Gly
    130                 135                 140

Leu Ser Glu Ile His Gly Val Asp Phe Ser Gln Glu Ser Ser Gly Tyr
145                 150                 155                 160

Glu Leu Thr Ser Met Phe Glu Asp Tyr Arg Ser Gln Arg Glu Ala Gly
                165                 170                 175

Glu Ala Asp Lys Asp Phe Ser Glu Ser Ile Ser Arg Ala Glu Ile Glu
            180                 185                 190

Gly Lys Asp Ile Phe Ala Asp Ala Asn Arg Thr Arg Thr Gly Val Ser
        195                 200                 205
```

```
Ala His Ala Gln Arg Leu Glu Gln Glu Arg Ala Leu Ser Ala Ala Gln
    210                 215                 220

Leu Met Ala Lys Leu Ala Gly Ile Ser Phe Gln Thr Glu Pro Val Leu
225                 230                 235                 240

Val Gly Ala Glu Glu Ser Phe Asp Ala Glu Gln Phe Leu Ala His Asp
                245                 250                 255

Leu Asp Asp Thr Ala Gly Met Ser Glu Trp Glu Arg Glu Val Thr Glu
            260                 265                 270

Phe Tyr Asn Glu Lys Ile Arg Ala Gln Glu Pro Val Val Glu Arg Glu
        275                 280                 285

Ala Glu Arg Asp Ser Asp Ile Glu Thr Glu Val Asp Ala Ala Pro Thr
    290                 295                 300

Val Ser Ala Ala Glu Ile Asn Asp Val Ile His Asp Leu Asp Glu Leu
305                 310                 315                 320

Glu Phe Asp Asp Val Ile Asp Leu Asp Ala Asp Asp Val Val Asn Thr
                325                 330                 335

Ala Glu Val Glu Ala Pro Ala Ser Val Ser Ala Ala Glu Ile Ser Ala
            340                 345                 350

Thr Glu Leu Asp Phe Asp Arg Glu Ser Arg Ala Lys Thr Ala Gln Arg
        355                 360                 365

Glu Ala Ser Arg Arg Val Ala Gln Lys Ile Gln Thr Gln Glu Ser Val
    370                 375                 380

Arg Glu Ala Tyr Ile Arg Glu Gln Lys His Gly Tyr Asp Ala Ser Pro
385                 390                 395                 400

Ala Glu Gly Arg Lys Phe Asp Glu Lys Ile Ala Glu Arg Gly Leu Asp
                405                 410                 415

Leu
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<210> 2301
<211> 819
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(796)
<223> RXA01546

<400> 2301
atagttagtt ggtgactagc tattgggggt tttgtctttt aatattataa aaagaaagtg 60

acaaacatac ttgcattaaa aaggaattga gataggcact atg gca cga gcg aaa 115
                                                Met Ala Arg Ala Lys
                                                  1   5

```
aat aag aaa cag cgt caa ttg cag cac gct cat gat gca gca cag gct   163
Asn Lys Lys Gln Arg Gln Leu Gln His Ala His Asp Ala Ala Gln Ala
                10                  15                  20

gag att gca gaa gcg gta gcg gtt aac acg gtt gaa cca att aat gca   211
Glu Ile Ala Glu Ala Val Ala Val Asn Thr Val Glu Pro Ile Asn Ala
            25                  30                  35

cgc acc ggt gga tgg cct tcg tgg gtc gat aag gtc tgg aag ctc act   259
Arg Thr Gly Gly Trp Pro Ser Trp Val Asp Lys Val Trp Lys Leu Thr
        40                  45                  50

ggt tca ctt ggt ggt tgg ttt gct ttc ctg gtt ttt gcc atc gcc gtg   307
Gly Ser Leu Gly Gly Trp Phe Ala Phe Leu Val Phe Ala Ile Ala Val
    55                  60                  65

tgg ccg gta gcg atc ctt gca gct ggc act gtg gtc acc atc atc ggt   355
Trp Pro Val Ala Ile Leu Ala Ala Gly Thr Val Val Thr Ile Ile Gly
70                  75                  80                  85

acg tgg gga gta tca gta ctg cca agt ctg gtt att tcc agc atc ggc   403
Thr Trp Gly Val Ser Val Leu Pro Ser Leu Val Ile Ser Ser Ile Gly
                90                  95                  100

gct tct gct ggt gtg att atc tcc act act gat ggg ttc ctc ttt agc   451
Ala Ser Ala Gly Val Ile Ile Ser Thr Thr Asp Gly Phe Leu Phe Ser
            105                 110                 115

tgg gtc atc ccg gtg ctg ttt ctc atg att gtg ctg gca ctg gtg gtc   499
Trp Val Ile Pro Val Leu Phe Leu Met Ile Val Leu Ala Leu Val Val
        120                 125                 130

atg aaa gtg ctc aat ctt att ttt ggt gca ttg tgg cgc ttc acc atg   547
Met Lys Val Leu Asn Leu Ile Phe Gly Ala Leu Trp Arg Phe Thr Met
    135                 140                 145

act ttg cga cag ggg tta tac gca ggt cgt gaa aag att tct cgc gac   595
Thr Leu Arg Gln Gly Leu Tyr Ala Gly Arg Glu Lys Ile Ser Arg Asp
150                 155                 160                 165

gac gcg aag cgc gca cga gca gaa aag aag ctg act aag cag cag gct   643
Asp Ala Lys Arg Ala Arg Ala Glu Lys Lys Leu Thr Lys Gln Gln Ala
                170                 175                 180

aaa gaa gcc aaa aag cag cgc aaa ctt gat gcc att tac tcg gct caa   691
Lys Glu Ala Lys Lys Gln Arg Lys Leu Asp Ala Ile Tyr Ser Ala Gln
            185                 190                 195

cag gct gaa gag act ctg gcg caa cag gca cag tct gag cca gaa gag   739
Gln Ala Glu Glu Thr Leu Ala Gln Gln Ala Gln Ser Glu Pro Glu Glu
        200                 205                 210

tca gac gat aag aac cga cac gac gcc ctc aac gac gct gtt gca gca   787
Ser Asp Asp Lys Asn Arg His Asp Ala Leu Asn Asp Ala Val Ala Ala
    215                 220                 225

gct cgc aac tagctagtta ccacgcctga cac                            819
Ala Arg Asn
230
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<210> 2302
<211> 232
<212> PRT
<213> Corynebacterium glutamicum

<400> 2302
Met Ala Arg Ala Lys Asn Lys Lys Gln Arg Gln Leu Gln His Ala His
1 5 10 15

Asp Ala Ala Gln Ala Glu Ile Ala Glu Ala Val Ala Val Asn Thr Val
20 25 30

Glu Pro Ile Asn Ala Arg Thr Gly Gly Trp Pro Ser Trp Val Asp Lys
35 40 45

Val Trp Lys Leu Thr Gly Ser Leu Gly Gly Trp Phe Ala Phe Leu Val
50 55 60

Phe Ala Ile Ala Val Trp Pro Val Ala Ile Leu Ala Ala Gly Thr Val
65 70 75 80

Val Thr Ile Ile Gly Thr Trp Gly Val Ser Val Leu Pro Ser Leu Val
85 90 95

Ile Ser Ser Ile Gly Ala Ser Ala Gly Val Ile Ile Ser Thr Thr Asp
100 105 110

Gly Phe Leu Phe Ser Trp Val Ile Pro Val Leu Phe Leu Met Ile Val
115 120 125

Leu Ala Leu Val Val Met Lys Val Leu Asn Leu Ile Phe Gly Ala Leu
130 135 140

Trp Arg Phe Thr Met Thr Leu Arg Gln Gly Leu Tyr Ala Gly Arg Glu
145 150 155 160

Lys Ile Ser Arg Asp Asp Ala Lys Arg Ala Arg Ala Glu Lys Lys Leu
165 170 175

Thr Lys Gln Gln Ala Lys Glu Ala Lys Lys Gln Arg Lys Leu Asp Ala
180 185 190

Ile Tyr Ser Ala Gln Gln Ala Glu Glu Thr Leu Ala Gln Gln Ala Gln
195 200 205

Ser Glu Pro Glu Glu Ser Asp Asp Lys Asn Arg His Asp Ala Leu Asn
210 215 220

Asp Ala Val Ala Ala Ala Arg Asn
225 230

<210> 2303
<211> 786
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(763)
<223> RXA01547

<400> 2303
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aaatgtagat aaccagagtg gtgtaactga ggacgagccg atg ttc gat cag gtc 115
Met Phe Asp Gln Val
1 5

aag cgc ttt ttt gtt cgc aat atc gtc atg atc att gcg ttg atc ttg 163
Lys Arg Phe Phe Val Arg Asn Ile Val Met Ile Ile Ala Leu Ile Leu
10 15 20

gca gtg gtg gtc att att gtt gcc acc agc acc tct gcg gat cga cat 211
Ala Val Val Val Ile Ile Val Ala Thr Ser Thr Ser Ala Asp Arg His
25 30 35

gct gta ctt aag cgt caa act ggt gag att atg gcc ttg caa cag gaa 259
Ala Val Leu Lys Arg Gln Thr Gly Glu Ile Met Ala Leu Gln Gln Glu
40 45 50

cgt gat gca tta aac agt aag ctt gag ggc caa ctt gag cag gtg gtg 307
Arg Asp Ala Leu Asn Ser Lys Leu Glu Gly Gln Leu Glu Gln Val Val
55 60 65

cgt gac gct acc ggt ggt atg gat att gaa cac aag gct gca gat gat 355
Arg Asp Ala Thr Gly Gly Met Asp Ile Glu His Lys Ala Ala Asp Asp
70 75 80 85

gct gtt gtt cga gaa ttt ttg tcc atg gcg ctg acg tgg gac agc gtg 403
Ala Val Val Arg Glu Phe Leu Ser Met Ala Leu Thr Trp Asp Ser Val
90 95 100

cgc gac tac ctt gat gtg cgc gag caa gtg atg cgg gtt tat gac ctg 451
Arg Asp Tyr Leu Asp Val Arg Glu Gln Val Met Arg Val Tyr Asp Leu
105 110 115

gat gaa gaa tca cag ttt atg tcg gtg ttt atg cct ggt gaa atg gcg 499
Asp Glu Glu Ser Gln Phe Met Ser Val Phe Met Pro Gly Glu Met Ala
120 125 130

ggc att gct cgc acc gat cca act ggc gaa gtg cac tat gcc tat gat 547
Gly Ile Ala Arg Thr Asp Pro Thr Gly Glu Val His Tyr Ala Tyr Asp
135 140 145

gca gat ctg tcc aac cgc ttt agc agc tta gaa tcc gtg gtt act cgc 595
Ala Asp Leu Ser Asn Arg Phe Ser Ser Leu Glu Ser Val Val Thr Arg
150 155 160 165

att aat ggt aca gag tac agc tat gta tcc acg gtg acg atg aag tcg 643
Ile Asn Gly Thr Glu Tyr Ser Tyr Val Ser Thr Val Thr Met Lys Ser
170 175 180

aag cgc tct ggt ggt gag gca gaa aca acc tct acc tca cgc ctt gcc 691
Lys Arg Ser Gly Gly Glu Ala Glu Thr Thr Ser Thr Ser Arg Leu Ala
185 190 195

tat gac gtg atc gac ggc aaa att cgt aac ctc gaa gca cgt act gtc 739
Tyr Asp Val Ile Asp Gly Lys Ile Arg Asn Leu Glu Ala Arg Thr Val
200 205 210

ccc ggt ggt gtg aaa tac tcg ggc taaaagtttc tggggcaacc ccc 786

Pro Gly Gly Val Lys Tyr Ser Gly
215 220

<210> 2304
<211> 221
<212> PRT
<213> Corynebacterium glutamicum

<400> 2304
Met Phe Asp Gln Val Lys Arg Phe Phe Val Arg Asn Ile Val Met Ile
1 5 10 15

Ile Ala Leu Ile Leu Ala Val Val Val Ile Ile Val Ala Thr Ser Thr
20 25 30

Ser Ala Asp Arg His Ala Val Leu Lys Arg Gln Thr Gly Glu Ile Met
35 40 45

Ala Leu Gln Gln Glu Arg Asp Ala Leu Asn Ser Lys Leu Glu Gly Gln
50 55 60

Leu Glu Gln Val Val Arg Asp Ala Thr Gly Gly Met Asp Ile Glu His
65 70 75 80

Lys Ala Ala Asp Asp Ala Val Val Arg Glu Phe Leu Ser Met Ala Leu
85 90 95

Thr Trp Asp Ser Val Arg Asp Tyr Leu Asp Val Arg Glu Gln Val Met
100 105 110

Arg Val Tyr Asp Leu Asp Glu Glu Ser Gln Phe Met Ser Val Phe Met
115 120 125

Pro Gly Glu Met Ala Gly Ile Ala Arg Thr Asp Pro Thr Gly Glu Val
130 135 140

His Tyr Ala Tyr Asp Ala Asp Leu Ser Asn Arg Phe Ser Ser Leu Glu
145 150 155 160

Ser Val Val Thr Arg Ile Asn Gly Thr Glu Tyr Ser Tyr Val Ser Thr
165 170 175

Val Thr Met Lys Ser Lys Arg Ser Gly Gly Glu Ala Glu Thr Thr Ser
180 185 190

Thr Ser Arg Leu Ala Tyr Asp Val Ile Asp Gly Lys Ile Arg Asn Leu
195 200 205

Glu Ala Arg Thr Val Pro Gly Gly Val Lys Tyr Ser Gly
210 215 220

<210> 2305
<211> 1131
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1108)

<223> RXA01548

<400> 2305

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agaaacttca ataacttagt aactttaaaa ggggtttaat atg gct gag aat aat   115
                                            Met Ala Glu Asn Asn
                                              1               5

ggc ggg tcg gat gac ctt aag ccc atc tct gtc gat ggg gtc gtc aat   163
Gly Gly Ser Asp Asp Leu Lys Pro Ile Ser Val Asp Gly Val Val Asn
                 10                  15                  20

ggg gaa gtg cgc agc gac aaa gaa aag cag gcg ttc gag aag att acc   211
Gly Glu Val Arg Ser Asp Lys Glu Lys Gln Ala Phe Glu Lys Ile Thr
             25                  30                  35

ggt gat gat ctg cgt cgt cgt gca gaa caa atc cgt aaa cgt cgt tta   259
Gly Asp Asp Leu Arg Arg Arg Ala Glu Gln Ile Arg Lys Arg Arg Leu
         40                  45                  50

gca aaa gcg caa gaa gat gca cgt aag cgt aag cca ttg ttt ggt ttg   307
Ala Lys Ala Gln Glu Asp Ala Arg Lys Arg Lys Pro Leu Phe Gly Leu
     55                  60                  65

ggt cgt atc gct gtc aca gta ctg gct ggc gcc gta ttt att ggt aca   355
Gly Arg Ile Ala Val Thr Val Leu Ala Gly Ala Val Phe Ile Gly Thr
 70                  75                  80                  85

acg ttg tgg atc agt acc acc tcg ggc ggc ttt gac gac aag gtg agt   403
Thr Leu Trp Ile Ser Thr Thr Ser Gly Gly Phe Asp Asp Lys Val Ser
                 90                  95                 100

gca aac aat gag cag att gtc act ctg cgt aat gaa gtc aac gac tta   451
Ala Asn Asn Glu Gln Ile Val Thr Leu Arg Asn Glu Val Asn Asp Leu
            105                 110                 115

aaa aac act gca gag aca atg ccc aaa aaa gag act ctt gct agt caa   499
Lys Asn Thr Ala Glu Thr Met Pro Lys Lys Glu Thr Leu Ala Ser Gln
        120                 125                 130

ttt gac gca gca acc tca cgt gca cag aat gtg gct gac tta cag aat   547
Phe Asp Ala Ala Thr Ser Arg Ala Gln Asn Val Ala Asp Leu Gln Asn
    135                 140                 145

cag tta gcc ggc att att acc agt gtt gat gat gat gcc gcg acc gag   595
Gln Leu Ala Gly Ile Ile Thr Ser Val Asp Asp Asp Ala Ala Thr Glu
150                 155                 160                 165

cag ttc aag aca att gtt gat gag ctg aaa ccg aaa ttc acg gtc tct   643
Gln Phe Lys Thr Ile Val Asp Glu Leu Lys Pro Lys Phe Thr Val Ser
                170                 175                 180

gct ggt acg aca ggt gaa ttt cct gcg gcg ggt cgt tgg tac cag cca   691
Ala Gly Thr Thr Gly Glu Phe Pro Ala Ala Gly Arg Trp Tyr Gln Pro
            185                 190                 195

caa gaa gtt gtt gtc gga gat aac aac cga ccc acc tgg gcg ccg atg   739
Gln Glu Val Val Val Gly Asp Asn Asn Arg Pro Thr Trp Ala Pro Met
        200                 205                 210
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ggg gct gag tcc tgg gga tgg act gtg acc cct aca ctg tcg atg tca   787
Gly Ala Glu Ser Trp Gly Trp Thr Val Thr Pro Thr Leu Ser Met Ser
    215                 220                 225

gat acc gag cac gtt gtg gtg atg tgg gag gcc cgc ttg acc gga ggt   835
Asp Thr Glu His Val Val Val Met Trp Glu Ala Arg Leu Thr Gly Gly
230                 235                 240                 245

gag cgt tac ggt gcg ctg ttg gcg tgg gtg aca gcc gat tac aac atc   883
Glu Arg Tyr Gly Ala Leu Leu Ala Trp Val Thr Ala Asp Tyr Asn Ile
                250                 255                 260

aac acc ggc gtg ttt agc tcg ctg gcg ttg gcg cat acc tat gaa gga   931
Asn Thr Gly Val Phe Ser Ser Leu Ala Leu Ala His Thr Tyr Glu Gly
            265                 270                 275

cac cag cgt att ggt gca acc acc tca cca agt gaa ttt ggt gcc cac   979
His Gln Arg Ile Gly Ala Thr Thr Ser Pro Ser Glu Phe Gly Ala His
        280                 285                 290

ggc aca aat gca gag gcg agc gct gca cgt gct ggc agt gaa ggc ggg   1027
Gly Thr Asn Ala Glu Ala Ser Ala Ala Arg Ala Gly Ser Glu Gly Gly
    295                 300                 305

ggg ctt gag ggc gag gct att ttc gtt gat gag ctg cag cgg gca cta   1075
Gly Leu Glu Gly Glu Ala Ile Phe Val Asp Glu Leu Gln Arg Ala Leu
310                 315                 320                 325

gag atc gct cag ctg aac aaa cag gag aac aga taatgacgac acgaaatgta 1128
Glu Ile Ala Gln Leu Asn Lys Gln Glu Asn Arg
                330                 335

gat                                                               1131


<210> 2306
<211> 336
<212> PRT
<213> Corynebacterium glutamicum

<400> 2306
Met Ala Glu Asn Asn Gly Gly Ser Asp Asp Leu Lys Pro Ile Ser Val
  1               5                  10                  15

Asp Gly Val Val Asn Gly Glu Val Arg Ser Asp Lys Glu Lys Gln Ala
             20                  25                  30

Phe Glu Lys Ile Thr Gly Asp Asp Leu Arg Arg Arg Ala Glu Gln Ile
         35                  40                  45

Arg Lys Arg Arg Leu Ala Lys Ala Gln Glu Asp Ala Arg Lys Arg Lys
     50                  55                  60

Pro Leu Phe Gly Leu Gly Arg Ile Ala Val Thr Val Leu Ala Gly Ala
 65                  70                  75                  80

Val Phe Ile Gly Thr Thr Leu Trp Ile Ser Thr Thr Ser Gly Gly Phe
                 85                  90                  95

Asp Asp Lys Val Ser Ala Asn Asn Glu Gln Ile Val Thr Leu Arg Asn
            100                 105                 110
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Glu Val Asn Asp Leu Lys Asn Thr Ala Glu Thr Met Pro Lys Lys Glu
        115                 120                 125

Thr Leu Ala Ser Gln Phe Asp Ala Ala Thr Ser Arg Ala Gln Asn Val
    130                 135                 140

Ala Asp Leu Gln Asn Gln Leu Ala Gly Ile Ile Thr Ser Val Asp Asp
145                 150                 155                 160

Asp Ala Ala Thr Glu Gln Phe Lys Thr Ile Val Asp Glu Leu Lys Pro
                165                 170                 175

Lys Phe Thr Val Ser Ala Gly Thr Thr Gly Glu Phe Pro Ala Ala Gly
            180                 185                 190

Arg Trp Tyr Gln Pro Gln Glu Val Val Val Gly Asp Asn Asn Arg Pro
        195                 200                 205

Thr Trp Ala Pro Met Gly Ala Glu Ser Trp Gly Trp Thr Val Thr Pro
    210                 215                 220

Thr Leu Ser Met Ser Asp Thr Glu His Val Val Val Met Trp Glu Ala
225                 230                 235                 240

Arg Leu Thr Gly Gly Glu Arg Tyr Gly Ala Leu Leu Ala Trp Val Thr
                245                 250                 255

Ala Asp Tyr Asn Ile Asn Thr Gly Val Phe Ser Ser Leu Ala Leu Ala
            260                 265                 270

His Thr Tyr Glu Gly His Gln Arg Ile Gly Ala Thr Thr Ser Pro Ser
        275                 280                 285

Glu Phe Gly Ala His Gly Thr Asn Ala Glu Ala Ser Ala Ala Arg Ala
    290                 295                 300

Gly Ser Glu Gly Gly Gly Leu Glu Gly Glu Ala Ile Phe Val Asp Glu
305                 310                 315                 320

Leu Gln Arg Ala Leu Glu Ile Ala Gln Leu Asn Lys Gln Glu Asn Arg
                325                 330                 335
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<210> 2307
<211> 1101
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1078)
<223> RXA01552

<400> 2307
actttgctct ttttatggcg ctgcacgaga ttcaactcaa agtgaaggtc agctatttga 60

actcagtgca aaagatgatc ggcataccaa actaatgaag atg tat ctg gga atg 115

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                                                    Met Tyr Leu Gly Met
                                                      1               5

aaa gaa gat tcc cta gcg cca ccc caa aat aga ttc gag tct cat aag   163
Lys Glu Asp Ser Leu Ala Pro Pro Gln Asn Arg Phe Glu Ser His Lys
                 10                  15                  20

act gtc ttt tcc cta aaa cag aaa aac atc cca att aag gat gct gct   211
Thr Val Phe Ser Leu Lys Gln Lys Asn Ile Pro Ile Lys Asp Ala Ala
             25                  30                  35

aaa tct gat cag gtg aat ctc act tgg cat gat tat cca ggt gaa tgg   259
Lys Ser Asp Gln Val Asn Leu Thr Trp His Asp Tyr Pro Gly Glu Trp
         40                  45                  50

ttt gag ggt gga gct gta acg gac tcg gaa aag cag gat aaa gtt gaa   307
Phe Glu Gly Gly Ala Val Thr Asp Ser Glu Lys Gln Asp Lys Val Glu
     55                  60                  65

acg ttt aga aac ctg ctg ggc tca gat gta gcg cta ttt tta gtt gac   355
Thr Phe Arg Asn Leu Leu Gly Ser Asp Val Ala Leu Phe Leu Val Asp
 70                  75                  80                  85

ggt caa aag ctg cat gat tac gcc aat gaa gag gag cgc tat ctt agc   403
Gly Gln Lys Leu His Asp Tyr Ala Asn Glu Glu Glu Arg Tyr Leu Ser
                 90                  95                 100

tat tta ttt gat gga ttc att gaa aac cta aat cag atc aaa gat gca   451
Tyr Leu Phe Asp Gly Phe Ile Glu Asn Leu Asn Gln Ile Lys Asp Ala
             105                 110                 115

atc ctg gag ggt ggg aaa cag ctc caa cag ttc cca cga att tgg gta   499
Ile Leu Glu Gly Gly Lys Gln Leu Gln Gln Phe Pro Arg Ile Trp Val
         120                 125                 130

att gct tta tcc aaa gct gat cta tgg cca gat ctc caa gta aaa gat   547
Ile Ala Leu Ser Lys Ala Asp Leu Trp Pro Asp Leu Gln Val Lys Asp
     135                 140                 145

ttt gag aat cta ctt aat aag aaa gct ggc aat gaa att att gcg ctg   595
Phe Glu Asn Leu Leu Asn Lys Lys Ala Gly Asn Glu Ile Ile Ala Leu
150                 155                 160                 165

cgt tca aag ctt ttg gag ttt atc gat aac gac gaa gct ttc tcc ttc   643
Arg Ser Lys Leu Leu Glu Phe Ile Asp Asn Asp Glu Ala Phe Ser Phe
                 170                 175                 180

ggt aaa gat ttc ctt ttg ctc tct tcg gcg aag ttc act cca ggc cat   691
Gly Lys Asp Phe Leu Leu Leu Ser Ser Ala Lys Phe Thr Pro Gly His
             185                 190                 195

att gat ata agc cag cgc aag ggt gtt gat gtc ctc ctc ccg ttg gct   739
Ile Asp Ile Ser Gln Arg Lys Gly Val Asp Val Leu Leu Pro Leu Ala
         200                 205                 210

tgt gta ttg ccc atg caa cgc cat ttg tgg tgg cag gag ctg aaa gtt   787
Cys Val Leu Pro Met Gln Arg His Leu Trp Trp Gln Glu Leu Lys Val
     215                 220                 225

ttg cca att aac ctg gct gat ata ctt ttg gga aat gaa att gcc caa   835
Leu Pro Ile Asn Leu Ala Asp Ile Leu Leu Gly Asn Glu Ile Ala Gln
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230                 235                 240                 245

atg ggt ttc aag atc gtt tcc aaa gtt ttg aaa aac aaa gta tct gga   883
Met Gly Phe Lys Ile Val Ser Lys Val Leu Lys Asn Lys Val Ser Gly
                250                 255                 260

aca aat aac aag gcg atg gcg gca ttg gtt ttc gct gaa ctt gtg agg   931
Thr Asn Asn Lys Ala Met Ala Ala Leu Val Phe Ala Glu Leu Val Arg
            265                 270                 275

gat atg gtt gat cag cca act gaa ttg ctt cag aag gct cgt gag gaa   979
Asp Met Val Asp Gln Pro Thr Glu Leu Leu Gln Lys Ala Arg Glu Glu
        280                 285                 290

gcc gtc gga agg cgt gaa ttc ctt aaa gcg att act gca gaa ttc acc   1027
Ala Val Gly Arg Arg Glu Phe Leu Lys Ala Ile Thr Ala Glu Phe Thr
    295                 300                 305

agg aag ctg aat caa gcc gaa gct gat cag gtt tta gtt cgg gac ttt   1075
Arg Lys Leu Asn Gln Ala Glu Ala Asp Gln Val Leu Val Arg Asp Phe
310                 315                 320                 325

gca tgacactcat gtgggcaacc cgt                                    1101
Ala
```

Sequence Listing - New Application - Not Entered

<210> 2308
<211> 326
<212> PRT
<213> Corynebacterium glutamicum

<400> 2308

```
Met Tyr Leu Gly Met Lys Glu Asp Ser Leu Ala Pro Pro Gln Asn Arg
  1               5                  10                  15

Phe Glu Ser His Lys Thr Val Phe Ser Leu Lys Gln Lys Asn Ile Pro
             20                  25                  30

Ile Lys Asp Ala Ala Lys Ser Asp Gln Val Asn Leu Thr Trp His Asp
         35                  40                  45

Tyr Pro Gly Glu Trp Phe Glu Gly Gly Ala Val Thr Asp Ser Glu Lys
     50                  55                  60

Gln Asp Lys Val Glu Thr Phe Arg Asn Leu Leu Gly Ser Asp Val Ala
 65                  70                  75                  80

Leu Phe Leu Val Asp Gly Gln Lys Leu His Asp Tyr Ala Asn Glu Glu
                 85                  90                  95

Glu Arg Tyr Leu Ser Tyr Leu Phe Asp Gly Phe Ile Glu Asn Leu Asn
            100                 105                 110

Gln Ile Lys Asp Ala Ile Leu Glu Gly Gly Lys Gln Leu Gln Gln Phe
        115                 120                 125

Pro Arg Ile Trp Val Ile Ala Leu Ser Lys Ala Asp Leu Trp Pro Asp
    130                 135                 140

Leu Gln Val Lys Asp Phe Glu Asn Leu Leu Asn Lys Lys Ala Gly Asn
```

```
145                 150                 155                 160

Glu Ile Ile Ala Leu Arg Ser Lys Leu Leu Glu Phe Ile Asp Asn Asp
                165                 170                 175

Glu Ala Phe Ser Phe Gly Lys Asp Phe Leu Leu Leu Ser Ser Ala Lys
            180                 185                 190

Phe Thr Pro Gly His Ile Asp Ile Ser Gln Arg Lys Gly Val Asp Val
        195                 200                 205

Leu Leu Pro Leu Ala Cys Val Leu Pro Met Gln Arg His Leu Trp Trp
    210                 215                 220

Gln Glu Leu Lys Val Leu Pro Ile Asn Leu Ala Asp Ile Leu Leu Gly
225                 230                 235                 240

Asn Glu Ile Ala Gln Met Gly Phe Lys Ile Val Ser Lys Val Leu Lys
                245                 250                 255

Asn Lys Val Ser Gly Thr Asn Asn Lys Ala Met Ala Ala Leu Val Phe
            260                 265                 270

Ala Glu Leu Val Arg Asp Met Val Asp Gln Pro Thr Glu Leu Leu Gln
        275                 280                 285

Lys Ala Arg Glu Glu Ala Val Gly Arg Arg Glu Phe Leu Lys Ala Ile
    290                 295                 300

Thr Ala Glu Phe Thr Arg Lys Leu Asn Gln Ala Glu Ala Asp Gln Val
305                 310                 315                 320

Leu Val Arg Asp Phe Ala
                325
```

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<210> 2309
<211> 2265
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2242)
<223> RXA01554

<400> 2309
tggcttaaac cttatttgta gttgtcaata aatatgaaat tccttagcaa cttgtttaaa 60

tagacgtata aacaagtttg aaaaaggaag gttatccatc ttg aaa aag cat gtg 115
                                            Leu Lys Lys His Val
                                              1   5

acc tca gcc gtt acc gcc gtg gtg acg gct ttt tca acg gct gcg ctt 163
Thr Ser Ala Val Thr Ala Val Val Thr Ala Phe Ser Thr Ala Ala Leu
                 10   15   20

ggt tta agt att gcc gtt tct cct gct gtt gcc caa gtg gct aat cca 211
Gly Leu Ser Ile Ala Val Ser Pro Ala Val Ala Gln Val Ala Asn Pro
             25   30   35

```
gct cca gat ctt tct gcg ccg tat aca tgg gtg gaa gag ttt gat tcc   259
Ala Pro Asp Leu Ser Ala Pro Tyr Thr Trp Val Glu Glu Phe Asp Ser
         40                  45                  50

gag gat gct ctc aaa ggg tgg aac att ttc cgc cag cca gat tat ggc   307
Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg Gln Pro Asp Tyr Gly
     55                  60                  65

agc gac aaa gtt ctc tat acc gaa gat gct tta agt atc gaa gat ggc   355
Ser Asp Lys Val Leu Tyr Thr Glu Asp Ala Leu Ser Ile Glu Asp Gly
 70                  75                  80                  85

aag ctc acc atc acc act cag cgc cac tgc gtt gac gaa gac ttc gcg   403
Lys Leu Thr Ile Thr Thr Gln Arg His Cys Val Asp Glu Asp Phe Ala
                 90                  95                 100

atc agt gat cct gtc aac cgc gga aag ctc aat gac agc acc gcg caa   451
Ile Ser Asp Pro Val Asn Arg Gly Lys Leu Asn Asp Ser Thr Ala Gln
            105                 110                 115

gtt gaa cct tgt gct cca ggt cag ttt gaa aag ttc acc agt gcg cgc   499
Val Glu Pro Cys Ala Pro Gly Gln Phe Glu Lys Phe Thr Ser Ala Arg
        120                 125                 130

atc gtc act ccg aaa att gct cgt gga gag ttc gac ctt tct gtc act   547
Ile Val Thr Pro Lys Ile Ala Arg Gly Glu Phe Asp Leu Ser Val Thr
    135                 140                 145

gca act ctt aac acc ggt ggc gtc gaa ggt gtc cga agt gcc att tgg   595
Ala Thr Leu Asn Thr Gly Gly Val Glu Gly Val Arg Ser Ala Ile Trp
150                 155                 160                 165

atg caa aac ggt gaa cag gcg tgt tcc tca gca acc aac aat ggc ctc   643
Met Gln Asn Gly Glu Gln Ala Cys Ser Ser Ala Thr Asn Asn Gly Leu
                170                 175                 180

tac gga gaa cta gac ctg gta gag cac ttt tct tac gat ctt cgc tcg   691
Tyr Gly Glu Leu Asp Leu Val Glu His Phe Ser Tyr Asp Leu Arg Ser
            185                 190                 195

cca tgg tct cca tca aac acc cac ttg ggt tgt gat cct gaa agt gtc   739
Pro Trp Ser Pro Ser Asn Thr His Leu Gly Cys Asp Pro Glu Ser Val
        200                 205                 210

aac ggc acc aac cgt gca cct cgt gaa ctt aaa cta gat gag tca ctc   787
Asn Gly Thr Asn Arg Ala Pro Arg Glu Leu Lys Leu Asp Glu Ser Leu
    215                 220                 225

gat ggc gtg gag cac acc tgg act gtg agc acc acc cgc gac ggc gtt   835
Asp Gly Val Glu His Thr Trp Thr Val Ser Thr Thr Arg Asp Gly Val
230                 235                 240                 245

gag tac ttc att gat gat gag gcg att aac cgc cag tca tgg cgc aac   883
Glu Tyr Phe Ile Asp Asp Glu Ala Ile Asn Arg Gln Ser Trp Arg Asn
                250                 255                 260

gat gtc act ttg ggg cat gcc gaa att gat gat ttc ggg atc tcc gcg   931
Asp Val Thr Leu Gly His Ala Glu Ile Asp Asp Phe Gly Ile Ser Ala
            265                 270                 275

cag acg ttt gat gag atc gtc gac cgc gaa tgg act ctc act ctt aat   979
```

```
Gln Thr Phe Asp Glu Ile Val Asp Arg Glu Trp Thr Leu Thr Leu Asn
        280                 285                 290

caa aag gta gaa agc gcc gac tgg gca aaa cca cgt tcc tct gag gaa   1027
Gln Lys Val Glu Ser Ala Asp Trp Ala Lys Pro Arg Ser Ser Glu Glu
    295                 300                 305

gat ttc cca gtc cgg tcc atg gtg att gac cgc atc gag gtc acc gga   1075
Asp Phe Pro Val Arg Ser Met Val Ile Asp Arg Ile Glu Val Thr Gly
310                 315                 320                 325

tct ccc gca gta tct gaa gac acc ccc atg cca gat acc acc cag ctt   1123
Ser Pro Ala Val Ser Glu Asp Thr Pro Met Pro Asp Thr Thr Gln Leu
                330                 335                 340

ttg acc caa gac act ctg gaa tac ctc ggt cgc atg cca gtg ctg gaa   1171
Leu Thr Gln Asp Thr Leu Glu Tyr Leu Gly Arg Met Pro Val Leu Glu
            345                 350                 355

cgc tac gag cca gca agt gct gat ttt gcc gat ggc cgc agg cct tcc   1219
Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp Gly Arg Arg Pro Ser
        360                 365                 370

tgg aac tac ttc aat ttg aag gaa tcg tgg cag aat cca gaa ctc gag   1267
Trp Asn Tyr Phe Asn Leu Lys Glu Ser Trp Gln Asn Pro Glu Leu Glu
    375                 380                 385

caa cgc cca gaa gct gtc gaa ttc gtt gat gga cgc atg gat atc gtg   1315
Gln Arg Pro Glu Ala Val Glu Phe Val Asp Gly Arg Met Asp Ile Val
390                 395                 400                 405

acc cgt cgc cac tgt ctg gcc acc act gat gac atc gcc act ccg gaa   1363
Thr Arg Arg His Cys Leu Ala Thr Thr Asp Asp Ile Ala Thr Pro Glu
                410                 415                 420

aac gca cag gag gaa ccg tgc gcg ccg ggt gag gtg aca cgc tac agc   1411
Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu Val Thr Arg Tyr Ser
            425                 430                 435

tca gcg cgt gtc cac ctt cca gag atc ccc gcc ggc aac ttc cgg ctc   1459
Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala Gly Asn Phe Arg Leu
        440                 445                 450

acc gtg cgc gca cgg gcg cag tcc gaa gag ctt gtc gac ggc gtc cgc   1507
Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu Val Asp Gly Val Arg
    455                 460                 465

ccc gct atc tgg atg cag aac aat acc aac ttc tgt gct gac aac gat   1555
Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe Cys Ala Asp Asn Asp
470                 475                 480                 485

gga cgc cct tat ggt gaa ctg gat att act gag ttc tac agc tct cgt   1603
Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu Phe Tyr Ser Ser Arg
                490                 495                 500

gtg aac acc cag tac tcg gca gta cac ctt gga tgt gct ggc aac cgc   1651
Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly Cys Ala Gly Asn Arg
            505                 510                 515

cca gag atg aag ctt cgc caa atg gaa atg gaa gag tcc atg ttt ggg   1699
Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu Glu Ser Met Phe Gly
```

```
        520                 525                 530

gat tgg cat gac tgg ggc gtc gaa gtc ttc gac ggc cag atc gta ttc   1747
Asp Trp His Asp Trp Gly Val Glu Val Phe Asp Gly Gln Ile Val Phe
    535                 540                 545

acc att gac ggc aag gca gta act tcc tct ggc aaa gat gtc ttt ggc   1795
Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly Lys Asp Val Phe Gly
550                 555                 560                 565

aac tct gtt acc cca gcc gct gca cct ctt cgc ccc gcg cac ttc aag   1843
Asn Ser Val Thr Pro Ala Ala Ala Pro Leu Arg Pro Ala His Phe Lys
                570                 575                 580

ttg tcg gaa gag gaa tac cgt gaa gtc atc ggg cag cct tgg cac ctt   1891
Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly Gln Pro Trp His Leu
            585                 590                 595

att ttg aac acc atg gtg gag cag tct ggc aaa gac agc tgg att aca   1939
Ile Leu Asn Thr Met Val Glu Gln Ser Gly Lys Asp Ser Trp Ile Thr
        600                 605                 610

gcg gtc gac aat aac gag gcg ttc cca gaa cac cgc ttc caa att gac   1987
Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His Arg Phe Gln Ile Asp
    615                 620                 625

cat gtg gca gta gat atc gag tct gac tct gtg gac aat gta tgg cct   2035
His Val Ala Val Asp Ile Glu Ser Asp Ser Val Asp Asn Val Trp Pro
630                 635                 640                 645

gac gct gcg aat gaa atc cca gac aat gtt ggt att gaa gac tct gat   2083
Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly Ile Glu Asp Ser Asp
                650                 655                 660

gat ggc agc gac ctg gag gtt ggt tcg acc gga agc tct aca gct gag   2131
Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly Ser Ser Thr Ala Glu
            665                 670                 675

acc gtg agc tgg atc tcg ttg ttc acc gcg ttg agc tcg ctg gtc ttc   2179
Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu Ser Ser Leu Val Phe
        680                 685                 690

aca ctg gct ctc aat caa gaa gca ttg cag aat ttg att aat cag ttc   2227
Thr Leu Ala Leu Asn Gln Glu Ala Leu Gln Asn Leu Ile Asn Gln Phe
    695                 700                 705

atg aga cag ttc aag taatccttgt gggcgctttg tct                    2265
Met Arg Gln Phe Lys
710
```

<210> 2310
<211> 714
<212> PRT
<213> Corynebacterium glutamicum

<400> 2310

```
Leu Lys Lys His Val Thr Ser Ala Val Thr Ala Val Val Thr Ala Phe
  1               5                  10                  15

Ser Thr Ala Ala Leu Gly Leu Ser Ile Ala Val Ser Pro Ala Val Ala
```

```
            20                  25                  30

Gln Val Ala Asn Pro Ala Pro Asp Leu Ser Ala Pro Tyr Thr Trp Val
         35                  40                  45

Glu Glu Phe Asp Ser Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg
     50                  55                  60

Gln Pro Asp Tyr Gly Ser Asp Lys Val Leu Tyr Thr Glu Asp Ala Leu
 65                  70                  75                  80

Ser Ile Glu Asp Gly Lys Leu Thr Ile Thr Thr Gln Arg His Cys Val
                 85                  90                  95

Asp Glu Asp Phe Ala Ile Ser Asp Pro Val Asn Arg Gly Lys Leu Asn
            100                 105                 110

Asp Ser Thr Ala Gln Val Glu Pro Cys Ala Pro Gly Gln Phe Glu Lys
        115                 120                 125

Phe Thr Ser Ala Arg Ile Val Thr Pro Lys Ile Ala Arg Gly Glu Phe
    130                 135                 140

Asp Leu Ser Val Thr Ala Thr Leu Asn Thr Gly Gly Val Glu Gly Val
145                 150                 155                 160

Arg Ser Ala Ile Trp Met Gln Asn Gly Glu Gln Ala Cys Ser Ser Ala
                165                 170                 175

Thr Asn Asn Gly Leu Tyr Gly Glu Leu Asp Leu Val Glu His Phe Ser
            180                 185                 190

Tyr Asp Leu Arg Ser Pro Trp Ser Pro Ser Asn Thr His Leu Gly Cys
        195                 200                 205

Asp Pro Glu Ser Val Asn Gly Thr Asn Arg Ala Pro Arg Glu Leu Lys
    210                 215                 220

Leu Asp Glu Ser Leu Asp Gly Val Glu His Thr Trp Thr Val Ser Thr
225                 230                 235                 240

Thr Arg Asp Gly Val Glu Tyr Phe Ile Asp Asp Glu Ala Ile Asn Arg
                245                 250                 255

Gln Ser Trp Arg Asn Asp Val Thr Leu Gly His Ala Glu Ile Asp Asp
            260                 265                 270

Phe Gly Ile Ser Ala Gln Thr Phe Asp Glu Ile Val Asp Arg Glu Trp
        275                 280                 285

Thr Leu Thr Leu Asn Gln Lys Val Glu Ser Ala Asp Trp Ala Lys Pro
    290                 295                 300

Arg Ser Ser Glu Glu Asp Phe Pro Val Arg Ser Met Val Ile Asp Arg
305                 310                 315                 320

Ile Glu Val Thr Gly Ser Pro Ala Val Ser Glu Asp Thr Pro Met Pro
                325                 330                 335

Asp Thr Thr Gln Leu Leu Thr Gln Asp Thr Leu Glu Tyr Leu Gly Arg
            340                 345                 350
```

```
Met Pro Val Leu Glu Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp
        355                 360                 365

Gly Arg Arg Pro Ser Trp Asn Tyr Phe Asn Leu Lys Glu Ser Trp Gln
    370                 375                 380

Asn Pro Glu Leu Glu Gln Arg Pro Glu Ala Val Glu Phe Val Asp Gly
385                 390                 395                 400

Arg Met Asp Ile Val Thr Arg Arg His Cys Leu Ala Thr Thr Asp Asp
                405                 410                 415

Ile Ala Thr Pro Glu Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu
            420                 425                 430

Val Thr Arg Tyr Ser Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala
        435                 440                 445

Gly Asn Phe Arg Leu Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu
    450                 455                 460

Val Asp Gly Val Arg Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe
465                 470                 475                 480

Cys Ala Asp Asn Asp Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu
                485                 490                 495

Phe Tyr Ser Ser Arg Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly
            500                 505                 510

Cys Ala Gly Asn Arg Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu
        515                 520                 525

Glu Ser Met Phe Gly Asp Trp His Asp Trp Gly Val Glu Val Phe Asp
    530                 535                 540

Gly Gln Ile Val Phe Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly
545                 550                 555                 560

Lys Asp Val Phe Gly Asn Ser Val Thr Pro Ala Ala Ala Pro Leu Arg
                565                 570                 575

Pro Ala His Phe Lys Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly
            580                 585                 590

Gln Pro Trp His Leu Ile Leu Asn Thr Met Val Glu Gln Ser Gly Lys
        595                 600                 605

Asp Ser Trp Ile Thr Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His
    610                 615                 620

Arg Phe Gln Ile Asp His Val Ala Val Asp Ile Glu Ser Asp Ser Val
625                 630                 635                 640

Asp Asn Val Trp Pro Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly
                645                 650                 655

Ile Glu Asp Ser Asp Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly
            660                 665                 670
```

```
Ser Ser Thr Ala Glu Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu
        675                 680                 685

Ser Ser Leu Val Phe Thr Leu Ala Leu Asn Gln Glu Ala Leu Gln Asn
    690                 695                 700

Leu Ile Asn Gln Phe Met Arg Gln Phe Lys
705                 710


<210> 2311
<211> 453
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(430)
<223> RXA01560

<400> 2311
atgggagcaa ggctcattta gctacttcga cgtggaagcg cacatcgttg agttgattcc 60

tgcatcagta agcgatgcgt tttaggcaca tctgcgatcc gtg ggc gtg tcc tac   115
                                              Val Gly Val Ser Tyr
                                                1               5

atc atc gcc ggc gat gag cag ctg gat atg gca gaa gcc gtt cgc aaa   163
Ile Ile Ala Gly Asp Glu Gln Leu Asp Met Ala Glu Ala Val Arg Lys
                10                  15                  20

att ggg gag acc ttt aaa act gag gaa att atc ctt ggt ggc gga gga   211
Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile Leu Gly Gly Gly Gly
            25                  30                  35

acc ctg aac tgg tcc atg ctc cgc gac ggt ttg tgc gac gag gtt agc   259
Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu Cys Asp Glu Val Ser
        40                  45                  50

atc gtg atg atg cca atc gcc gat ggt gaa aag cac acc cac tct ttg   307
Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys His Thr His Ser Leu
    55                  60                  65

ttc gaa gcc gat gaa aaa tac tca gca ccg ttg ccg atc ggt ttt tca   355
Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu Pro Ile Gly Phe Ser
70                  75                  80                  85

ctc gcc agc gtt gaa cca cta gaa gat gga agc gtt tgg atg cgt tac   403
Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser Val Trp Met Arg Tyr
                90                  95                  100

ggg gtc aat ggc cca gtg gac gcg aac taggtagcaa atactcgctc         450
Gly Val Asn Gly Pro Val Asp Ala Asn
            105                 110

ttt                                                              453


<210> 2312
<211> 110
<212> PRT
```

<213> Corynebacterium glutamicum

<400> 2312

```
Val Gly Val Ser Tyr Ile Ile Ala Gly Asp Glu Gln Leu Asp Met Ala
  1               5                  10                  15

Glu Ala Val Arg Lys Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile
             20                  25                  30

Leu Gly Gly Gly Gly Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu
         35                  40                  45

Cys Asp Glu Val Ser Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys
     50                  55                  60

His Thr His Ser Leu Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu
 65                  70                  75                  80

Pro Ile Gly Phe Ser Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser
                 85                  90                  95

Val Trp Met Arg Tyr Gly Val Asn Gly Pro Val Asp Ala Asn
            100                 105                 110
```

<210> 2313
<211> 1143
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1120)
<223> RXA01575

<400> 2313

```
gctgtttttt gatgcatcca tgataggaat agagcctagt gcatgatggc tgattttcct 60

gttaggtgcc accgacccca gtgatgataa cttgattgtc atg aaa tcc att gat   115
                                            Met Lys Ser Ile Asp
                                              1               5

ctt gag cag ctg gcg ggc acg caa tcg cgc acg tat caa tcg cga aag   163
Leu Glu Gln Leu Ala Gly Thr Gln Ser Arg Thr Tyr Gln Ser Arg Lys
                 10                  15                  20

atc acc gat gag atg gtc gcc cgg ccg gtg cat gtg gcg atc gcg ctg   211
Ile Thr Asp Glu Met Val Ala Arg Pro Val His Val Ala Ile Ala Leu
             25                  30                  35

tgg gaa gtg ccg tgg gag tcg gca aaa tcc ggc aag att gag ggt tgg   259
Trp Glu Val Pro Trp Glu Ser Ala Lys Ser Gly Lys Ile Glu Gly Trp
         40                  45                  50

gtc att gcc gtg gat tcg ccg cgt ggg cgg ttt gtg cgc agc ggg cag   307
Val Ile Ala Val Asp Ser Pro Arg Gly Arg Phe Val Arg Ser Gly Gln
     55                  60                  65

acc aaa aat ggc gac gcc gtc aac cgg act gtg tcg atg ctg aaa tca   355
Thr Lys Asn Gly Asp Ala Val Asn Arg Thr Val Ser Met Leu Lys Ser
 70                  75                  80                  85
```

```
gcg ttg aaa ggg gtc cgc ggg aag gcg tgg att gta act ggg cgt cga   403
Ala Leu Lys Gly Val Arg Gly Lys Ala Trp Ile Val Thr Gly Arg Arg
                 90                  95                 100

caa gca gct tta cgc gca gcc ctg gtg cgc gaa aac tac ctg gtc acc   451
Gln Ala Ala Leu Arg Ala Ala Leu Val Arg Glu Asn Tyr Leu Val Thr
            105                 110                 115

gga agc ttc gcc gag caa aat agg gcc ggc gtg aag gcg tcg gcg atc   499
Gly Ser Phe Ala Glu Gln Asn Arg Ala Gly Val Lys Ala Ser Ala Ile
        120                 125                 130

tcg cgc cgc gcc gaa caa tcc gcg ctc tac aag gcg aaa aaa atc ggc   547
Ser Arg Arg Ala Glu Gln Ser Ala Leu Tyr Lys Ala Lys Lys Ile Gly
    135                 140                 145

gaa ttc gcc gag cgc gcc cca cgc gtc aaa gag cgg caa gag gca cat   595
Glu Phe Ala Glu Arg Ala Pro Arg Val Lys Glu Arg Gln Glu Ala His
150                 155                 160                 165

tgg tgg cca cgg ttg tca cgc acg caa ggc acc gca ggc gtt tta cgc   643
Trp Trp Pro Arg Leu Ser Arg Thr Gln Gly Thr Ala Gly Val Leu Arg
                170                 175                 180

tta gcg acg gac gcc tct acc gat ggg gtc ttc cgc ggc gcc atg tgc   691
Leu Ala Thr Asp Ala Ser Thr Asp Gly Val Phe Arg Gly Ala Met Cys
            185                 190                 195

ttc gta gcc tca aac ggc gac tac ctc ctg gag acc caa gac acc acc   739
Phe Val Ala Ser Asn Gly Asp Tyr Leu Leu Glu Thr Gln Asp Thr Thr
        200                 205                 210

gca agc tcc gac gaa tta gaa ctc gaa agc atc acc cac gcc ctg atc   787
Ala Ser Ser Asp Glu Leu Glu Leu Glu Ser Ile Thr His Ala Leu Ile
    215                 220                 225

tac ctc aaa acc atc ggc gcg acc caa gcc atc atc gaa tcc gac agc   835
Tyr Leu Lys Thr Ile Gly Ala Thr Gln Ala Ile Ile Glu Ser Asp Ser
230                 235                 240                 245

aaa gcc gca ctt gaa gcc atc gac ttc atc ctc aac aac cga ccg cgc   883
Lys Ala Ala Leu Glu Ala Ile Asp Phe Ile Leu Asn Asn Arg Pro Arg
                250                 255                 260

cgg ggc agg tgg cgc ggc atc acc gca tgc gcc cgc aac cgg ttc cgg   931
Arg Gly Arg Trp Arg Gly Ile Thr Ala Cys Ala Arg Asn Arg Phe Arg
            265                 270                 275

gat gcc tgg gaa gcg ctt atc gac gac tgc gtt gtg gaa tta tcc cgc   979
Asp Ala Trp Glu Ala Leu Ile Asp Asp Cys Val Val Glu Leu Ser Arg
        280                 285                 290

gta cta ggg cac gcc ggg gat cca ctg aac caa gca gcc gac caa atc   1027
Val Leu Gly His Ala Gly Asp Pro Leu Asn Gln Ala Ala Asp Gln Ile
    295                 300                 305

gca tac atg ggc atg cgc gcc gta att ttt gaa caa aaa tcc gca cac   1075
Ala Tyr Met Gly Met Arg Ala Val Ile Phe Glu Gln Lys Ser Ala His
310                 315                 320                 325
```

```
ccc aca ttg ctc aaa gga att gac aag gcg ctt cgc aag gcc gag       1120
Pro Thr Leu Leu Lys Gly Ile Asp Lys Ala Leu Arg Lys Ala Glu
                330                 335                 340

taaggtgggc aacgagtcgg tga                                       1143


<210> 2314
<211> 340
<212> PRT
<213> Corynebacterium glutamicum

<400> 2314
Met Lys Ser Ile Asp Leu Glu Gln Leu Ala Gly Thr Gln Ser Arg Thr
  1               5                  10                  15

Tyr Gln Ser Arg Lys Ile Thr Asp Glu Met Val Ala Arg Pro Val His
             20                  25                  30

Val Ala Ile Ala Leu Trp Glu Val Pro Trp Glu Ser Ala Lys Ser Gly
         35                  40                  45

Lys Ile Glu Gly Trp Val Ile Ala Val Asp Ser Pro Arg Gly Arg Phe
     50                  55                  60

Val Arg Ser Gly Gln Thr Lys Asn Gly Asp Ala Val Asn Arg Thr Val
 65                  70                  75                  80

Ser Met Leu Lys Ser Ala Leu Lys Gly Val Arg Gly Lys Ala Trp Ile
                 85                  90                  95

Val Thr Gly Arg Arg Gln Ala Ala Leu Arg Ala Ala Leu Val Arg Glu
            100                 105                 110

Asn Tyr Leu Val Thr Gly Ser Phe Ala Glu Gln Asn Arg Ala Gly Val
        115                 120                 125

Lys Ala Ser Ala Ile Ser Arg Arg Ala Glu Gln Ser Ala Leu Tyr Lys
    130                 135                 140

Ala Lys Lys Ile Gly Glu Phe Ala Glu Arg Ala Pro Arg Val Lys Glu
145                 150                 155                 160

Arg Gln Glu Ala His Trp Trp Pro Arg Leu Ser Arg Thr Gln Gly Thr
                165                 170                 175

Ala Gly Val Leu Arg Leu Ala Thr Asp Ala Ser Thr Asp Gly Val Phe
            180                 185                 190

Arg Gly Ala Met Cys Phe Val Ala Ser Asn Gly Asp Tyr Leu Leu Glu
        195                 200                 205

Thr Gln Asp Thr Thr Ala Ser Ser Asp Glu Leu Glu Leu Glu Ser Ile
    210                 215                 220

Thr His Ala Leu Ile Tyr Leu Lys Thr Ile Gly Ala Thr Gln Ala Ile
225                 230                 235                 240

Ile Glu Ser Asp Ser Lys Ala Ala Leu Glu Ala Ile Asp Phe Ile Leu
                245                 250                 255
```

```
Asn Asn Arg Pro Arg Arg Gly Arg Trp Arg Gly Ile Thr Ala Cys Ala
            260                 265                 270

Arg Asn Arg Phe Arg Asp Ala Trp Glu Ala Leu Ile Asp Asp Cys Val
        275                 280                 285

Val Glu Leu Ser Arg Val Leu Gly His Ala Gly Asp Pro Leu Asn Gln
    290                 295                 300

Ala Ala Asp Gln Ile Ala Tyr Met Gly Met Arg Ala Val Ile Phe Glu
305                 310                 315                 320

Gln Lys Ser Ala His Pro Thr Leu Leu Lys Gly Ile Asp Lys Ala Leu
                325                 330                 335

Arg Lys Ala Glu
            340
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<210> 2315
<211> 498
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(475)
<223> RXA01577

<400> 2315

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ccgtagacat cctctacacc gaatactcca tgagcaaggg gcaatccctg ctcaacggcg 60

taaacatcct ggccgacggc ttcctagcga ggagactccc atg acg cag acc acc   115
                                              Met Thr Gln Thr Thr
                                                1               5

acc caa atc atc atc cag ata ctg ctt ctc ctg gca acc gca gca ctg   163
Thr Gln Ile Ile Ile Gln Ile Leu Leu Leu Leu Ala Thr Ala Ala Leu
                10                  15                  20

gca cta tat ttc ctc cga aac cgc cgc aaa gcc cgc gcc aaa gca tgg   211
Ala Leu Tyr Phe Leu Arg Asn Arg Arg Lys Ala Arg Ala Lys Ala Trp
            25                  30                  35

gtg aaa atc ggc ttc gta gta ttc att ttc gcc gca gta tgg gca gtg   259
Val Lys Ile Gly Phe Val Val Phe Ile Phe Ala Ala Val Trp Ala Val
        40                  45                  50

ctc cgc ccc gat gac ctc acc caa cta gcc aac ttt gtg ggc gtg gac   307
Leu Arg Pro Asp Asp Leu Thr Gln Leu Ala Asn Phe Val Gly Val Asp
    55                  60                  65

cgc ggc acc gac cta atg ctt tac gcc ctg gtt gtg gca ttt atg ttc   355
Arg Gly Thr Asp Leu Met Leu Tyr Ala Leu Val Val Ala Phe Met Phe
70                  75                  80                  85

acc acg ctg tcc agt tat gtg cgt ttc cgt gaa caa gag ctg cgt tat   403
Thr Thr Leu Ser Ser Tyr Val Arg Phe Arg Glu Gln Glu Leu Arg Tyr
                90                  95                  100

tcc aag ctg gcc cgc gct gtc gct ttg caa aat gtg gtg ctg ccg gag   451
```

```
Ser Lys Leu Ala Arg Ala Val Ala Leu Gln Asn Val Val Leu Pro Glu
            105                 110                 115

gat tcc cag ggt tct gac ccc gct taggaaagcg cttggcctct gga         498
Asp Ser Gln Gly Ser Asp Pro Ala
        120                 125


<210> 2316
<211> 125
<212> PRT
<213> Corynebacterium glutamicum

<400> 2316
Met Thr Gln Thr Thr Thr Gln Ile Ile Ile Gln Ile Leu Leu Leu Leu
  1               5                  10                  15

Ala Thr Ala Ala Leu Ala Leu Tyr Phe Leu Arg Asn Arg Arg Lys Ala
             20                  25                  30

Arg Ala Lys Ala Trp Val Lys Ile Gly Phe Val Val Phe Ile Phe Ala
         35                  40                  45

Ala Val Trp Ala Val Leu Arg Pro Asp Asp Leu Thr Gln Leu Ala Asn
     50                  55                  60

Phe Val Gly Val Asp Arg Gly Thr Asp Leu Met Leu Tyr Ala Leu Val
 65                  70                  75                  80

Val Ala Phe Met Phe Thr Thr Leu Ser Ser Tyr Val Arg Phe Arg Glu
                 85                  90                  95

Gln Glu Leu Arg Tyr Ser Lys Leu Ala Arg Ala Val Ala Leu Gln Asn
            100                 105                 110

Val Val Leu Pro Glu Asp Ser Gln Gly Ser Asp Pro Ala
        115                 120                 125


<210> 2317
<211> 507
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(484)
<223> RXA01579

<400> 2317
tggcagcatc ctgcgcaagg ttgggcagca gaccattcat tacggcgaat acaccggtca  60

ttgtgagaag ggtgctcagc agcaatgccc aggtgcgtcg ttg acc gag gta ttc   115
                                               Leu Thr Glu Val Phe
                                                 1               5

aac act gac cag cgg gtg ctt aac gcg ctt ttc aat gtt gta gaa gaa   163
Asn Thr Asp Gln Arg Val Leu Asn Ala Leu Phe Asn Val Val Glu Glu
                 10                  15                  20

gat gac tcc ggc gat acc gat gat gaa cag cac aac cac cag aat cca   211
```

```
Asp Asp Ser Gly Asp Thr Asp Asp Glu Gln His Asn His Gln Asn Pro
             25                  30                  35

gtt cgc ggc acc gag ttt gcc ggc ctc gtt gaa agc cat gag caa aga   259
Val Arg Gly Thr Glu Phe Ala Gly Leu Val Glu Ser His Glu Gln Arg
         40                  45                  50

tcc aat gga cac cgc cag tgg cag cac acc aag cca gtc cat ctt cgg   307
Ser Asn Gly His Arg Gln Trp Gln His Thr Lys Pro Val His Leu Arg
     55                  60                  65

ggt ttc ttc agc ggt gga ttc ctt cac gct gaa agg cag tgc gag ggc   355
Gly Phe Phe Ser Gly Gly Phe Leu His Ala Glu Arg Gln Cys Glu Gly
 70                  75                  80                  85

agc gac agc gca gaa agc agc cat gac cca gaa gat gga acg gaa acc   403
Ser Asp Ser Ala Glu Ser Ser His Asp Pro Glu Asp Gly Thr Glu Thr
                 90                  95                 100

aag tgt ttc agc caa cca gcc acc agc aag cgc gtc cac gcc gcc gat   451
Lys Cys Phe Ser Gln Pro Ala Thr Ser Lys Arg Val His Ala Ala Asp
            105                 110                 115

acc acc gtt gac aga ggt aac aat tcc gag aag tagcgcatat tgcttttcat 504
Thr Thr Val Asp Arg Gly Asn Asn Ser Glu Lys
        120                 125

tgg                                                               507


<210> 2318
<211> 128
<212> PRT
<213> Corynebacterium glutamicum

<400> 2318
Leu Thr Glu Val Phe Asn Thr Asp Gln Arg Val Leu Asn Ala Leu Phe
  1               5                  10                  15

Asn Val Val Glu Glu Asp Asp Ser Gly Asp Thr Asp Asp Glu Gln His
             20                  25                  30

Asn His Gln Asn Pro Val Arg Gly Thr Glu Phe Ala Gly Leu Val Glu
         35                  40                  45

Ser His Glu Gln Arg Ser Asn Gly His Arg Gln Trp Gln His Thr Lys
     50                  55                  60

Pro Val His Leu Arg Gly Phe Phe Ser Gly Gly Phe Leu His Ala Glu
 65                  70                  75                  80

Arg Gln Cys Glu Gly Ser Asp Ser Ala Glu Ser Ser His Asp Pro Glu
                 85                  90                  95

Asp Gly Thr Glu Thr Lys Cys Phe Ser Gln Pro Ala Thr Ser Lys Arg
            100                 105                 110

Val His Ala Ala Asp Thr Thr Val Asp Arg Gly Asn Asn Ser Glu Lys
        115                 120                 125
```

<210> 2319
<211> 750
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(727)
<223> RXA01585

<400> 2319
tgcagactgc tgcgccccgt tccatcagca aggtggagcg caaggtgctg accgctgtcg 60

ctactgatga ggtgcagtcg caggaagctc tagaaaagta gtg gtt gag act ctt 115
Val Val Glu Thr Leu
1 5

tct atc acc tca ggt gcg gct ggc ctg cag gcg ctt gtt gcg cgt gcg 163
Ser Ile Thr Ser Gly Ala Ala Gly Leu Gln Ala Leu Val Ala Arg Ala
10 15 20

gtt ggt ttg aat gag ttg gcg agc gcg cgt ttc cgc cag ctc acg cca 211
Val Gly Leu Asn Glu Leu Ala Ser Ala Arg Phe Arg Gln Leu Thr Pro
25 30 35

gag gtc gtt gat gtt ttt gtc acc act ccg ttc aac gtg acg gcg tcg 259
Glu Val Val Asp Val Phe Val Thr Thr Pro Phe Asn Val Thr Ala Ser
40 45 50

cgc cgg gta ttt ggt gtg gcg ggt cgc gat ggc gct gca gtt ggc gcg 307
Arg Arg Val Phe Gly Val Ala Gly Arg Asp Gly Ala Ala Val Gly Ala
55 60 65

aag gat ttg ctg cag gca ctc agc gag ggc cgg gaa gac gta ggc acc 355
Lys Asp Leu Leu Gln Ala Leu Ser Glu Gly Arg Glu Asp Val Gly Thr
70 75 80 85

tcc cgc gac gcc agc tgg ccg ggc tca ttg ccg cca gcc acg ggc ttt 403
Ser Arg Asp Ala Ser Trp Pro Gly Ser Leu Pro Pro Ala Thr Gly Phe
90 95 100

acg ctt gtc gac gaa ctc ccc acc cac gtg gtg cgc act ttg gct gat 451
Thr Leu Val Asp Glu Leu Pro Thr His Val Val Arg Thr Leu Ala Asp
105 110 115

cag ggt cag gca ttg gct cgc cag ttc tcc ggc ccg ctt ggc cct ccg 499
Gln Gly Gln Ala Leu Ala Arg Gln Phe Ser Gly Pro Leu Gly Pro Pro
120 125 130

gct tcg ttg atg gat cag gaa gtt att tca gca gaa ggc aat ggc aag 547
Ala Ser Leu Met Asp Gln Glu Val Ile Ser Ala Glu Gly Asn Gly Lys
135 140 145

aag gcc gga atc ccg atg cgc acg gta ttt acc tgc act tcg ctt ggt 595
Lys Ala Gly Ile Pro Met Arg Thr Val Phe Thr Cys Thr Ser Leu Gly
150 155 160 165

ttg atc cca ggt ttt gag gca gcc aat gat gtg ccg agg cac ctg cgg 643

```
Leu Ile Pro Gly Phe Glu Ala Ala Asn Asp Val Pro Arg His Leu Arg
                170                 175                 180

gta tcg gtg aat ggt cgt tgg acc cgc gtt gat gct ccc tat ggc agt   691
Val Ser Val Asn Gly Arg Trp Thr Arg Val Asp Ala Pro Tyr Gly Ser
            185                 190                 195

gtt tat cac tcg tca ggt ttg ggt ctg agc gtt ttc taaagcaaga        737
Val Tyr His Ser Ser Gly Leu Gly Leu Ser Val Phe
        200                 205

cccagcctgc aag                                                   750


<210> 2320
<211> 209
<212> PRT
<213> Corynebacterium glutamicum

<400> 2320
Val Val Glu Thr Leu Ser Ile Thr Ser Gly Ala Ala Gly Leu Gln Ala
  1               5                  10                  15

Leu Val Ala Arg Ala Val Gly Leu Asn Glu Leu Ala Ser Ala Arg Phe
             20                  25                  30

Arg Gln Leu Thr Pro Glu Val Val Asp Val Phe Val Thr Thr Pro Phe
         35                  40                  45

Asn Val Thr Ala Ser Arg Arg Val Phe Gly Val Ala Gly Arg Asp Gly
     50                  55                  60

Ala Ala Val Gly Ala Lys Asp Leu Leu Gln Ala Leu Ser Glu Gly Arg
 65                  70                  75                  80

Glu Asp Val Gly Thr Ser Arg Asp Ala Ser Trp Pro Gly Ser Leu Pro
                 85                  90                  95

Pro Ala Thr Gly Phe Thr Leu Val Asp Glu Leu Pro Thr His Val Val
            100                 105                 110

Arg Thr Leu Ala Asp Gln Gly Gln Ala Leu Ala Arg Gln Phe Ser Gly
        115                 120                 125

Pro Leu Gly Pro Pro Ala Ser Leu Met Asp Gln Glu Val Ile Ser Ala
    130                 135                 140

Glu Gly Asn Gly Lys Lys Ala Gly Ile Pro Met Arg Thr Val Phe Thr
145                 150                 155                 160

Cys Thr Ser Leu Gly Leu Ile Pro Gly Phe Glu Ala Ala Asn Asp Val
                165                 170                 175

Pro Arg His Leu Arg Val Ser Val Asn Gly Arg Trp Thr Arg Val Asp
            180                 185                 190

Ala Pro Tyr Gly Ser Val Tyr His Ser Ser Gly Leu Gly Leu Ser Val
        195                 200                 205

Phe
```

<210> 2321
<211> 392
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(369)
<223> RXA01586

<400> 2321
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aac aac gcg gcg ttc att gag atc gcg cag gaa gct cga ttg gcg ttt   48
Asn Asn Ala Ala Phe Ile Glu Ile Ala Gln Glu Ala Arg Leu Ala Phe
  1               5                  10                  15

gcg gag gat cag ttc cgt gag cgt ggc tat gag atc cct gct gtg ttt   96
Ala Glu Asp Gln Phe Arg Glu Arg Gly Tyr Glu Ile Pro Ala Val Phe
             20                  25                  30

gtg cgc cac ttg gaa gtt gat tat ttg cgt gcg atc ttg ccg gat acc   144
Val Arg His Leu Glu Val Asp Tyr Leu Arg Ala Ile Leu Pro Asp Thr
         35                  40                  45

acc cag gct gtc gtg gag aca cag gtg acc aag atc ggt aat act tcc   192
Thr Gln Ala Val Val Glu Thr Gln Val Thr Lys Ile Gly Asn Thr Ser
     50                  55                  60

ttc agc act cgt caa gag gtc aag gat cgt aac ggt cgt gtg tgc tgc   240
Phe Ser Thr Arg Gln Glu Val Lys Asp Arg Asn Gly Arg Val Cys Cys
 65                  70                  75                  80

gtg gtt gag tgc gtg cag gtg gct gtc aat gtg cag act gct gcg ccc   288
Val Val Glu Cys Val Gln Val Ala Val Asn Val Gln Thr Ala Ala Pro
                 85                  90                  95

cgt tcc atc agc aag gtg gag cgc aag gtg ctg acc gct gtc gct act   336
Arg Ser Ile Ser Lys Val Glu Arg Lys Val Leu Thr Ala Val Ala Thr
            100                 105                 110

gat gag gtg cag tcg cag gaa gct cta gaa aag tagtggttga gactctttct 389
Asp Glu Val Gln Ser Gln Glu Ala Leu Glu Lys
        115                 120

atc                                                               392
```

<210> 2322
<211> 123
<212> PRT
<213> Corynebacterium glutamicum

<400> 2322
```
Asn Asn Ala Ala Phe Ile Glu Ile Ala Gln Glu Ala Arg Leu Ala Phe
  1               5                  10                  15

Ala Glu Asp Gln Phe Arg Glu Arg Gly Tyr Glu Ile Pro Ala Val Phe
             20                  25                  30

Val Arg His Leu Glu Val Asp Tyr Leu Arg Ala Ile Leu Pro Asp Thr
```

```
         35                  40                  45

Thr Gln Ala Val Val Glu Thr Gln Val Thr Lys Ile Gly Asn Thr Ser
     50                  55                  60

Phe Ser Thr Arg Gln Glu Val Lys Asp Arg Asn Gly Arg Val Cys Cys
 65                  70                  75                  80

Val Val Glu Cys Val Gln Val Ala Val Asn Val Gln Thr Ala Ala Pro
                 85                  90                  95

Arg Ser Ile Ser Lys Val Glu Arg Lys Val Leu Thr Ala Val Ala Thr
            100                 105                 110

Asp Glu Val Gln Ser Gln Glu Ala Leu Glu Lys
        115                 120


<210> 2323
<211> 1083
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1060)
<223> RXA01595

<400> 2323
aatacttcct gtggctggtt aaagatggtg gcgcttcaat gccggatgac cagcaattgt 60

cggcaatgat tgacacggct gtaaaggaag gtccgcaata atg act gca ccc acg   115
                                              Met Thr Ala Pro Thr
                                                1               5

aac gct ggg gaa ctc agg cga gtt ttg ctg gtt cca cac acc ggg cgt   163
Asn Ala Gly Glu Leu Arg Arg Val Leu Leu Val Pro His Thr Gly Arg
                10                  15                  20

tct tcc aat att gaa tcc gcc atc ttg gca gcc aag ctg ctc gac gat   211
Ser Ser Asn Ile Glu Ser Ala Ile Leu Ala Ala Lys Leu Leu Asp Asp
            25                  30                  35

gct gga atc gat gtg agg gtg ctg atc aat gat gca gat gat cca att   259
Ala Gly Ile Asp Val Arg Val Leu Ile Asn Asp Ala Asp Asp Pro Ile
        40                  45                  50

gca gag cac tcc gtt tta ggc cgt ttc acc cat gtc agg cac gct gca   307
Ala Glu His Ser Val Leu Gly Arg Phe Thr His Val Arg His Ala Ala
    55                  60                  65

gac gcc gct gac ggc gca gaa cta gtt ctg gtg ctg ggt gga gat ggc   355
Asp Ala Ala Asp Gly Ala Glu Leu Val Leu Val Leu Gly Gly Asp Gly
70                  75                  80                  85

acc ttc ctc cgc gca gca gat atg gcc cac gct gtt gat ttg cct gtt   403
Thr Phe Leu Arg Ala Ala Asp Met Ala His Ala Val Asp Leu Pro Val
                90                  95                 100

ctg ggc atc aac cta ggc cat gtg gga ttc ttg gct gaa tgg gag tct   451
Leu Gly Ile Asn Leu Gly His Val Gly Phe Leu Ala Glu Trp Glu Ser
```

```
            105                 110                 115

gac tca ctt gaa gag gca ctc aaa cgt gtg atc gac cgc gat tac cgt   499
Asp Ser Leu Glu Glu Ala Leu Lys Arg Val Ile Asp Arg Asp Tyr Arg
        120                 125                 130

att gaa gat cgc atg acc tta act gtc gtt gtc cta gac ggc ggt gga   547
Ile Glu Asp Arg Met Thr Leu Thr Val Val Val Leu Asp Gly Gly Gly
    135                 140                 145

gaa gaa atc ggc cga ggc tgg gct ctc aat gag gtc agt att gaa aac   595
Glu Glu Ile Gly Arg Gly Trp Ala Leu Asn Glu Val Ser Ile Glu Asn
150                 155                 160                 165

tta aac cgc agg gga gtg ctc gat gca acc ctc gag gta gat gca cga   643
Leu Asn Arg Arg Gly Val Leu Asp Ala Thr Leu Glu Val Asp Ala Arg
                170                 175                 180

cca gtt gct tcc ttt ggt tgc gat ggc gtg ctg att tcc acc cca acc   691
Pro Val Ala Ser Phe Gly Cys Asp Gly Val Leu Ile Ser Thr Pro Thr
            185                 190                 195

ggc tcc acc gct tat gca ttt tcc gcc ggt ggt cct gta ctg tgg cca   739
Gly Ser Thr Ala Tyr Ala Phe Ser Ala Gly Gly Pro Val Leu Trp Pro
        200                 205                 210

gaa ctc gat gcc atc ttg gtg gtt cct aat aac gcc cac gcg ctg ttt   787
Glu Leu Asp Ala Ile Leu Val Val Pro Asn Asn Ala His Ala Leu Phe
    215                 220                 225

acc aaa ccg ctg gtt gtg agc cca aaa tcc acc gta gct gtg gaa tcc   835
Thr Lys Pro Leu Val Val Ser Pro Lys Ser Thr Val Ala Val Glu Ser
230                 235                 240                 245

aat tca gat act tca gca gcg atg gcc gtc atg gat ggt ttc cgt ccc   883
Asn Ser Asp Thr Ser Ala Ala Met Ala Val Met Asp Gly Phe Arg Pro
                250                 255                 260

att cct atg cct cca gga tcc cgt gtt gag gtc acc agg ggt gag cgt   931
Ile Pro Met Pro Pro Gly Ser Arg Val Glu Val Thr Arg Gly Glu Arg
            265                 270                 275

ccc gtg cgt tgg gtg agg ctt gat tct tca ccg ttt acc gac cga ctt   979
Pro Val Arg Trp Val Arg Leu Asp Ser Ser Pro Phe Thr Asp Arg Leu
        280                 285                 290

gtg agc aaa tta agg ctc ccc gtt acc ggt tgg cgg ggt ccg caa aaa   1027
Val Ser Lys Leu Arg Leu Pro Val Thr Gly Trp Arg Gly Pro Gln Lys
    295                 300                 305

cag gcg gaa aat aaa gat ccc agg tca gcg ggg taattcgaaa accattcgaa 1080
Gln Ala Glu Asn Lys Asp Pro Arg Ser Ala Gly
310                 315                 320

caa                                                               1083


<210> 2324
<211> 320
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 2324

```
Met Thr Ala Pro Thr Asn Ala Gly Glu Leu Arg Arg Val Leu Leu Val
  1               5                  10                  15

Pro His Thr Gly Arg Ser Ser Asn Ile Glu Ser Ala Ile Leu Ala Ala
             20                  25                  30

Lys Leu Leu Asp Asp Ala Gly Ile Asp Val Arg Val Leu Ile Asn Asp
         35                  40                  45

Ala Asp Asp Pro Ile Ala Glu His Ser Val Leu Gly Arg Phe Thr His
     50                  55                  60

Val Arg His Ala Ala Asp Ala Ala Asp Gly Ala Glu Leu Val Leu Val
 65                  70                  75                  80

Leu Gly Gly Asp Gly Thr Phe Leu Arg Ala Ala Asp Met Ala His Ala
                 85                  90                  95

Val Asp Leu Pro Val Leu Gly Ile Asn Leu Gly His Val Gly Phe Leu
            100                 105                 110

Ala Glu Trp Glu Ser Asp Ser Leu Glu Glu Ala Leu Lys Arg Val Ile
        115                 120                 125

Asp Arg Asp Tyr Arg Ile Glu Asp Arg Met Thr Leu Thr Val Val Val
    130                 135                 140

Leu Asp Gly Gly Gly Glu Glu Ile Gly Arg Gly Trp Ala Leu Asn Glu
145                 150                 155                 160

Val Ser Ile Glu Asn Leu Asn Arg Arg Gly Val Leu Asp Ala Thr Leu
                165                 170                 175

Glu Val Asp Ala Arg Pro Val Ala Ser Phe Gly Cys Asp Gly Val Leu
            180                 185                 190

Ile Ser Thr Pro Thr Gly Ser Thr Ala Tyr Ala Phe Ser Ala Gly Gly
        195                 200                 205

Pro Val Leu Trp Pro Glu Leu Asp Ala Ile Leu Val Val Pro Asn Asn
    210                 215                 220

Ala His Ala Leu Phe Thr Lys Pro Leu Val Val Ser Pro Lys Ser Thr
225                 230                 235                 240

Val Ala Val Glu Ser Asn Ser Asp Thr Ser Ala Ala Met Ala Val Met
                245                 250                 255

Asp Gly Phe Arg Pro Ile Pro Met Pro Pro Gly Ser Arg Val Glu Val
            260                 265                 270

Thr Arg Gly Glu Arg Pro Val Arg Trp Val Arg Leu Asp Ser Ser Pro
        275                 280                 285

Phe Thr Asp Arg Leu Val Ser Lys Leu Arg Leu Pro Val Thr Gly Trp
    290                 295                 300

Arg Gly Pro Gln Lys Gln Ala Glu Asn Lys Asp Pro Arg Ser Ala Gly
305                 310                 315                 320
```

<210> 2325
<211> 792
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(769)
<223> RXA01600

<400> 2325
tgagtacaaa tctcgtccaa cccatgctca tccactgttt tacggcctgg tgaagaccgc 60

tttggagctg cgtgtccacc cttagatcta caatgtgatc atg gtt tcg aag atg 115
Met Val Ser Lys Met
1 5

cac att ccc ggt acc cat gag ttc acg gtg aca gat act gaa ctg ttg 163
His Ile Pro Gly Thr His Glu Phe Thr Val Thr Asp Thr Glu Leu Leu
10 15 20

tta gag tcc cca att ttg ggc gtt cgt cga gat tca ttg atc atg ccg 211
Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp Ser Leu Ile Met Pro
25 30 35

ggt ggt tcc act gcc cgc cgt gaa gtg gtt gaa cac ttt ggg gcg gtc 259
Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu His Phe Gly Ala Val
40 45 50

gca gtg gtt gcc ttt gat ggt gaa aac att gcg atg gtc aag cag tac 307
Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala Met Val Lys Gln Tyr
55 60 65

cgt cgc agc gtg ggg gat tcc ttg tgg gag ctg cct gca ggt ttg ttg 355
Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu Pro Ala Gly Leu Leu
70 75 80 85

gat att gct gat gag gat gaa ctc acg ggc gcg cag cgc gag ctc atg 403
Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala Gln Arg Glu Leu Met
90 95 100

gag gag gct ggt ttg gag gcc agt gag tgg tcc gtg ctc act gat ttg 451
Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser Val Leu Thr Asp Leu
105 110 115

att acc tcg cct ggt ttc tgc gat gaa gcg gtg cgt gtc ttt cta gcc 499
Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val Arg Val Phe Leu Ala
120 125 130

cga ggc ctc aca aag gtt gag cgc ccg aag gtt atg ggc gat gaa gaa 547
Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val Met Gly Asp Glu Glu
135 140 145

gcg gac atg att aac cag tgg gtt ccg cta cat gag gca gtg gga atg 595
Ala Asp Met Ile Asn Gln Trp Val Pro Leu His Glu Ala Val Gly Met
150 155 160 165

```
gtg ttt agt ggc cag ttg gtt aac tcc att gcc att gcg ggt gtc atg   643
Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala Ile Ala Gly Val Met
                170                 175                 180

gct gct gat gct gtg att gcg ggt cgt gcg tct gcg cgt gcc gtc acc   691
Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser Ala Arg Ala Val Thr
            185                 190                 195

gcg ccg ttt acc tat cgc cct acg gcg ttg gcg cag cgt cga aaa gcg   739
Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala Gln Arg Arg Lys Ala
        200                 205                 210

cac ggc att gtt cct gac atg aaa aaa cta tgaaggctcg cgttttagcg     789
His Gly Ile Val Pro Asp Met Lys Lys Leu
    215                 220

aaa                                                               792
```

<210> 2326
<211> 223
<212> PRT
<213> Corynebacterium glutamicum

<400> 2326

```
Met Val Ser Lys Met His Ile Pro Gly Thr His Glu Phe Thr Val Thr
  1               5                  10                  15

Asp Thr Glu Leu Leu Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp
             20                  25                  30

Ser Leu Ile Met Pro Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu
         35                  40                  45

His Phe Gly Ala Val Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala
     50                  55                  60

Met Val Lys Gln Tyr Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu
 65                  70                  75                  80

Pro Ala Gly Leu Leu Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala
                 85                  90                  95

Gln Arg Glu Leu Met Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser
            100                 105                 110

Val Leu Thr Asp Leu Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val
        115                 120                 125

Arg Val Phe Leu Ala Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val
    130                 135                 140

Met Gly Asp Glu Glu Ala Asp Met Ile Asn Gln Trp Val Pro Leu His
145                 150                 155                 160

Glu Ala Val Gly Met Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala
                165                 170                 175

Ile Ala Gly Val Met Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser
            180                 185                 190
```

```
Ala Arg Ala Val Thr Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala
        195                 200                 205

Gln Arg Arg Lys Ala His Gly Ile Val Pro Asp Met Lys Lys Leu
    210                 215                 220


<210> 2327
<211> 1653
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1630)
<223> RXA01602

<400> 2327
tgcaggccac atgcctccca gtgccgtctc tgcacgttga ttttcccctg ccacgactgg 60

tcgcagggcg actttctagc acttttaaag gaatttttta atg gct aaa acc cat   115
                                              Met Ala Lys Thr His
                                                1               5

att cgg tta cag gac ctt tcc ctg tca tac acc tca acc ccg tta att   163
Ile Arg Leu Gln Asp Leu Ser Leu Ser Tyr Thr Ser Thr Pro Leu Ile
                10                  15                  20

acg aag ctc aat atc act gtt tct tct gga cag tgc gca gtg att gtt   211
Thr Lys Leu Asn Ile Thr Val Ser Ser Gly Gln Cys Ala Val Ile Val
            25                  30                  35

ggt gag aat ggt cga ggt aaa acc aca ctt ctg cga gca ctg gct cga   259
Gly Glu Asn Gly Arg Gly Lys Thr Thr Leu Leu Arg Ala Leu Ala Arg
        40                  45                  50

gaa ttc ccg cca tct gca ggt gag att ctc act cat ggc acg gta gca   307
Glu Phe Pro Pro Ser Ala Gly Glu Ile Leu Thr His Gly Thr Val Ala
    55                  60                  65

att gct cat caa cac atg cct gca ggt gat ctg tcc gtc gga gag atc   355
Ile Ala His Gln His Met Pro Ala Gly Asp Leu Ser Val Gly Glu Ile
70                  75                  80                  85

tgt gat gag gca att cgt gat tca aag aat gct ctc gaa gag ctt gag   403
Cys Asp Glu Ala Ile Arg Asp Ser Lys Asn Ala Leu Glu Glu Leu Glu
                90                  95                  100

aga gct gga gct cta ctt gag aca aac act gcg cac gca ctt gat gga   451
Arg Ala Gly Ala Leu Leu Glu Thr Asn Thr Ala His Ala Leu Asp Gly
            105                 110                 115

tat caa caa gcc ctt gat gcc gct gaa gtg ctt gac gca tgg aac gct   499
Tyr Gln Gln Ala Leu Asp Ala Ala Glu Val Leu Asp Ala Trp Asn Ala
        120                 125                 130

gaa cat cga tta gaa aaa gct ctg cgc agc ttt ggc gcg atc acc gat   547
Glu His Arg Leu Glu Lys Ala Leu Arg Ser Phe Gly Ala Ile Thr Asp
    135                 140                 145
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aga tcc cgt gca ctc agt gag cta tcg atc ggg caa agg tat cgg gta   595
Arg Ser Arg Ala Leu Ser Glu Leu Ser Ile Gly Gln Arg Tyr Arg Val
150                 155                 160                 165

cgg ctg gcc tgc ctc atc ggt ggc gat gct gat att ttg ctt ctc gat   643
Arg Leu Ala Cys Leu Ile Gly Gly Asp Ala Asp Ile Leu Leu Leu Asp
                170                 175                 180

gaa ccc acc aat cat ctt gac cgg ggc gcg ctt aac tat ctc acc gaa   691
Glu Pro Thr Asn His Leu Asp Arg Gly Ala Leu Asn Tyr Leu Thr Glu
            185                 190                 195

gcc ata acc tcc cac aaa ggt gtg gta ctt gtt gtt tct cat gat caa   739
Ala Ile Thr Ser His Lys Gly Val Val Leu Val Val Ser His Asp Gln
        200                 205                 210

gca ctg atc aaa gat gtc gcg gat ttc atc atc gat att gat tca acc   787
Ala Leu Ile Lys Asp Val Ala Asp Phe Ile Ile Asp Ile Asp Ser Thr
    215                 220                 225

cca gac ggc cta cca cgg atc tat cat gag ggt ttt gat tct tat cga   835
Pro Asp Gly Leu Pro Arg Ile Tyr His Glu Gly Phe Asp Ser Tyr Arg
230                 235                 240                 245

cgc caa agg agt gcg ctt ctt gaa act tgg agg cag gat tat gcc gct   883
Arg Gln Arg Ser Ala Leu Leu Glu Thr Trp Arg Gln Asp Tyr Ala Ala
                250                 255                 260

gca caa act gtg caa cag caa ttg cag gag gat cta gag cac gca cgc   931
Ala Gln Thr Val Gln Gln Gln Leu Gln Glu Asp Leu Glu His Ala Arg
            265                 270                 275

cag cgg gtg aat tct tcg tgg aaa cct cca aaa gga acg gga aaa cac   979
Gln Arg Val Asn Ser Ser Trp Lys Pro Pro Lys Gly Thr Gly Lys His
        280                 285                 290

act cgc gca tct cgg gct ccc gga gtg gtg cag gcc tta aag cga gca   1027
Thr Arg Ala Ser Arg Ala Pro Gly Val Val Gln Ala Leu Lys Arg Ala
    295                 300                 305

cag gat gcg ttg gat agc aaa gcg ttg gac gtt ccc ccg gct ccg gcc   1075
Gln Asp Ala Leu Asp Ser Lys Ala Leu Asp Val Pro Pro Ala Pro Ala
310                 315                 320                 325

cca ttg ctt ctg cct acc ttg aaa gtg cga cca gat aaa ccc atg gtg   1123
Pro Leu Leu Leu Pro Thr Leu Lys Val Arg Pro Asp Lys Pro Met Val
                330                 335                 340

gac ttt tcg gac ctt ttt gta ccc cac cgc ttg cgt ctg cca ggc tca   1171
Asp Phe Ser Asp Leu Phe Val Pro His Arg Leu Arg Leu Pro Gly Ser
            345                 350                 355

cat tca gtg gta tca ggt gac aaa ata gtg atc act ggt gac aac ggc   1219
His Ser Val Val Ser Gly Asp Lys Ile Val Ile Thr Gly Asp Asn Gly
        360                 365                 370

gct ggc aaa tca acg ctc atc gaa gtc ttg tct ggg gtt ttg act ccg   1267
Ala Gly Lys Ser Thr Leu Ile Glu Val Leu Ser Gly Val Leu Thr Pro
    375                 380                 385

gca agt ggt tcg gtt gca aac cat gcc cga act ggg gtt ctc ggc caa   1315
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Ala Ser Gly Ser Val Ala Asn His Ala Arg Thr Gly Val Leu Gly Gln
390                 395                 400                 405

gaa tca ctt gtc ggc gag gtg cca tca ata gca cga gat cac gca gtt   1363
Glu Ser Leu Val Gly Glu Val Pro Ser Ile Ala Arg Asp His Ala Val
                410                 415                 420

aag tgg gga ctt tta agt gtt gag gag agc cga ttt gcc cta cag gaa   1411
Lys Trp Gly Leu Leu Ser Val Glu Glu Ser Arg Phe Ala Leu Gln Glu
            425                 430                 435

ttc tca att ggt caa cgc aga aga cta gat ttg gcc atg tcg tta gct   1459
Phe Ser Ile Gly Gln Arg Arg Arg Leu Asp Leu Ala Met Ser Leu Ala
        440                 445                 450

ggc aat cct gaa ctg ttg ctt ctc gat gaa cct tcg aac cat ctg tct   1507
Gly Asn Pro Glu Leu Leu Leu Leu Asp Glu Pro Ser Asn His Leu Ser
    455                 460                 465

atg cac ttg gtt tcc gca ctt aca gag tgg ctg gac acg acc gcg gct   1555
Met His Leu Val Ser Ala Leu Thr Glu Trp Leu Asp Thr Thr Ala Ala
470                 475                 480                 485

gca gtg atc atg gta acg cat gat cga cag cta ctc cgc gat acg gct   1603
Ala Val Ile Met Val Thr His Asp Arg Gln Leu Leu Arg Asp Thr Ala
                490                 495                 500

cat tgg agg cac atc gag ttg aaa tct taagaattcg caagggcttt         1650
His Trp Arg His Ile Glu Leu Lys Ser
            505                 510

cac                                                               1653


<210> 2328
<211> 510
<212> PRT
<213> Corynebacterium glutamicum

<400> 2328
Met Ala Lys Thr His Ile Arg Leu Gln Asp Leu Ser Leu Ser Tyr Thr
  1               5                  10                  15

Ser Thr Pro Leu Ile Thr Lys Leu Asn Ile Thr Val Ser Ser Gly Gln
             20                  25                  30

Cys Ala Val Ile Val Gly Glu Asn Gly Arg Gly Lys Thr Thr Leu Leu
         35                  40                  45

Arg Ala Leu Ala Arg Glu Phe Pro Pro Ser Ala Gly Glu Ile Leu Thr
     50                  55                  60

His Gly Thr Val Ala Ile Ala His Gln His Met Pro Ala Gly Asp Leu
 65                  70                  75                  80

Ser Val Gly Glu Ile Cys Asp Glu Ala Ile Arg Asp Ser Lys Asn Ala
                 85                  90                  95

Leu Glu Glu Leu Glu Arg Ala Gly Ala Leu Leu Glu Thr Asn Thr Ala
            100                 105                 110
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```
His Ala Leu Asp Gly Tyr Gln Gln Ala Leu Asp Ala Ala Glu Val Leu
        115                 120                 125

Asp Ala Trp Asn Ala Glu His Arg Leu Glu Lys Ala Leu Arg Ser Phe
    130                 135                 140

Gly Ala Ile Thr Asp Arg Ser Arg Ala Leu Ser Glu Leu Ser Ile Gly
145                 150                 155                 160

Gln Arg Tyr Arg Val Arg Leu Ala Cys Leu Ile Gly Gly Asp Ala Asp
                165                 170                 175

Ile Leu Leu Leu Asp Glu Pro Thr Asn His Leu Asp Arg Gly Ala Leu
            180                 185                 190

Asn Tyr Leu Thr Glu Ala Ile Thr Ser His Lys Gly Val Val Leu Val
        195                 200                 205

Val Ser His Asp Gln Ala Leu Ile Lys Asp Val Ala Asp Phe Ile Ile
    210                 215                 220

Asp Ile Asp Ser Thr Pro Asp Gly Leu Pro Arg Ile Tyr His Glu Gly
225                 230                 235                 240

Phe Asp Ser Tyr Arg Arg Gln Arg Ser Ala Leu Leu Glu Thr Trp Arg
                245                 250                 255

Gln Asp Tyr Ala Ala Ala Gln Thr Val Gln Gln Gln Leu Gln Glu Asp
            260                 265                 270

Leu Glu His Ala Arg Gln Arg Val Asn Ser Ser Trp Lys Pro Pro Lys
        275                 280                 285

Gly Thr Gly Lys His Thr Arg Ala Ser Arg Ala Pro Gly Val Val Gln
    290                 295                 300

Ala Leu Lys Arg Ala Gln Asp Ala Leu Asp Ser Lys Ala Leu Asp Val
305                 310                 315                 320

Pro Pro Ala Pro Ala Pro Leu Leu Leu Pro Thr Leu Lys Val Arg Pro
                325                 330                 335

Asp Lys Pro Met Val Asp Phe Ser Asp Leu Phe Val Pro His Arg Leu
            340                 345                 350

Arg Leu Pro Gly Ser His Ser Val Val Ser Gly Asp Lys Ile Val Ile
        355                 360                 365

Thr Gly Asp Asn Gly Ala Gly Lys Ser Thr Leu Ile Glu Val Leu Ser
    370                 375                 380

Gly Val Leu Thr Pro Ala Ser Gly Ser Val Ala Asn His Ala Arg Thr
385                 390                 395                 400

Gly Val Leu Gly Gln Glu Ser Leu Val Gly Glu Val Pro Ser Ile Ala
                405                 410                 415

Arg Asp His Ala Val Lys Trp Gly Leu Leu Ser Val Glu Glu Ser Arg
            420                 425                 430

Phe Ala Leu Gln Glu Phe Ser Ile Gly Gln Arg Arg Arg Leu Asp Leu
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        435                 440                 445

Ala Met Ser Leu Ala Gly Asn Pro Glu Leu Leu Leu Leu Asp Glu Pro
    450                 455                 460

Ser Asn His Leu Ser Met His Leu Val Ser Ala Leu Thr Glu Trp Leu
465                 470                 475                 480

Asp Thr Thr Ala Ala Ala Val Ile Met Val Thr His Asp Arg Gln Leu
                485                 490                 495

Leu Arg Asp Thr Ala His Trp Arg His Ile Glu Leu Lys Ser
            500                 505                 510


<210> 2329
<211> 1638
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1615)
<223> RXA01605

<400> 2329
agtcaagcgc cgaagaaagg cccgngaagg naatcagacg acgggcacct actacttcgg 60

cattgaaatt ccgaagaact tcagcgattc tattgccagc gtg acc agc gat tca   115
                                            Val Thr Ser Asp Ser
                                              1               5

ccc gcg cca gca acc gtc aac gcg gta ttc aac aac agc aac ggc ttc   163
Pro Ala Pro Ala Thr Val Asn Ala Val Phe Asn Asn Ser Asn Gly Phe
                10                  15                  20

att gcc tcc atg ctg ggc aac cag gtg gtc aac act gtt gtg gag acc   211
Ile Ala Ser Met Leu Gly Asn Gln Val Val Asn Thr Val Val Glu Thr
            25                  30                  35

atg gac acg gaa ttc ggc gtc cgc att gtg gat aac atg ctc gtc ggt   259
Met Asp Thr Glu Phe Gly Val Arg Ile Val Asp Asn Met Leu Val Gly
        40                  45                  50

ttc tcc acc ttg ggc gac ggc atg aac caa gcc gcc gaa ggt gcc act   307
Phe Ser Thr Leu Gly Asp Gly Met Asn Gln Ala Ala Glu Gly Ala Thr
    55                  60                  65

acg ctc agc gat ggc gtc ggt tcc gcc aac gac ggt gca gtt cag ctt   355
Thr Leu Ser Asp Gly Val Gly Ser Ala Asn Asp Gly Ala Val Gln Leu
70                  75                  80                  85

gcc gac ggc gcg gtc acc ctg cgc gac ggc atc gca agt gcc aat gag   403
Ala Asp Gly Ala Val Thr Leu Arg Asp Gly Ile Ala Ser Ala Asn Glu
                90                  95                  100

ggt gcg caa tcg ctt gcc gac ggc gcc agc cag ctc gac acc ggc ctc   451
Gly Ala Gln Ser Leu Ala Asp Gly Ala Ser Gln Leu Asp Thr Gly Leu
            105                 110                 115

ggc tcc gcg gct aca ggc agc caa acg ctc gcc gac ggt cta tcc agc   499
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Gly Ser Ala Ala Thr Gly Ser Gln Thr Leu Ala Asp Gly Leu Ser Ser
        120                 125                 130

ctg tct gcg ggc acc gcc caa cta ggc caa ggc gca acc cag gtt tca   547
Leu Ser Ala Gly Thr Ala Gln Leu Gly Gln Gly Ala Thr Gln Val Ser
    135                 140                 145

gat ggc gtg ggc caa ctt gtc gac caa gta gca cca ctg acc gcc tat   595
Asp Gly Val Gly Gln Leu Val Asp Gln Val Ala Pro Leu Thr Ala Tyr
150                 155                 160                 165

gtt cca gac atc aac tct cag ttg atc acc ctg cgc gac ggc gca gcc   643
Val Pro Asp Ile Asn Ser Gln Leu Ile Thr Leu Arg Asp Gly Ala Ala
                170                 175                 180

acc att gcc tct gaa cta tct gat ccc tcc agc acc tac cgc tcc ggc   691
Thr Ile Ala Ser Glu Leu Ser Asp Pro Ser Ser Thr Tyr Arg Ser Gly
            185                 190                 195

gtg gac tcc gct gtg agc gca tcc cag caa cta gca gcc ggc ctg caa   739
Val Asp Ser Ala Val Ser Ala Ser Gln Gln Leu Ala Ala Gly Leu Gln
        200                 205                 210

acc ctg aaa gac gga tcc agc caa ctc agc atc ggt gca cgc acc ctc   787
Thr Leu Lys Asp Gly Ser Ser Gln Leu Ser Ile Gly Ala Arg Thr Leu
    215                 220                 225

gct gat ggc acc agc caa ttg gcc gca ggt tcc gaa cag cta gtt gtt   835
Ala Asp Gly Thr Ser Gln Leu Ala Ala Gly Ser Glu Gln Leu Val Val
230                 235                 240                 245

ggc gca caa gca ctg cgc gac ggc acc gtc cag ctt gat gaa ggc tcc   883
Gly Ala Gln Ala Leu Arg Asp Gly Thr Val Gln Leu Asp Glu Gly Ser
                250                 255                 260

agc gaa ctc gcc ctc aaa ctc acc gac ggc gca agc caa gta cca acc   931
Ser Glu Leu Ala Leu Lys Leu Thr Asp Gly Ala Ser Gln Val Pro Thr
            265                 270                 275

ttc gct gac ggc gca gac acc acc atc gca acc cca gtt gaa aca gaa   979
Phe Ala Asp Gly Ala Asp Thr Thr Ile Ala Thr Pro Val Glu Thr Glu
        280                 285                 290

caa gca gga gac acc aca ccg ctc ttc ggt att ggt ctc gca cca ttc   1027
Gln Ala Gly Asp Thr Thr Pro Leu Phe Gly Ile Gly Leu Ala Pro Phe
    295                 300                 305

ttc atg gct gtc ggc ctg ttc atg gga gca acc gtt gcc tgg atg atc   1075
Phe Met Ala Val Gly Leu Phe Met Gly Ala Thr Val Ala Trp Met Ile
310                 315                 320                 325

ctg cac cca atc agt cgc cgc gca ctc gac tcc cgc atg gga ggc ttc   1123
Leu His Pro Ile Ser Arg Arg Ala Leu Asp Ser Arg Met Gly Gly Phe
                330                 335                 340

cga ggc acc ctg gca agc tac ctt cca tca aca gtc tta ggc ctt ggc   1171
Arg Gly Thr Leu Ala Ser Tyr Leu Pro Ser Thr Val Leu Gly Leu Gly
            345                 350                 355

caa gca acc atc atg tgg gca gta ctg tac ttc ctg ctc gac ctc aat   1219
Gln Ala Thr Ile Met Trp Ala Val Leu Tyr Phe Leu Leu Asp Leu Asn
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        360                 365                 370

cca gct cac cca gct gga ctg tgg atg gcg atg gtc gcc atc tca tgg   1267
Pro Ala His Pro Ala Gly Leu Trp Met Ala Met Val Ala Ile Ser Trp
    375                 380                 385

gta ttc atc tcc att acc cat atg ttc aac aac gtg gca gga ccc tcc   1315
Val Phe Ile Ser Ile Thr His Met Phe Asn Asn Val Ala Gly Pro Ser
390                 395                 400                 405

gca ggc cgt gtg ctg tcc atc gtg atg atg tcc ttc cag cta gtc tcc   1363
Ala Gly Arg Val Leu Ser Ile Val Met Met Ser Phe Gln Leu Val Ser
                410                 415                 420

tcc ggt ggc cta tac cca cca gaa acc cag cca gca ttc ttc cac tgg   1411
Ser Gly Gly Leu Tyr Pro Pro Glu Thr Gln Pro Ala Phe Phe His Trp
            425                 430                 435

ttc cac acc tac gac ccg atc acc tac gca gtc aac ctc gtg cgc caa   1459
Phe His Thr Tyr Asp Pro Ile Thr Tyr Ala Val Asn Leu Val Arg Gln
        440                 445                 450

atg atc ttc aac gaa acc cca tcc aac gac cca cgc ttc ata caa gca   1507
Met Ile Phe Asn Glu Thr Pro Ser Asn Asp Pro Arg Phe Ile Gln Ala
    455                 460                 465

atc tgg gta ctg ctc ttc atc tgg gca ctg atg ctc gcc atc tcc acc   1555
Ile Trp Val Leu Leu Phe Ile Trp Ala Leu Met Leu Ala Ile Ser Thr
470                 475                 480                 485

ctg gcg aat aga aca aac aag gtt ctt cgc atg aag gac tac cac cca   1603
Leu Ala Asn Arg Thr Asn Lys Val Leu Arg Met Lys Asp Tyr His Pro
                490                 495                 500

gaa ctg aag gtc taaaagcttt tcccgcccgg ttc                        1638
Glu Leu Lys Val
            505
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<210> 2330
<211> 505
<212> PRT
<213> Corynebacterium glutamicum

<400> 2330

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Val Thr Ser Asp Ser Pro Ala Pro Ala Thr Val Asn Ala Val Phe Asn
  1               5                  10                  15

Asn Ser Asn Gly Phe Ile Ala Ser Met Leu Gly Asn Gln Val Val Asn
             20                  25                  30

Thr Val Val Glu Thr Met Asp Thr Glu Phe Gly Val Arg Ile Val Asp
         35                  40                  45

Asn Met Leu Val Gly Phe Ser Thr Leu Gly Asp Gly Met Asn Gln Ala
     50                  55                  60

Ala Glu Gly Ala Thr Thr Leu Ser Asp Gly Val Gly Ser Ala Asn Asp
 65                  70                  75                  80

Gly Ala Val Gln Leu Ala Asp Gly Ala Val Thr Leu Arg Asp Gly Ile
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                  85                  90                  95

Ala Ser Ala Asn Glu Gly Ala Gln Ser Leu Ala Asp Gly Ala Ser Gln
            100                 105                 110

Leu Asp Thr Gly Leu Gly Ser Ala Ala Thr Gly Ser Gln Thr Leu Ala
        115                 120                 125

Asp Gly Leu Ser Ser Leu Ser Ala Gly Thr Ala Gln Leu Gly Gln Gly
    130                 135                 140

Ala Thr Gln Val Ser Asp Gly Val Gly Gln Leu Val Asp Gln Val Ala
145                 150                 155                 160

Pro Leu Thr Ala Tyr Val Pro Asp Ile Asn Ser Gln Leu Ile Thr Leu
                165                 170                 175

Arg Asp Gly Ala Ala Thr Ile Ala Ser Glu Leu Ser Asp Pro Ser Ser
            180                 185                 190

Thr Tyr Arg Ser Gly Val Asp Ser Ala Val Ser Ala Ser Gln Gln Leu
        195                 200                 205

Ala Ala Gly Leu Gln Thr Leu Lys Asp Gly Ser Ser Gln Leu Ser Ile
    210                 215                 220

Gly Ala Arg Thr Leu Ala Asp Gly Thr Ser Gln Leu Ala Ala Gly Ser
225                 230                 235                 240

Glu Gln Leu Val Val Gly Ala Gln Ala Leu Arg Asp Gly Thr Val Gln
                245                 250                 255

Leu Asp Glu Gly Ser Ser Glu Leu Ala Leu Lys Leu Thr Asp Gly Ala
            260                 265                 270

Ser Gln Val Pro Thr Phe Ala Asp Gly Ala Asp Thr Thr Ile Ala Thr
        275                 280                 285

Pro Val Glu Thr Glu Gln Ala Gly Asp Thr Thr Pro Leu Phe Gly Ile
    290                 295                 300

Gly Leu Ala Pro Phe Phe Met Ala Val Gly Leu Phe Met Gly Ala Thr
305                 310                 315                 320

Val Ala Trp Met Ile Leu His Pro Ile Ser Arg Arg Ala Leu Asp Ser
                325                 330                 335

Arg Met Gly Gly Phe Arg Gly Thr Leu Ala Ser Tyr Leu Pro Ser Thr
            340                 345                 350

Val Leu Gly Leu Gly Gln Ala Thr Ile Met Trp Ala Val Leu Tyr Phe
        355                 360                 365

Leu Leu Asp Leu Asn Pro Ala His Pro Ala Gly Leu Trp Met Ala Met
    370                 375                 380

Val Ala Ile Ser Trp Val Phe Ile Ser Ile Thr His Met Phe Asn Asn
385                 390                 395                 400

Val Ala Gly Pro Ser Ala Gly Arg Val Leu Ser Ile Val Met Met Ser
                405                 410                 415
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```
Phe Gln Leu Val Ser Ser Gly Gly Leu Tyr Pro Pro Glu Thr Gln Pro
            420                 425                 430

Ala Phe Phe His Trp Phe His Thr Tyr Asp Pro Ile Thr Tyr Ala Val
        435                 440                 445

Asn Leu Val Arg Gln Met Ile Phe Asn Glu Thr Pro Ser Asn Asp Pro
    450                 455                 460

Arg Phe Ile Gln Ala Ile Trp Val Leu Leu Phe Ile Trp Ala Leu Met
465                 470                 475                 480

Leu Ala Ile Ser Thr Leu Ala Asn Arg Thr Asn Lys Val Leu Arg Met
                485                 490                 495

Lys Asp Tyr His Pro Glu Leu Lys Val
            500                 505


<210> 2331
<211> 852
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(829)
<223> RXA01610

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tccatatctt tagtttgcga aagcgatcaa cttaaaacac gtg tcc ggt ttt ctt   115
                                            Val Ser Gly Phe Leu
                                              1               5

act ccc cca gct aca ccc cat att cgg acg gca act gcc agt att gct   163
Thr Pro Pro Ala Thr Pro His Ile Arg Thr Ala Thr Ala Ser Ile Ala
                10                  15                  20

acc gca gtt gcc gta gca ctg tca gtg ttc gct gct gca ctc att cca   211
Thr Ala Val Ala Val Ala Leu Ser Val Phe Ala Ala Ala Leu Ile Pro
            25                  30                  35

gga agc gct ctg tat tct gtg ctg acc gct gga ggg gtg gca ctt gga   259
Gly Ser Ala Leu Tyr Ser Val Leu Thr Ala Gly Gly Val Ala Leu Gly
        40                  45                  50

gca gca tca ggc gtt gcc gcg tta cgc cat cgc gga ggg ctt cgc att   307
Ala Ala Ser Gly Val Ala Ala Leu Arg His Arg Gly Gly Leu Arg Ile
    55                  60                  65

ttt caa tgg ctg tct gcg ctt ggt gga atc gtc att ttg ctg atc ggt   355
Phe Gln Trp Leu Ser Ala Leu Gly Gly Ile Val Ile Leu Leu Ile Gly
70                  75                  80                  85

atc gta gtg gca gtt gca aag ttt ggg gcc tcg gca aaa ctt gcc acg   403
Ile Val Val Ala Val Ala Lys Phe Gly Ala Ser Ala Lys Leu Ala Thr
                90                  95                  100
```

```
tta ggc ctg gtg acc tcg tat tat ctc atg ccg tct gcg gca ttg gcc   451
Leu Gly Leu Val Thr Ser Tyr Tyr Leu Met Pro Ser Ala Ala Leu Ala
            105                 110                 115

tgt tat atc gga ggg ctt ggc cag cta cca gcc aaa tgg att gcg cca   499
Cys Tyr Ile Gly Gly Leu Gly Gln Leu Pro Ala Lys Trp Ile Ala Pro
        120                 125                 130

gcg ttt atg gct acg gct ggt gca ggt gct gcg gga tgg ttt tca ttg   547
Ala Phe Met Ala Thr Ala Gly Ala Gly Ala Ala Gly Trp Phe Ser Leu
    135                 140                 145

ggg gca ggc acc ggt ttt gaa cgg ttc ctc att gct gtt gca gcg gtg   595
Gly Ala Gly Thr Gly Phe Glu Arg Phe Leu Ile Ala Val Ala Ala Val
150                 155                 160                 165

ttt tca ctg atg gga tgt gta tac cca gtg tgg gga tgc gtc gta aag   643
Phe Ser Leu Met Gly Cys Val Tyr Pro Val Trp Gly Cys Val Val Lys
                170                 175                 180

cgt cca cgt caa gtg gct gca tgg ctg gtc gcg ctg gcg gcc ctg gtg   691
Arg Pro Arg Gln Val Ala Ala Trp Leu Val Ala Leu Ala Ala Leu Val
            185                 190                 195

ctt ggg gcg ctc atg ctt ttt atg gtg agc atg gtg gtg gcg ccg ggt   739
Leu Gly Ala Leu Met Leu Phe Met Val Ser Met Val Val Ala Pro Gly
        200                 205                 210

ttg ctg tgg ctg cag ccc acg acg gtc gca tgg ggt ttt atg att gcc   787
Leu Leu Trp Leu Gln Pro Thr Thr Val Ala Trp Gly Phe Met Ile Ala
    215                 220                 225

ggg gtt ctt gcg acg gtc gca ggc ttg tgg cct agg cgt ttt           829
Gly Val Leu Ala Thr Val Ala Gly Leu Trp Pro Arg Arg Phe
230                 235                 240

tagacggaat cgtctgggag ggt                                        852


<210> 2332
<211> 243
<212> PRT
<213> Corynebacterium glutamicum

<400> 2332
Val Ser Gly Phe Leu Thr Pro Pro Ala Thr Pro His Ile Arg Thr Ala
  1               5                  10                  15

Thr Ala Ser Ile Ala Thr Ala Val Ala Val Ala Leu Ser Val Phe Ala
             20                  25                  30

Ala Ala Leu Ile Pro Gly Ser Ala Leu Tyr Ser Val Leu Thr Ala Gly
         35                  40                  45

Gly Val Ala Leu Gly Ala Ala Ser Gly Val Ala Ala Leu Arg His Arg
     50                  55                  60

Gly Gly Leu Arg Ile Phe Gln Trp Leu Ser Ala Leu Gly Gly Ile Val
 65                  70                  75                  80

Ile Leu Leu Ile Gly Ile Val Val Ala Val Ala Lys Phe Gly Ala Ser
```

```
                85                  90                  95

Ala Lys Leu Ala Thr Leu Gly Leu Val Thr Ser Tyr Tyr Leu Met Pro
            100                 105                 110

Ser Ala Ala Leu Ala Cys Tyr Ile Gly Gly Leu Gly Gln Leu Pro Ala
        115                 120                 125

Lys Trp Ile Ala Pro Ala Phe Met Ala Thr Ala Gly Ala Gly Ala Ala
    130                 135                 140

Gly Trp Phe Ser Leu Gly Ala Gly Thr Gly Phe Glu Arg Phe Leu Ile
145                 150                 155                 160

Ala Val Ala Ala Val Phe Ser Leu Met Gly Cys Val Tyr Pro Val Trp
                165                 170                 175

Gly Cys Val Val Lys Arg Pro Arg Gln Val Ala Ala Trp Leu Val Ala
            180                 185                 190

Leu Ala Ala Leu Val Leu Gly Ala Leu Met Leu Phe Met Val Ser Met
        195                 200                 205

Val Val Ala Pro Gly Leu Leu Trp Leu Gln Pro Thr Thr Val Ala Trp
    210                 215                 220

Gly Phe Met Ile Ala Gly Val Leu Ala Thr Val Ala Gly Leu Trp Pro
225                 230                 235                 240

Arg Arg Phe
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<210> 2333
<211> 480
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(457)
<223> RXA01611

<400> 2333
cccgcttaca actacttggt ttacaccggt gttatcaagg gctaaatcgc ctaacctcta 60

tcttcatcta tagcttagct ttactgaaag gcttttcatc atg cgt aaa ttc cgc 115
                                            Met Arg Lys Phe Arg
                                              1   5

aac act gca att gca cta gtt tct gca gct gca atc acc ttg ggt ggc 163
Asn Thr Ala Ile Ala Leu Val Ser Ala Ala Ala Ile Thr Leu Gly Gly
                10   15   20

gtt acc gct gct acc gct cag gaa gac gaa act cct cct gca gca gag 211
Val Thr Ala Ala Thr Ala Gln Glu Asp Glu Thr Pro Pro Ala Ala Glu
            25   30   35

acc gag acc act tct cct tcc ggt tcc tca ggc tct tcc tgg aac gac 259
Thr Glu Thr Thr Ser Pro Ser Gly Ser Ser Gly Ser Ser Trp Asn Asp
        40   45   50

```
tac aac gaa gag tac gaa ggc gac caa gag ggc tac gga atc gac ggc   307
Tyr Asn Glu Glu Tyr Glu Gly Asp Gln Glu Gly Tyr Gly Ile Asp Gly
     55                  60                  65

ttt ggt tct tcc cgc gat gac tcc gga gaa gaa gtt cca cgt tgg ttg   355
Phe Gly Ser Ser Arg Asp Asp Ser Gly Glu Glu Val Pro Arg Trp Leu
 70                  75                  80                  85

gag acc tgg ggc aag gta ttt gac gct ttg acc att acc tcc gtt ctt   403
Glu Thr Trp Gly Lys Val Phe Asp Ala Leu Thr Ile Thr Ser Val Leu
                90                  95                 100

ggt ctt gtt gtc ttc cct gtt gtt aac ttc ctg aag tac aac ggc ctc   451
Gly Leu Val Val Phe Pro Val Val Asn Phe Leu Lys Tyr Asn Gly Leu
            105                 110                 115

att aag taatctgcaa tttcctgtca aat                                480
Ile Lys
```

<210> 2334
<211> 119
<212> PRT
<213> Corynebacterium glutamicum

<400> 2334

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Met Arg Lys Phe Arg Asn Thr Ala Ile Ala Leu Val Ser Ala Ala Ala
  1               5                  10                  15

Ile Thr Leu Gly Gly Val Thr Ala Ala Thr Ala Gln Glu Asp Glu Thr
             20                  25                  30

Pro Pro Ala Ala Glu Thr Glu Thr Thr Ser Pro Ser Gly Ser Ser Gly
         35                  40                  45

Ser Ser Trp Asn Asp Tyr Asn Glu Glu Tyr Glu Gly Asp Gln Glu Gly
     50                  55                  60

Tyr Gly Ile Asp Gly Phe Gly Ser Ser Arg Asp Asp Ser Gly Glu Glu
 65                  70                  75                  80

Val Pro Arg Trp Leu Glu Thr Trp Gly Lys Val Phe Asp Ala Leu Thr
                 85                  90                  95

Ile Thr Ser Val Leu Gly Leu Val Val Phe Pro Val Val Asn Phe Leu
            100                 105                 110

Lys Tyr Asn Gly Leu Ile Lys
        115
```

<210> 2335
<211> 468
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(445)

<223> RXA01612

<400> 2335
gaaaaaacga cgttggttcg tagtcgctgg aaatttaata attcctccgt ccccttcaac 60

```
taggggtgg aaacccgact atttccgaag gactattctc atg cgt tct ttc cgt   115
                                            Met Arg Ser Phe Arg
                                              1               5

acc gcg gca gtt gca ggc ctt act gca gtt gca ctt tcc gta ggt tcc   163
Thr Ala Ala Val Ala Gly Leu Thr Ala Val Ala Leu Ser Val Gly Ser
                 10                  15                  20

gcc acc gtg gca act gcg gaa gaa tct gat caa aac ctc tca tcc ggc   211
Ala Thr Val Ala Thr Ala Glu Glu Ser Asp Gln Asn Leu Ser Ser Gly
             25                  30                  35

ttc tca gca ctt tct tcc ggt ggc gca gcg gcc gta ggt gag gac tgg   259
Phe Ser Ala Leu Ser Ser Gly Gly Ala Ala Ala Val Gly Glu Asp Trp
         40                  45                  50

gat gca gac cag ccc gtc aca ggt gaa gac atc ttt ggt gaa gag cac   307
Asp Ala Asp Gln Pro Val Thr Gly Glu Asp Ile Phe Gly Glu Glu His
     55                  60                  65

gag cgc gat aac gaa aac acc cca gcg tgg gct aag aac atg tac gat   355
Glu Arg Asp Asn Glu Asn Thr Pro Ala Trp Ala Lys Asn Met Tyr Asp
 70                  75                  80                  85

cta acc gtc ttg ggt ggc att gct tcc ctt ctc ggt gtc atc gta ttc   403
Leu Thr Val Leu Gly Gly Ile Ala Ser Leu Leu Gly Val Ile Val Phe
                 90                  95                 100

ccc gct tac aac tac ttg gtt tac acc ggt gtt atc aag ggc           445
Pro Ala Tyr Asn Tyr Leu Val Tyr Thr Gly Val Ile Lys Gly
             105                 110                 115

taaatcgcct aacctctatc ttc                                        468
```

<210> 2336
<211> 115
<212> PRT
<213> Corynebacterium glutamicum

<400> 2336

```
Met Arg Ser Phe Arg Thr Ala Ala Val Ala Gly Leu Thr Ala Val Ala
  1               5                  10                  15

Leu Ser Val Gly Ser Ala Thr Val Ala Thr Ala Glu Glu Ser Asp Gln
             20                  25                  30

Asn Leu Ser Ser Gly Phe Ser Ala Leu Ser Ser Gly Gly Ala Ala Ala
         35                  40                  45

Val Gly Glu Asp Trp Asp Ala Asp Gln Pro Val Thr Gly Glu Asp Ile
     50                  55                  60

Phe Gly Glu Glu His Glu Arg Asp Asn Glu Asn Thr Pro Ala Trp Ala
 65                  70                  75                  80
```

```
Lys Asn Met Tyr Asp Leu Thr Val Leu Gly Gly Ile Ala Ser Leu Leu
                 85                  90                  95

Gly Val Ile Val Phe Pro Ala Tyr Asn Tyr Leu Val Tyr Thr Gly Val
            100                 105                 110

Ile Lys Gly
        115
```

<210> 2337
<211> 1098
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1075)
<223> RXA01619

<400> 2337

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cctgcaagtt tactgctcgg ccgtcacggg ggaatggaaa aagtacgctt ggtgttcata 60

tagcgaaccc attttctatt gcgatgagag gaacaccacc atg cgc gca atc act   115
                                             Met Arg Ala Ile Thr
                                               1               5

cac aac act ttc ggc gac ccc gcc gac gtc cta cag att acc gag aag   163
His Asn Thr Phe Gly Asp Pro Ala Asp Val Leu Gln Ile Thr Glu Lys
                10                  15                  20

gaa att ccc act ccc ggc cca ggt cag gtt cgt att caa gtg acg ctg   211
Glu Ile Pro Thr Pro Gly Pro Gly Gln Val Arg Ile Gln Val Thr Leu
            25                  30                  35

gca acc atc cac aac cat gat ttg tgg acc gtg aag ggc tct tac ggc   259
Ala Thr Ile His Asn His Asp Leu Trp Thr Val Lys Gly Ser Tyr Gly
        40                  45                  50

ttc gtc cca gat ctg ccg gcc gcc gca ggc acc gag gca gtc ggc atc   307
Phe Val Pro Asp Leu Pro Ala Ala Ala Gly Thr Glu Ala Val Gly Ile
    55                  60                  65

gtc gac gcc ctg ggc gag ggc gtc gaa ggt ttg cag gtc ggt cag cgt   355
Val Asp Ala Leu Gly Glu Gly Val Glu Gly Leu Gln Val Gly Gln Arg
70                  75                  80                  85

gtt gcg tcc ggc acc agc ttt ggc atc tgg gcg gag tac gcg ctt gtc   403
Val Ala Ser Gly Thr Ser Phe Gly Ile Trp Ala Glu Tyr Ala Leu Val
                90                  95                 100

gac gcc tcc ggc ctc att ccc gta cca gaa cag ctc tcc gac gaa agc   451
Asp Ala Ser Gly Leu Ile Pro Val Pro Glu Gln Leu Ser Asp Glu Ser
            105                 110                 115

gca gct cag ctc gtc gca atg cct ttc agc gcc atc agc ctt ctt gat   499
Ala Ala Gln Leu Val Ala Met Pro Phe Ser Ala Ile Ser Leu Leu Asp
        120                 125                 130

ttc ctg gat atg aaa cca ggg gag tgg ctg atc caa aac tcc gca aac   547
Phe Leu Asp Met Lys Pro Gly Glu Trp Leu Ile Gln Asn Ser Ala Asn
```

```
    135                 140                 145

ggt gcc gtc ggc cgc atg ctc gca cag ctg gca gaa tcc cgc ggc atc   595
Gly Ala Val Gly Arg Met Leu Ala Gln Leu Ala Glu Ser Arg Gly Ile
150                 155                 160                 165

cat gtc gtt ggt ctc gtc cgc cgt gac gcc ggt gtc caa gaa ctc gct   643
His Val Val Gly Leu Val Arg Arg Asp Ala Gly Val Gln Glu Leu Ala
                170                 175                 180

gct caa aac atc agc ggc gtc gtt tcc act gag acc cca ggc tgg gaa   691
Ala Gln Asn Ile Ser Gly Val Val Ser Thr Glu Thr Pro Gly Trp Glu
            185                 190                 195

aag cag gtc gaa gac atc acc ggt ggc gca agc atc gcc gtc gca ctt   739
Lys Gln Val Glu Asp Ile Thr Gly Gly Ala Ser Ile Ala Val Ala Leu
        200                 205                 210

gat tcc gtc ggt gga tcc tcc gca gct gac ctg gtg aaa ctg ctt ggc   787
Asp Ser Val Gly Gly Ser Ser Ala Ala Asp Leu Val Lys Leu Leu Gly
    215                 220                 225

gaa ggc ggc acc ctc gtc tcc ttc ggc gcc atg ggc aac cca atc atg   835
Glu Gly Gly Thr Leu Val Ser Phe Gly Ala Met Gly Asn Pro Ile Met
230                 235                 240                 245

gaa atc cca tcc ggc ccc gtc atc ttc aag cac atc acc gtc aag ggc   883
Glu Ile Pro Ser Gly Pro Val Ile Phe Lys His Ile Thr Val Lys Gly
                250                 255                 260

ttc tgg gga agc aaa gtc agc cgc gaa atg cca gca gag aag aaa acc   931
Phe Trp Gly Ser Lys Val Ser Arg Glu Met Pro Ala Glu Lys Lys Thr
            265                 270                 275

cag ttg ttc ggc gag ctc att gcg cgc ata ctt gat gga aca ttg acc   979
Gln Leu Phe Gly Glu Leu Ile Ala Arg Ile Leu Asp Gly Thr Leu Thr
        280                 285                 290

ctt cca gtt gat tcc acc ttt gat gcc gct gac atc gtc tcg gcc gtg   1027
Leu Pro Val Asp Ser Thr Phe Asp Ala Ala Asp Ile Val Ser Ala Val
    295                 300                 305

cgc gcc tcc agc gag cct ggc cgt gcc gga aaa gtg ctc att cgt ttc   1075
Arg Ala Ser Ser Glu Pro Gly Arg Ala Gly Lys Val Leu Ile Arg Phe
310                 315                 320                 325

taaacgttta aggcccatta gac                                        1098
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<210> 2338
<211> 325
<212> PRT
<213> Corynebacterium glutamicum

<400> 2338

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Met Arg Ala Ile Thr His Asn Thr Phe Gly Asp Pro Ala Asp Val Leu
  1               5                  10                  15

Gln Ile Thr Glu Lys Glu Ile Pro Thr Pro Gly Pro Gly Gln Val Arg
             20                  25                  30
```

```
Ile Gln Val Thr Leu Ala Thr Ile His Asn His Asp Leu Trp Thr Val
          35                  40                  45

Lys Gly Ser Tyr Gly Phe Val Pro Asp Leu Pro Ala Ala Ala Gly Thr
      50                  55                  60

Glu Ala Val Gly Ile Val Asp Ala Leu Gly Glu Gly Val Glu Gly Leu
 65                  70                  75                  80

Gln Val Gly Gln Arg Val Ala Ser Gly Thr Ser Phe Gly Ile Trp Ala
                 85                  90                  95

Glu Tyr Ala Leu Val Asp Ala Ser Gly Leu Ile Pro Val Pro Glu Gln
            100                 105                 110

Leu Ser Asp Glu Ser Ala Ala Gln Leu Val Ala Met Pro Phe Ser Ala
        115                 120                 125

Ile Ser Leu Leu Asp Phe Leu Asp Met Lys Pro Gly Glu Trp Leu Ile
    130                 135                 140

Gln Asn Ser Ala Asn Gly Ala Val Gly Arg Met Leu Ala Gln Leu Ala
145                 150                 155                 160

Glu Ser Arg Gly Ile His Val Val Gly Leu Val Arg Arg Asp Ala Gly
                165                 170                 175

Val Gln Glu Leu Ala Ala Gln Asn Ile Ser Gly Val Val Ser Thr Glu
            180                 185                 190

Thr Pro Gly Trp Glu Lys Gln Val Glu Asp Ile Thr Gly Gly Ala Ser
        195                 200                 205

Ile Ala Val Ala Leu Asp Ser Val Gly Gly Ser Ser Ala Ala Asp Leu
    210                 215                 220

Val Lys Leu Leu Gly Glu Gly Gly Thr Leu Val Ser Phe Gly Ala Met
225                 230                 235                 240

Gly Asn Pro Ile Met Glu Ile Pro Ser Gly Pro Val Ile Phe Lys His
                245                 250                 255

Ile Thr Val Lys Gly Phe Trp Gly Ser Lys Val Ser Arg Glu Met Pro
            260                 265                 270

Ala Glu Lys Lys Thr Gln Leu Phe Gly Glu Leu Ile Ala Arg Ile Leu
        275                 280                 285

Asp Gly Thr Leu Thr Leu Pro Val Asp Ser Thr Phe Asp Ala Ala Asp
    290                 295                 300

Ile Val Ser Ala Val Arg Ala Ser Ser Glu Pro Gly Arg Ala Gly Lys
305                 310                 315                 320

Val Leu Ile Arg Phe
                325
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<210> 2339
<211> 726
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(703)
<223> RXA01622

<400> 2339
aaggcgtggg cgtttttgaa ggagcttcgt ttggagcgcg gtcctttgga tcgtgaagtt 60

gccatcgcag agctgaagag ctggtgggaa ggagaaaaca atg agt gat ttt tat 115
Met Ser Asp Phe Tyr
1 5

gcc gac agg ttg ttt aac gcg atg gag cgc aat gag gta gct cca ggc 163
Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn Glu Val Ala Pro Gly
10 15 20

atg ttg ttg gtg gct gcg ccc gat atg gcg tcg gag gat ttt gag cgc 211
Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser Glu Asp Phe Glu Arg
25 30 35

agc atc gtg ttg atc atc gag cat tct cct gcc acc act ttt ggt gtg 259
Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala Thr Thr Phe Gly Val
40 45 50

aac att tct tca cgt tcc gat gtt gct gtg gcc aat gtg ttg ccc gag 307
Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala Asn Val Leu Pro Glu
55 60 65

tgg gtg gac ctc acc tcg aag cca cag gca ctg tac atc ggt ggg ccg 355
Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu Tyr Ile Gly Gly Pro
70 75 80 85

ttg agc cag cag gct gtg gtt ggt ttg ggc gtg acc aag ccg ggc gtg 403
Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val Thr Lys Pro Gly Val
90 95 100

gat att gaa aat tcc acc agc ttc aac aag ctc gcc aac cgc ctg gtg 451
Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu Ala Asn Arg Leu Val
105 110 115

cac gtg gat ctg cgt tct gca cct gaa gat gtg gct gat gat ctt gag 499
His Val Asp Leu Arg Ser Ala Pro Glu Asp Val Ala Asp Asp Leu Glu
120 125 130

ggc atg cgc ttt ttt gcg ggc tac gcg gag tgg gct ccg ggc cag ctc 547
Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp Ala Pro Gly Gln Leu
135 140 145

aac gag gaa att gag cag ggt gat tgg ttc gtc aca cct gcg ttg ccg 595
Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val Thr Pro Ala Leu Pro
150 155 160 165

tcg gac att atc gcg ccg ggc cgc gtc gat att tgg ggc gac gtg atg 643
Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile Trp Gly Asp Val Met
170 175 180

cgt cga caa gca atg cct ttg ccg ttg tat tcc acg ttt ccg tcg gac 691
Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser Thr Phe Pro Ser Asp
185 190 195

cct tca gat aat tagatgagtt ccgaaaattt aaa 726
Pro Ser Asp Asn
200

<210> 2340
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 2340
Met Ser Asp Phe Tyr Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn
1 5 10 15

Glu Val Ala Pro Gly Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser
20 25 30

Glu Asp Phe Glu Arg Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala
35 40 45

Thr Thr Phe Gly Val Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala
50 55 60

Asn Val Leu Pro Glu Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu
65 70 75 80

Tyr Ile Gly Gly Pro Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val
85 90 95

Thr Lys Pro Gly Val Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu
100 105 110

Ala Asn Arg Leu Val His Val Asp Leu Arg Ser Ala Pro Glu Asp Val
115 120 125

Ala Asp Asp Leu Glu Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp
130 135 140

Ala Pro Gly Gln Leu Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val
145 150 155 160

Thr Pro Ala Leu Pro Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile
165 170 175

Trp Gly Asp Val Met Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser
180 185 190

Thr Phe Pro Ser Asp Pro Ser Asp Asn
195 200

<210> 2341
<211> 834
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(811)
<223> RXA01623

<400> 2341
cgcgccgggc cgcgtcgata tttggggcga cgtgatgcgt cgacaagcaa tgcctttgcc 60

gttgtattcc acgtttccgt cggacccttc agataattag atg agt tcc gaa aat 115
Met Ser Ser Glu Asn
1 5

tta aaa gaa att cgc ggc gga atc ggt gag act tta acg gtc ggt ttg 163
Leu Lys Glu Ile Arg Gly Gly Ile Gly Glu Thr Leu Thr Val Gly Leu
10 15 20

ggg ctg att ccg ctg ggt ttg gcc ttt ggg ctg ttg atg gtc cag aca 211
Gly Leu Ile Pro Leu Gly Leu Ala Phe Gly Leu Leu Met Val Gln Thr
25 30 35

ggt ttc gcc tgg tgg tgg acg ccg att ttc tcc ttc gtg atc tat gcc 259
Gly Phe Ala Trp Trp Trp Thr Pro Ile Phe Ser Phe Val Ile Tyr Ala
40 45 50

ggt tcg atg gaa ttt ctg gca atc ggc atg gtc acc gca ggt atc ggc 307
Gly Ser Met Glu Phe Leu Ala Ile Gly Met Val Thr Ala Gly Ile Gly
55 60 65

ccg ttt tcg gcg gcg gtc gct ggt ttc atg gtg aat ttc cgc cac att 355
Pro Phe Ser Ala Ala Val Ala Gly Phe Met Val Asn Phe Arg His Ile
70 75 80 85

ttc tac ggt ctc acc ttc cca cgc cac cgc atc aag tcc ggc gcc ggc 403
Phe Tyr Gly Leu Thr Phe Pro Arg His Arg Ile Lys Ser Gly Ala Gly
90 95 100

cgc gcc tat tcc acc tac gcg ctt acc gac gag tcc tac gcc atc gtg 451
Arg Ala Tyr Ser Thr Tyr Ala Leu Thr Asp Glu Ser Tyr Ala Ile Val
105 110 115

tca gcc cgc cca cct ggc gat atc agt ggc acg cgg gtg ctt acc gtt 499
Ser Ala Arg Pro Pro Gly Asp Ile Ser Gly Thr Arg Val Leu Thr Val
120 125 130

caa att ttg tgc caa gct ctg tgg gtt atc cca gga att att ggc gcc 547
Gln Ile Leu Cys Gln Ala Leu Trp Val Ile Pro Gly Ile Ile Gly Ala
135 140 145

ttg gtt ggt caa gtg ctg ccc gat gat cta aaa ggc atg gat ttt gcc 595
Leu Val Gly Gln Val Leu Pro Asp Asp Leu Lys Gly Met Asp Phe Ala
150 155 160 165

ctg acc gcg ctg ttt gtg gtg ctg gcg tgg gag gca ttc aaa aat aac 643
Leu Thr Ala Leu Phe Val Val Leu Ala Trp Glu Ala Phe Lys Asn Asn
170 175 180

aag gat tat tcg ctg cca tta ttc gcg gtg gta ttg gct ctg gtt tcc 691
Lys Asp Tyr Ser Leu Pro Leu Phe Ala Val Val Leu Ala Leu Val Ser
185 190 195

ggt ttt gtg gcg ccc gag cag atg ctg gtt atc gct ttg acc acg tac 739
Gly Phe Val Ala Pro Glu Gln Met Leu Val Ile Ala Leu Thr Thr Tyr
200 205 210

ttt ttg atc ctt ctt ctc cgc gtc cgc ttc ccc aac ctg gac aag aaa 787

```
Phe Leu Ile Leu Leu Leu Arg Val Arg Phe Pro Asn Leu Asp Lys Lys
    215                 220                 225

ctg gag atc agg act tcc cat gag tgagtttggc ctgccagaag gcg         834
Leu Glu Ile Arg Thr Ser His Glu
230                 235


<210> 2342
<211> 237
<212> PRT
<213> Corynebacterium glutamicum

<400> 2342
Met Ser Ser Glu Asn Leu Lys Glu Ile Arg Gly Gly Ile Gly Glu Thr
  1               5                  10                  15

Leu Thr Val Gly Leu Gly Leu Ile Pro Leu Gly Leu Ala Phe Gly Leu
             20                  25                  30

Leu Met Val Gln Thr Gly Phe Ala Trp Trp Trp Thr Pro Ile Phe Ser
         35                  40                  45

Phe Val Ile Tyr Ala Gly Ser Met Glu Phe Leu Ala Ile Gly Met Val
     50                  55                  60

Thr Ala Gly Ile Gly Pro Phe Ser Ala Ala Val Ala Gly Phe Met Val
 65                  70                  75                  80

Asn Phe Arg His Ile Phe Tyr Gly Leu Thr Phe Pro Arg His Arg Ile
                 85                  90                  95

Lys Ser Gly Ala Gly Arg Ala Tyr Ser Thr Tyr Ala Leu Thr Asp Glu
            100                 105                 110

Ser Tyr Ala Ile Val Ser Ala Arg Pro Pro Gly Asp Ile Ser Gly Thr
        115                 120                 125

Arg Val Leu Thr Val Gln Ile Leu Cys Gln Ala Leu Trp Val Ile Pro
    130                 135                 140

Gly Ile Ile Gly Ala Leu Val Gly Gln Val Leu Pro Asp Asp Leu Lys
145                 150                 155                 160

Gly Met Asp Phe Ala Leu Thr Ala Leu Phe Val Val Leu Ala Trp Glu
                165                 170                 175

Ala Phe Lys Asn Asn Lys Asp Tyr Ser Leu Pro Leu Phe Ala Val Val
            180                 185                 190

Leu Ala Leu Val Ser Gly Phe Val Ala Pro Glu Gln Met Leu Val Ile
        195                 200                 205

Ala Leu Thr Thr Tyr Phe Leu Ile Leu Leu Leu Arg Val Arg Phe Pro
    210                 215                 220

Asn Leu Asp Lys Lys Leu Glu Ile Arg Thr Ser His Glu
225                 230                 235


<210> 2343
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<211> 468
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(445)
<223> RXA01624

<400> 2343
gagcagatgc tggttatcgc tttgaccacg tacttttttga tccttcttct ccgcgtccgc 60

ttccccaacc tggacaagaa actggagatc aggacttccc atg agt gag ttt ggc 115
Met Ser Glu Phe Gly
1 5

ctg cca gaa ggc gtc acg ctg ctc aac gtc gcc gcc gtg ttg atc ccc 163
Leu Pro Glu Gly Val Thr Leu Leu Asn Val Ala Ala Val Leu Ile Pro
10 15 20

atc gcg atc atc acc ttg ctg ctg cgc atc ttc ccc ttc gcc gcg atg 211
Ile Ala Ile Ile Thr Leu Leu Leu Arg Ile Phe Pro Phe Ala Ala Met
25 30 35

aaa cgc gtc aac agc aac caa ctc atg gga gtt ttg ggg cgc aca atg 259
Lys Arg Val Asn Ser Asn Gln Leu Met Gly Val Leu Gly Arg Thr Met
40 45 50

cca gtc gga gtg atg gtc gta ttg gtc att tac acg ctc ttt ggc cag 307
Pro Val Gly Val Met Val Val Leu Val Ile Tyr Thr Leu Phe Gly Gln
55 60 65

gtc agt gcg cca ggt ggt gtg ggt gct tca ctg atc gcg gtg gca ttc 355
Val Ser Ala Pro Gly Gly Val Gly Ala Ser Leu Ile Ala Val Ala Phe
70 75 80 85

acc gcg ctg ctg cac tgg ttg aaa ggc tcc gcc ggg ctg tcc atc gtc 403
Thr Ala Leu Leu His Trp Leu Lys Gly Ser Ala Gly Leu Ser Ile Val
90 95 100

ggt ggc acc ttg gcc tac atg ttt ctg gtc aac gtc gtt ttt 445
Gly Gly Thr Leu Ala Tyr Met Phe Leu Val Asn Val Val Phe
105 110 115

taaaagatgc ttctcgacgc aaa 468

<210> 2344
<211> 115
<212> PRT
<213> Corynebacterium glutamicum

<400> 2344
Met Ser Glu Phe Gly Leu Pro Glu Gly Val Thr Leu Leu Asn Val Ala
1 5 10 15

Ala Val Leu Ile Pro Ile Ala Ile Ile Thr Leu Leu Leu Arg Ile Phe
20 25 30

Pro Phe Ala Ala Met Lys Arg Val Asn Ser Asn Gln Leu Met Gly Val
35 40 45

```
Leu Gly Arg Thr Met Pro Val Gly Val Met Val Val Leu Val Ile Tyr
     50                  55                  60

Thr Leu Phe Gly Gln Val Ser Ala Pro Gly Gly Val Gly Ala Ser Leu
 65                  70                  75                  80

Ile Ala Val Ala Phe Thr Ala Leu Leu His Trp Leu Lys Gly Ser Ala
                 85                  90                  95

Gly Leu Ser Ile Val Gly Gly Thr Leu Ala Tyr Met Phe Leu Val Asn
            100                 105                 110

Val Val Phe
        115


<210> 2345
<211> 1137
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1114)
<223> RXA01628

<400> 2345
cttccccttt cagcccgttg aagaaccaat gagccctgcc cgcacccagc cccgagcggc 60

tttcctaagg aagctccgac ccatcacatg tagcctttcc ttg gtt ctc gta ggg   115
                                          Leu Val Leu Val Gly
                                            1               5

tgc agc aac acg gca gag tcc acg acc acc gat acg gca ggc tcc act   163
Cys Ser Asn Thr Ala Glu Ser Thr Thr Thr Asp Thr Ala Gly Ser Thr
                10                  15                  20

gaa act tca tca cag att tca ccc acc act cca gtc agc acc acc gaa   211
Glu Thr Ser Ser Gln Ile Ser Pro Thr Thr Pro Val Ser Thr Thr Glu
            25                  30                  35

gca gcg ccg cct gaa gat cca agc gca aac gct ttg gaa gag tat gct   259
Ala Ala Pro Pro Glu Asp Pro Ser Ala Asn Ala Leu Glu Glu Tyr Ala
        40                  45                  50

cag atc ctt gcc aat cca agc atc tac ccc tta acc gaa att tca caa   307
Gln Ile Leu Ala Asn Pro Ser Ile Tyr Pro Leu Thr Glu Ile Ser Gln
     55                  60                  65

ttc gtc ccc aca ggc aca tat gcc tac aca ctt gtt gaa gca act tcc   355
Phe Val Pro Thr Gly Thr Tyr Ala Tyr Thr Leu Val Glu Ala Thr Ser
 70                  75                  80                  85

gat tcc atc cca gaa cta cta ctc cgc gcc gat agt cac gaa ttc gcg   403
Asp Ser Ile Pro Glu Leu Leu Leu Arg Ala Asp Ser His Glu Phe Ala
                90                  95                 100

cca att ttg gtt ttc acc tat gac gaa aac aca caa tcc gca acc caa   451
Pro Ile Leu Val Phe Thr Tyr Asp Glu Asn Thr Gln Ser Ala Thr Gln
            105                 110                 115
```

```
gct gga gga gtc cta att gac ggt gtc gcc agc gcc ggc ggt tca cga   499
Ala Gly Gly Val Leu Ile Asp Gly Val Ala Ser Ala Gly Gly Ser Arg
        120                 125                 130

gtc aag gtc aga gct tca aat tca gga gca gga atc tac caa ttg aat   547
Val Lys Val Arg Ala Ser Asn Ser Gly Ala Gly Ile Tyr Gln Leu Asn
    135                 140                 145

tgg tac tcg ata caa cca gtt ggc gaa agc tct ttg tac gga atc caa   595
Trp Tyr Ser Ile Gln Pro Val Gly Glu Ser Ser Leu Tyr Gly Ile Gln
150                 155                 160                 165

gga aac tcc ctg aca caa atc gca gac ccc gag gat ttc atg gtc cgt   643
Gly Asn Ser Leu Thr Gln Ile Ala Asp Pro Glu Asp Phe Met Val Arg
                170                 175                 180

gaa cta tta cct gac cac cac gaa att acc tgg gtt gat tcc aac gac   691
Glu Leu Leu Pro Asp His His Glu Ile Thr Trp Val Asp Ser Asn Asp
            185                 190                 195

ccc tcc ggc cta tca acc gtt cag act ggt gga gcc aac att caa caa   739
Pro Ser Gly Leu Ser Thr Val Gln Thr Gly Gly Ala Asn Ile Gln Gln
        200                 205                 210

gca gcc cca act ccc gtt caa cag cct gcg tca aac ctg cac tac ttc   787
Ala Ala Pro Thr Pro Val Gln Gln Pro Ala Ser Asn Leu His Tyr Phe
    215                 220                 225

tct ggt gta gta acg atg cag acc gcc ggc gaa ctc atg cga ggt gaa   835
Ser Gly Val Val Thr Met Gln Thr Ala Gly Glu Leu Met Arg Gly Glu
230                 235                 240                 245

cga act ccc aat ggt gag cct gcc act gat ctc tat ctc gta ctg gtc   883
Arg Thr Pro Asn Gly Glu Pro Ala Thr Asp Leu Tyr Leu Val Leu Val
                250                 255                 260

ctt gat tcc cca att gaa atc aca gca cga aac gca gct aca gac cct   931
Leu Asp Ser Pro Ile Glu Ile Thr Ala Arg Asn Ala Ala Thr Asp Pro
            265                 270                 275

cag act cgt acc att tcc gaa gtc agc ctc ggc cga tac atc ccc gct   979
Gln Thr Arg Thr Ile Ser Glu Val Ser Leu Gly Arg Tyr Ile Pro Ala
        280                 285                 290

gat ggt gac aat gat tgg ata ggc tac ctc gac acc cac gtg gaa atc   1027
Asp Gly Asp Asn Asp Trp Ile Gly Tyr Leu Asp Thr His Val Glu Ile
    295                 300                 305

act gca aca acg gat cag gtc tgg ttc cca acc gac acc ggt cta cct   1075
Thr Ala Thr Thr Asp Gln Val Trp Phe Pro Thr Asp Thr Gly Leu Pro
310                 315                 320                 325

ctt gga atg ctt cgt cta gcg gac tac aaa agc atc tca taaaccgacg    1124
Leu Gly Met Leu Arg Leu Ala Asp Tyr Lys Ser Ile Ser
                330                 335

cagcactcgt cga                                                   1137
```

<210> 2346

<211> 338
<212> PRT
<213> Corynebacterium glutamicum

<400> 2346

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Leu Val Leu Val Gly Cys Ser Asn Thr Ala Glu Ser Thr Thr Thr Asp
  1               5                  10                  15

Thr Ala Gly Ser Thr Glu Thr Ser Ser Gln Ile Ser Pro Thr Thr Pro
             20                  25                  30

Val Ser Thr Thr Glu Ala Ala Pro Pro Glu Asp Pro Ser Ala Asn Ala
         35                  40                  45

Leu Glu Glu Tyr Ala Gln Ile Leu Ala Asn Pro Ser Ile Tyr Pro Leu
     50                  55                  60

Thr Glu Ile Ser Gln Phe Val Pro Thr Gly Thr Tyr Ala Tyr Thr Leu
 65                  70                  75                  80

Val Glu Ala Thr Ser Asp Ser Ile Pro Glu Leu Leu Leu Arg Ala Asp
                 85                  90                  95

Ser His Glu Phe Ala Pro Ile Leu Val Phe Thr Tyr Asp Glu Asn Thr
            100                 105                 110

Gln Ser Ala Thr Gln Ala Gly Gly Val Leu Ile Asp Gly Val Ala Ser
        115                 120                 125

Ala Gly Gly Ser Arg Val Lys Val Arg Ala Ser Asn Ser Gly Ala Gly
    130                 135                 140

Ile Tyr Gln Leu Asn Trp Tyr Ser Ile Gln Pro Val Gly Glu Ser Ser
145                 150                 155                 160

Leu Tyr Gly Ile Gln Gly Asn Ser Leu Thr Gln Ile Ala Asp Pro Glu
                165                 170                 175

Asp Phe Met Val Arg Glu Leu Leu Pro Asp His His Glu Ile Thr Trp
            180                 185                 190

Val Asp Ser Asn Asp Pro Ser Gly Leu Ser Thr Val Gln Thr Gly Gly
        195                 200                 205

Ala Asn Ile Gln Gln Ala Ala Pro Thr Pro Val Gln Gln Pro Ala Ser
    210                 215                 220

Asn Leu His Tyr Phe Ser Gly Val Val Thr Met Gln Thr Ala Gly Glu
225                 230                 235                 240

Leu Met Arg Gly Glu Arg Thr Pro Asn Gly Glu Pro Ala Thr Asp Leu
                245                 250                 255

Tyr Leu Val Leu Val Leu Asp Ser Pro Ile Glu Ile Thr Ala Arg Asn
            260                 265                 270

Ala Ala Thr Asp Pro Gln Thr Arg Thr Ile Ser Glu Val Ser Leu Gly
        275                 280                 285

Arg Tyr Ile Pro Ala Asp Gly Asp Asn Asp Trp Ile Gly Tyr Leu Asp
    290                 295                 300
```

```
Thr His Val Glu Ile Thr Ala Thr Thr Asp Gln Val Trp Phe Pro Thr
305                 310                 315                 320

Asp Thr Gly Leu Pro Leu Gly Met Leu Arg Leu Ala Asp Tyr Lys Ser
                325                 330                 335

Ile Ser
```

<210> 2347
<211> 1200
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1177)
<223> RXA01630

<400> 2347

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gtaggtgagt cttcgtgaga taccccggc cagtcataca gttcaaccaa gctccaccac 60

ccagataaaa acctgcgggt tgcgttttag gagaattccc atg agt gat caa aaa   115
                                            Met Ser Asp Gln Lys
                                              1               5

att gtt gtt ggc ctg cta ggc atc acc cac ccg cat gcg tcg gcg cgg   163
Ile Val Val Gly Leu Leu Gly Ile Thr His Pro His Ala Ser Ala Arg
                10                  15                  20

gtg cgt gcc ctc cgt gaa att gat ggg gta gag gtc gtc gcc gcc gcg   211
Val Arg Ala Leu Arg Glu Ile Asp Gly Val Glu Val Val Ala Ala Ala
            25                  30                  35

gat act gat tcc cgc ctc cag tac ttc acc gac aaa tat gat gtt gaa   259
Asp Thr Asp Ser Arg Leu Gln Tyr Phe Thr Asp Lys Tyr Asp Val Glu
        40                  45                  50

ccc cgc gag atc gat gac gtc ttg aac gac gat cgc atc aac gcc atc   307
Pro Arg Glu Ile Asp Asp Val Leu Asn Asp Asp Arg Ile Asn Ala Ile
    55                  60                  65

atg gtt cac tcc aag agc aag gac atg gtc cct cac gcc aag cgc gcg   355
Met Val His Ser Lys Ser Lys Asp Met Val Pro His Ala Lys Arg Ala
70                  75                  80                  85

ctc gcg gcc gga aaa tcc gtc gtc gtg gag aag ccc ggc ggg gga aca   403
Leu Ala Ala Gly Lys Ser Val Val Val Glu Lys Pro Gly Gly Gly Thr
                90                  95                  100

gtg gcg gat ctt gag gag ctc ctg gcc ctc aaa gaa gct gcc gat cct   451
Val Ala Asp Leu Glu Glu Leu Leu Ala Leu Lys Glu Ala Ala Asp Pro
            105                 110                 115

cag cga atc gtg cag gtc ggg tac aac gtc cgc ctg tct gaa tcg gtt   499
Gln Arg Ile Val Gln Val Gly Tyr Asn Val Arg Leu Ser Glu Ser Val
        120                 125                 130

cag aga tta aaa gag ctt ctc gac gcc ggc ctc atc ggc gaa gtc gtc   547
```

```
Gln Arg Leu Lys Glu Leu Leu Asp Ala Gly Leu Ile Gly Glu Val Val
    135                 140                 145

agc gtg caa gca cgc ggc gcc gca aaa gta ggt gag cat atc acc gag   595
Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly Glu His Ile Thr Glu
150                 155                 160                 165

cac ctc aac caa ccc gca gac atg ggc ggt gtg ttg tgg att ctt ggc   643
His Leu Asn Gln Pro Ala Asp Met Gly Gly Val Leu Trp Ile Leu Gly
                170                 175                 180

tgc cac atg ctc gat gca ttg gtg gaa gtc ttc gga gct cca gaa tcc   691
Cys His Met Leu Asp Ala Leu Val Glu Val Phe Gly Ala Pro Glu Ser
            185                 190                 195

gtg aac gcc cga gtg cat aag acc gca aaa ctc tct gac gac acc agc   739
Val Asn Ala Arg Val His Lys Thr Ala Lys Leu Ser Asp Asp Thr Ser
        200                 205                 210

cgc gaa gac tca gcc tcc gca ctg ctg tac tac cca gat ttc tcc gtc   787
Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr Pro Asp Phe Ser Val
    215                 220                 225

agc ttc agc ttc gac ggc cac gat gat ctg gaa tgg ttc gaa agc tcc   835
Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu Trp Phe Glu Ser Ser
230                 235                 240                 245

cga ctc acg gtc tat gga acc aag ggc atg atc gaa gcc gga atc ctc   883
Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile Glu Ala Gly Ile Leu
                250                 255                 260

cct cag aca ctg cgc gta tac ctc aat gag tca cgc cag ggc tgg cca   931
Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser Arg Gln Gly Trp Pro
            265                 270                 275

cag ggt tgg acc gag tgg acc cag agc tac ttc acc cca ccg ttt gct   979
Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe Thr Pro Pro Phe Ala
        280                 285                 290

cgc aca gaa tcc aac aaa ttc tca gag ctt cca gag cta gaa aac atc   1027
Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro Glu Leu Glu Asn Ile
    295                 300                 305

agc aac ttc cgc aca gaa atg cag ggg tgg gtg aat tcc att cgc act   1075
Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val Asn Ser Ile Arg Thr
310                 315                 320                 325

gga tcc cgc aat gtg gcg cca gtt gag gat gct ctc aca gtc gct cgc   1123
Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala Leu Thr Val Ala Arg
                330                 335                 340

att gtc agt gca tgc tac gaa tcc gac aac aac cag ggc att tcc gta   1171
Ile Val Ser Ala Cys Tyr Glu Ser Asp Asn Asn Gln Gly Ile Ser Val
            345                 350                 355

aac atc taagaggagc actccatgaa acc                                1200
Asn Ile
```

<210> 2348

<211> 359
<212> PRT
<213> Corynebacterium glutamicum

<400> 2348

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Met Ser Asp Gln Lys Ile Val Val Gly Leu Leu Gly Ile Thr His Pro
  1               5                  10                  15

His Ala Ser Ala Arg Val Arg Ala Leu Arg Glu Ile Asp Gly Val Glu
             20                  25                  30

Val Val Ala Ala Ala Asp Thr Asp Ser Arg Leu Gln Tyr Phe Thr Asp
         35                  40                  45

Lys Tyr Asp Val Glu Pro Arg Glu Ile Asp Asp Val Leu Asn Asp Asp
     50                  55                  60

Arg Ile Asn Ala Ile Met Val His Ser Lys Ser Lys Asp Met Val Pro
 65                  70                  75                  80

His Ala Lys Arg Ala Leu Ala Ala Gly Lys Ser Val Val Val Glu Lys
                 85                  90                  95

Pro Gly Gly Gly Thr Val Ala Asp Leu Glu Glu Leu Leu Ala Leu Lys
            100                 105                 110

Glu Ala Ala Asp Pro Gln Arg Ile Val Gln Val Gly Tyr Asn Val Arg
        115                 120                 125

Leu Ser Glu Ser Val Gln Arg Leu Lys Glu Leu Leu Asp Ala Gly Leu
    130                 135                 140

Ile Gly Glu Val Val Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly
145                 150                 155                 160

Glu His Ile Thr Glu His Leu Asn Gln Pro Ala Asp Met Gly Gly Val
                165                 170                 175

Leu Trp Ile Leu Gly Cys His Met Leu Asp Ala Leu Val Glu Val Phe
            180                 185                 190

Gly Ala Pro Glu Ser Val Asn Ala Arg Val His Lys Thr Ala Lys Leu
        195                 200                 205

Ser Asp Asp Thr Ser Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr
    210                 215                 220

Pro Asp Phe Ser Val Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu
225                 230                 235                 240

Trp Phe Glu Ser Ser Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile
                245                 250                 255

Glu Ala Gly Ile Leu Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser
            260                 265                 270

Arg Gln Gly Trp Pro Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe
        275                 280                 285

Thr Pro Pro Phe Ala Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro
    290                 295                 300
```

```
Glu Leu Glu Asn Ile Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val
305                 310                 315                 320

Asn Ser Ile Arg Thr Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala
                325                 330                 335

Leu Thr Val Ala Arg Ile Val Ser Ala Cys Tyr Glu Ser Asp Asn Asn
            340                 345                 350

Gln Gly Ile Ser Val Asn Ile
        355
```

<210> 2349
<211> 1494
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1471)
<223> RXA01641

<400> 2349

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gtgaaattag gggaattctc accaacgctg ctcccccgtcc ccttttgctg gcatactcaa 60

agacacattt gttgggggac aattttgggg gttggttatt ttg gca atc gat aat   115
                                              Leu Ala Ile Asp Asn
                                                1               5

gcg ctg cgc gtg agc atc cgc ata gat ctc acc gtt ggc gat gcg ccc   163
Ala Leu Arg Val Ser Ile Arg Ile Asp Leu Thr Val Gly Asp Ala Pro
                10                  15                  20

gct gct gtg gct gat gtg gcg cta cct gca ggt tcg agt ctg gcg gac   211
Ala Ala Val Ala Asp Val Ala Leu Pro Ala Gly Ser Ser Leu Ala Asp
            25                  30                  35

att ttg gat gaa att tta gaa ctc acc gat gca ccc cgg att tcc agg   259
Ile Leu Asp Glu Ile Leu Glu Leu Thr Asp Ala Pro Arg Ile Ser Arg
        40                  45                  50

ccg tgg gtg gct cac act gct gcg gga agt ccc att gat tgc ggg att   307
Pro Trp Val Ala His Thr Ala Ala Gly Ser Pro Ile Asp Cys Gly Ile
    55                  60                  65

ccg ctt gca gaa aca caa gtg gaa caa ggc agc gtg gtg gtc ctt tca   355
Pro Leu Ala Glu Thr Gln Val Glu Gln Gly Ser Val Val Val Leu Ser
70                  75                  80                  85

ccc gaa agg gac ttg gaa gcc ccc gtg ttg cgt gat gtc gcc gaa gcg   403
Pro Glu Arg Asp Leu Glu Ala Pro Val Leu Arg Asp Val Ala Glu Ala
                90                  95                  100

ttg gtg gag ttt tct tcc acg aac cgc gcc ggg cac ctc gtg gaa ttg   451
Leu Val Glu Phe Ser Ser Thr Asn Arg Ala Gly His Leu Val Glu Leu
            105                 110                 115

atg act ttc gcg ggg ctc atc ggg gct gcc gtg tta atg aca agt cct   499
Met Thr Phe Ala Gly Leu Ile Gly Ala Ala Val Leu Met Thr Ser Pro
```

```
        120                 125                 130

gct gcc tcc gga att att gtg ccc ggc cgc atg gga atc ttc gtc gca   547
Ala Ala Ser Gly Ile Ile Val Pro Gly Arg Met Gly Ile Phe Val Ala
    135                 140                 145

atc tgc gct cta ctg ctt ctg tgg ctc cca ccc gcg cac acc ccg atc   595
Ile Cys Ala Leu Leu Leu Leu Trp Leu Pro Pro Ala His Thr Pro Ile
150                 155                 160                 165

ctt cga aac gtc ctg ccg att acc ctg atc ttg ggc gca ggc gga gcg   643
Leu Arg Asn Val Leu Pro Ile Thr Leu Ile Leu Gly Ala Gly Gly Ala
                170                 175                 180

gta tca gtg ctg gtt gca ggc act tct ggg act tct ccc ggc gcg ctt   691
Val Ser Val Leu Val Ala Gly Thr Ser Gly Thr Ser Pro Gly Ala Leu
            185                 190                 195

acc tgg acg att ttc gct ggc gcg tgc act att ctt gcc agt tcg ctg   739
Thr Trp Thr Ile Phe Ala Gly Ala Cys Thr Ile Leu Ala Ser Ser Leu
        200                 205                 210

ctg gtt cat gtg gtg tat cgt cca gca att ctt ctg gtg gca aca ctg   787
Leu Val His Val Val Tyr Arg Pro Ala Ile Leu Leu Val Ala Thr Leu
    215                 220                 225

tcc aca ttg ggg ctc ggt ctc tta gtc ctt gca gca acc acc act ctg   835
Ser Thr Leu Gly Leu Gly Leu Leu Val Leu Ala Ala Thr Thr Thr Leu
230                 235                 240                 245

tgg aag ctc aaa gct acc gaa gat ttc agc ggt cca gca gcg atc acg   883
Trp Lys Leu Lys Ala Thr Glu Asp Phe Ser Gly Pro Ala Ala Ile Thr
                250                 255                 260

gtc acc gct tcc acc atc acc atg tgc ttc gcc ccg aaa atc gca gca   931
Val Thr Ala Ser Thr Ile Thr Met Cys Phe Ala Pro Lys Ile Ala Ala
            265                 270                 275

tcg cta gca ggc ctg cgc gtc cca tcg ctt ccc acc gcc ggc gaa gat   979
Ser Leu Ala Gly Leu Arg Val Pro Ser Leu Pro Thr Ala Gly Glu Asp
        280                 285                 290

ctc tcc gtc agc gac ctc acc atg act gat ccc gag aaa aga ata aaa   1027
Leu Ser Val Ser Asp Leu Thr Met Thr Asp Pro Glu Lys Arg Ile Lys
    295                 300                 305

aca aca aag acg ctt ttc gac gcc cag atc ctt ggc ctt ggc gtt ttg   1075
Thr Thr Lys Thr Leu Phe Asp Ala Gln Ile Leu Gly Leu Gly Val Leu
310                 315                 320                 325

agc ggg cct ttg gcg ttg ttg tcg gtt acc ccg ggc acc tgg aca acc   1123
Ser Gly Pro Leu Ala Leu Leu Ser Val Thr Pro Gly Thr Trp Thr Thr
                330                 335                 340

acc gtt ttt agt tta tgc atc gcg gtg gct tcg ctg ctt cac gct aat   1171
Thr Val Phe Ser Leu Cys Ile Ala Val Ala Ser Leu Leu His Ala Asn
            345                 350                 355

cgt cat caa gca cca att ccc acg tgg aca ttg atg ggg tta tct gcc   1219
Arg His Gln Ala Pro Ile Pro Thr Trp Thr Leu Met Gly Leu Ser Ala
        360                 365                 370
```

```
ctt ggt ttc att tcc atg gcg tta tcc gca agc cga tca ggt tca cta   1267
Leu Gly Phe Ile Ser Met Ala Leu Ser Ala Ser Arg Ser Gly Ser Leu
    375                 380                 385

att gca ctg atc ggt tct gtg gtt atc atc gct gtg ctg gtc agc gtg   1315
Ile Ala Leu Ile Gly Ser Val Val Ile Ile Ala Val Leu Val Ser Val
390                 395                 400                 405

gca ttg tgg atc agt aca gtc ccc acg ctg gaa ccc acc acc att gtg   1363
Ala Leu Trp Ile Ser Thr Val Pro Thr Leu Glu Pro Thr Thr Ile Val
                410                 415                 420

tgg ctt gaa agg ttg gaa tca ctg tgt ctt gca gct agt ctg cca ctc   1411
Trp Leu Glu Arg Leu Glu Ser Leu Cys Leu Ala Ala Ser Leu Pro Leu
            425                 430                 435

gca ctg cat ttg ctg gat gta ttt gga atg ctg cgc ggt ctt gat att   1459
Ala Leu His Leu Leu Asp Val Phe Gly Met Leu Arg Gly Leu Asp Ile
        440                 445                 450

gga ttc ggt gga taagatgcgc agactcatcg cgg                        1494
Gly Phe Gly Gly
    455
```

<210> 2350
<211> 457
<212> PRT
<213> Corynebacterium glutamicum

<400> 2350

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Leu Ala Ile Asp Asn Ala Leu Arg Val Ser Ile Arg Ile Asp Leu Thr
  1               5                  10                  15

Val Gly Asp Ala Pro Ala Ala Val Ala Asp Val Ala Leu Pro Ala Gly
             20                  25                  30

Ser Ser Leu Ala Asp Ile Leu Asp Glu Ile Leu Glu Leu Thr Asp Ala
         35                  40                  45

Pro Arg Ile Ser Arg Pro Trp Val Ala His Thr Ala Ala Gly Ser Pro
     50                  55                  60

Ile Asp Cys Gly Ile Pro Leu Ala Glu Thr Gln Val Glu Gln Gly Ser
 65                  70                  75                  80

Val Val Val Leu Ser Pro Glu Arg Asp Leu Glu Ala Pro Val Leu Arg
                 85                  90                  95

Asp Val Ala Glu Ala Leu Val Glu Phe Ser Ser Thr Asn Arg Ala Gly
            100                 105                 110

His Leu Val Glu Leu Met Thr Phe Ala Gly Leu Ile Gly Ala Ala Val
        115                 120                 125

Leu Met Thr Ser Pro Ala Ala Ser Gly Ile Ile Val Pro Gly Arg Met
    130                 135                 140

Gly Ile Phe Val Ala Ile Cys Ala Leu Leu Leu Leu Trp Leu Pro Pro
145                 150                 155                 160
```

```
Ala His Thr Pro Ile Leu Arg Asn Val Leu Pro Ile Thr Leu Ile Leu
               165                 170                 175

Gly Ala Gly Gly Ala Val Ser Val Leu Val Ala Gly Thr Ser Gly Thr
           180                 185                 190

Ser Pro Gly Ala Leu Thr Trp Thr Ile Phe Ala Gly Ala Cys Thr Ile
       195                 200                 205

Leu Ala Ser Ser Leu Leu Val His Val Val Tyr Arg Pro Ala Ile Leu
   210                 215                 220

Leu Val Ala Thr Leu Ser Thr Leu Gly Leu Gly Leu Leu Val Leu Ala
225                 230                 235                 240

Ala Thr Thr Thr Leu Trp Lys Leu Lys Ala Thr Glu Asp Phe Ser Gly
               245                 250                 255

Pro Ala Ala Ile Thr Val Thr Ala Ser Thr Ile Thr Met Cys Phe Ala
           260                 265                 270

Pro Lys Ile Ala Ala Ser Leu Ala Gly Leu Arg Val Pro Ser Leu Pro
       275                 280                 285

Thr Ala Gly Glu Asp Leu Ser Val Ser Asp Leu Thr Met Thr Asp Pro
   290                 295                 300

Glu Lys Arg Ile Lys Thr Thr Lys Thr Leu Phe Asp Ala Gln Ile Leu
305                 310                 315                 320

Gly Leu Gly Val Leu Ser Gly Pro Leu Ala Leu Leu Ser Val Thr Pro
               325                 330                 335

Gly Thr Trp Thr Thr Thr Val Phe Ser Leu Cys Ile Ala Val Ala Ser
           340                 345                 350

Leu Leu His Ala Asn Arg His Gln Ala Pro Ile Pro Thr Trp Thr Leu
       355                 360                 365

Met Gly Leu Ser Ala Leu Gly Phe Ile Ser Met Ala Leu Ser Ala Ser
   370                 375                 380

Arg Ser Gly Ser Leu Ile Ala Leu Ile Gly Ser Val Val Ile Ile Ala
385                 390                 395                 400

Val Leu Val Ser Val Ala Leu Trp Ile Ser Thr Val Pro Thr Leu Glu
               405                 410                 415

Pro Thr Thr Ile Val Trp Leu Glu Arg Leu Glu Ser Leu Cys Leu Ala
           420                 425                 430

Ala Ser Leu Pro Leu Ala Leu His Leu Leu Asp Val Phe Gly Met Leu
       435                 440                 445

Arg Gly Leu Asp Ile Gly Phe Gly Gly
   450                 455
```

<210> 2351
<211> 1365

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1342)
<223> RXA01642

<400> 2351
ttggaatcac tgtgtcttgc agctagtctg ccactcgcac tgcatttgct ggatgtattt 60

ggaatgctgc gcggtcttga tattggattc ggtggataag atg cgc aga ctc atc 115
Met Arg Arg Leu Ile
1 5

gcg gtt agc ttg gcc gct ctg ttt atg ttg gct tcc act cca gcg acg 163
Ala Val Ser Leu Ala Ala Leu Phe Met Leu Ala Ser Thr Pro Ala Thr
10 15 20

agg gca cag gaa gta gaa gct ctc gct tgc ccc gag gta gcg atc gcc 211
Arg Ala Gln Glu Val Glu Ala Leu Ala Cys Pro Glu Val Ala Ile Ala
25 30 35

gat cct tcc tcc gca gtt tta gat gaa cac ctt tcg cag tca tta tcc 259
Asp Pro Ser Ser Ala Val Leu Asp Glu His Leu Ser Gln Ser Leu Ser
40 45 50

caa gct cac caa cta gca act ggc gcc ggt gtg atg gtg gca gtc atc 307
Gln Ala His Gln Leu Ala Thr Gly Ala Gly Val Met Val Ala Val Ile
55 60 65

gac acc gga gta tcc ctg cat cca cgt ctg ccc cac tta att ccc ggc 355
Asp Thr Gly Val Ser Leu His Pro Arg Leu Pro His Leu Ile Pro Gly
70 75 80 85

ggt gat ttc gtg ggc gcc cac caa agc ccc gat gtg cca ggt gaa ctt 403
Gly Asp Phe Val Gly Ala His Gln Ser Pro Asp Val Pro Gly Glu Leu
90 95 100

atc gat tgc gac ggc cac ggc acc atc gtc gcc gga atc atc gcc tcc 451
Ile Asp Cys Asp Gly His Gly Thr Ile Val Ala Gly Ile Ile Ala Ser
105 110 115

caa gga aac ccc ggc acc ggc tgg cca tat gac ggc agc tcc gat cct 499
Gln Gly Asn Pro Gly Thr Gly Trp Pro Tyr Asp Gly Ser Ser Asp Pro
120 125 130

tat atc ggt gtc gcc cca gat tcc gga atc atc tcc att aaa caa acc 547
Tyr Ile Gly Val Ala Pro Asp Ser Gly Ile Ile Ser Ile Lys Gln Thr
135 140 145

agc tca tat gtg cgt act cgt gaa gat tcc aac gtc gga acg ctg agc 595
Ser Ser Tyr Val Arg Thr Arg Glu Asp Ser Asn Val Gly Thr Leu Ser
150 155 160 165

acc ctg gcg gaa tcc atc cac cga gct ctc gat tcc ggt gcc cac gtg 643
Thr Leu Ala Glu Ser Ile His Arg Ala Leu Asp Ser Gly Ala His Val
170 175 180

atc aat att tcc gtg gtg tcc tgt ttg ccc caa tca ccc gac gag gcc 691
Ile Asn Ile Ser Val Val Ser Cys Leu Pro Gln Ser Pro Asp Glu Ala

```
            185                 190                 195

gca tcg ttc cag cct ctg acg gat gct ctt aac aga gca gaa ctt caa   739
Ala Ser Phe Gln Pro Leu Thr Asp Ala Leu Asn Arg Ala Glu Leu Gln
        200                 205                 210

ggg gtg ata gtg gtg gca gca gca gga aac ctc ggg cag gat tgt cca   787
Gly Val Ile Val Val Ala Ala Ala Gly Asn Leu Gly Gln Asp Cys Pro
    215                 220                 225

gtt gga tct acc gtt tat cct gca cat tca gac act gtg ctc tct gtg   835
Val Gly Ser Thr Val Tyr Pro Ala His Ser Asp Thr Val Leu Ser Val
230                 235                 240                 245

tcg gca cgt ttt gat tct cac acg ctt gca gaa tat tcc atg cct ggc   883
Ser Ala Arg Phe Asp Ser His Thr Leu Ala Glu Tyr Ser Met Pro Gly
                250                 255                 260

aac caa caa atc ctc tct gca cca agc cac att cag gct ggt cta tca   931
Asn Gln Gln Ile Leu Ser Ala Pro Ser His Ile Gln Ala Gly Leu Ser
            265                 270                 275

ccg cgt ggc gac ggc ttc gcc agc cac atg atc acc acc gct ggc gaa   979
Pro Arg Gly Asp Gly Phe Ala Ser His Met Ile Thr Thr Ala Gly Glu
        280                 285                 290

agc ccc ttc gag ggc acc agt ttt gcc gct cca gtt gtc agc gcc aca   1027
Ser Pro Phe Glu Gly Thr Ser Phe Ala Ala Pro Val Val Ser Ala Thr
    295                 300                 305

gct gca ctg ctt cgc cag cat ttt ccc ttt gcc aca ccc tat gaa att   1075
Ala Ala Leu Leu Arg Gln His Phe Pro Phe Ala Thr Pro Tyr Glu Ile
310                 315                 320                 325

cgt gca cga atc ttc aac agc atc gac cct gca aga ggc gct att gat   1123
Arg Ala Arg Ile Phe Asn Ser Ile Asp Pro Ala Arg Gly Ala Ile Asp
                330                 335                 340

ccc tac ctg gca ctt act caa gaa atc tat ccc acc act ccc ctg gtt   1171
Pro Tyr Leu Ala Leu Thr Gln Glu Ile Tyr Pro Thr Thr Pro Leu Val
            345                 350                 355

cat gag atc gca cta agt gtt ccc acg ccg ccg gat gat tct cca cgg   1219
His Glu Ile Ala Leu Ser Val Pro Thr Pro Pro Asp Asp Ser Pro Arg
        360                 365                 370

gag cgg ggc atc cta gtt acc gca atc att gtt ggg ttg ctc gca gtg   1267
Glu Arg Gly Ile Leu Val Thr Ala Ile Ile Val Gly Leu Leu Ala Val
    375                 380                 385

tta gct gtg ctg atg gga cta cgc cga att cat cat cac tcg gcc ttt   1315
Leu Ala Val Leu Met Gly Leu Arg Arg Ile His His His Ser Ala Phe
390                 395                 400                 405

caa aaa gct agc tca agt gtt atc act taatctatga ggcaccgttc         1362
Gln Lys Ala Ser Ser Ser Val Ile Thr
                410

aga                                                              1365
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<210> 2352
<211> 414
<212> PRT
<213> Corynebacterium glutamicum

<400> 2352
Met Arg Arg Leu Ile Ala Val Ser Leu Ala Ala Leu Phe Met Leu Ala
1 5 10 15

Ser Thr Pro Ala Thr Arg Ala Gln Glu Val Glu Ala Leu Ala Cys Pro
20 25 30

Glu Val Ala Ile Ala Asp Pro Ser Ser Ala Val Leu Asp Glu His Leu
35 40 45

Ser Gln Ser Leu Ser Gln Ala His Gln Leu Ala Thr Gly Ala Gly Val
50 55 60

Met Val Ala Val Ile Asp Thr Gly Val Ser Leu His Pro Arg Leu Pro
65 70 75 80

His Leu Ile Pro Gly Gly Asp Phe Val Gly Ala His Gln Ser Pro Asp
85 90 95

Val Pro Gly Glu Leu Ile Asp Cys Asp Gly His Gly Thr Ile Val Ala
100 105 110

Gly Ile Ile Ala Ser Gln Gly Asn Pro Gly Thr Gly Trp Pro Tyr Asp
115 120 125

Gly Ser Ser Asp Pro Tyr Ile Gly Val Ala Pro Asp Ser Gly Ile Ile
130 135 140

Ser Ile Lys Gln Thr Ser Ser Tyr Val Arg Thr Arg Glu Asp Ser Asn
145 150 155 160

Val Gly Thr Leu Ser Thr Leu Ala Glu Ser Ile His Arg Ala Leu Asp
165 170 175

Ser Gly Ala His Val Ile Asn Ile Ser Val Val Ser Cys Leu Pro Gln
180 185 190

Ser Pro Asp Glu Ala Ala Ser Phe Gln Pro Leu Thr Asp Ala Leu Asn
195 200 205

Arg Ala Glu Leu Gln Gly Val Ile Val Val Ala Ala Ala Gly Asn Leu
210 215 220

Gly Gln Asp Cys Pro Val Gly Ser Thr Val Tyr Pro Ala His Ser Asp
225 230 235 240

Thr Val Leu Ser Val Ser Ala Arg Phe Asp Ser His Thr Leu Ala Glu
245 250 255

Tyr Ser Met Pro Gly Asn Gln Gln Ile Leu Ser Ala Pro Ser His Ile
260 265 270

Gln Ala Gly Leu Ser Pro Arg Gly Asp Gly Phe Ala Ser His Met Ile
275 280 285

Thr Thr Ala Gly Glu Ser Pro Phe Glu Gly Thr Ser Phe Ala Ala Pro

```
    290                 295                 300

Val Val Ser Ala Thr Ala Ala Leu Leu Arg Gln His Phe Pro Phe Ala
305                 310                 315                 320

Thr Pro Tyr Glu Ile Arg Ala Arg Ile Phe Asn Ser Ile Asp Pro Ala
                325                 330                 335

Arg Gly Ala Ile Asp Pro Tyr Leu Ala Leu Thr Gln Glu Ile Tyr Pro
            340                 345                 350

Thr Thr Pro Leu Val His Glu Ile Ala Leu Ser Val Pro Thr Pro Pro
        355                 360                 365

Asp Asp Ser Pro Arg Glu Arg Gly Ile Leu Val Thr Ala Ile Ile Val
    370                 375                 380

Gly Leu Leu Ala Val Leu Ala Val Leu Met Gly Leu Arg Arg Ile His
385                 390                 395                 400

His His Ser Ala Phe Gln Lys Ala Ser Ser Ser Val Ile Thr
                405                 410
```

Sequence Listing

<210> 2353
<211> 549
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(526)
<223> RXA01643

<400> 2353

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cggatttcaa cactttcagg atgcatctgt aactatgccc atgccacacc ccatgtttat 60

cgatgtctcc ttcccacccg cggagacctg tagttaaccc atg ggc acg atg cga   115
                                             Met Gly Thr Met Arg
                                               1               5

gaa atg gtc agt gac cgc att gac cga cta caa gaa gca cac gcg cga   163
Glu Met Val Ser Asp Arg Ile Asp Arg Leu Gln Glu Ala His Ala Arg
                 10                  15                  20

tca aag cag aag aag ttc ggc ttc tta gtt cgg cca ggc acc ctg atc   211
Ser Lys Gln Lys Lys Phe Gly Phe Leu Val Arg Pro Gly Thr Leu Ile
             25                  30                  35

ctt gga tgg ttg gtc acg atc atc ggt ctg atc acc att cca ctt ccc   259
Leu Gly Trp Leu Val Thr Ile Ile Gly Leu Ile Thr Ile Pro Leu Pro
         40                  45                  50

ggc caa ggc tgg ctg acc acc ttc att ggt gtg ggc att ttg tct ctg   307
Gly Gln Gly Trp Leu Thr Thr Phe Ile Gly Val Gly Ile Leu Ser Leu
     55                  60                  65

gag ctt aaa tgg gcg aag aac ctc ctg gcc tgg gga gtg cat cag tat   355
Glu Leu Lys Trp Ala Lys Asn Leu Leu Ala Trp Gly Val His Gln Tyr
 70                  75                  80                  85
```

```
gat cgc ttc ttc acc tgg tac ggc aag aaa tca ttc cgc ttc cgc atg   403
Asp Arg Phe Phe Thr Trp Tyr Gly Lys Lys Ser Phe Arg Phe Arg Met
                 90                  95                  100

gcg atg ttg gca ctg atg att ctg ctg att tgg gtg gtg ttc atc gtg   451
Ala Met Leu Ala Leu Met Ile Leu Leu Ile Trp Val Val Phe Ile Val
            105                 110                 115

aca ttt tgg ttg atg tgg cac gcc gga act atc ccg tgg gca gat gag   499
Thr Phe Trp Leu Met Trp His Ala Gly Thr Ile Pro Trp Ala Asp Glu
        120                 125                 130

ttc ttc acc tgg ctt ggg ttg agc cgc tagcaactat tcgctttgaa        546
Phe Phe Thr Trp Leu Gly Leu Ser Arg
    135                 140

ggc                                                              549
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<210> 2354
<211> 142
<212> PRT
<213> Corynebacterium glutamicum

<400> 2354

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Met Gly Thr Met Arg Glu Met Val Ser Asp Arg Ile Asp Arg Leu Gln
  1               5                  10                  15

Glu Ala His Ala Arg Ser Lys Gln Lys Lys Phe Gly Phe Leu Val Arg
             20                  25                  30

Pro Gly Thr Leu Ile Leu Gly Trp Leu Val Thr Ile Ile Gly Leu Ile
         35                  40                  45

Thr Ile Pro Leu Pro Gly Gln Gly Trp Leu Thr Thr Phe Ile Gly Val
     50                  55                  60

Gly Ile Leu Ser Leu Glu Leu Lys Trp Ala Lys Asn Leu Leu Ala Trp
 65                  70                  75                  80

Gly Val His Gln Tyr Asp Arg Phe Phe Thr Trp Tyr Gly Lys Lys Ser
                 85                  90                  95

Phe Arg Phe Arg Met Ala Met Leu Ala Leu Met Ile Leu Leu Ile Trp
            100                 105                 110

Val Val Phe Ile Val Thr Phe Trp Leu Met Trp His Ala Gly Thr Ile
        115                 120                 125

Pro Trp Ala Asp Glu Phe Phe Thr Trp Leu Gly Leu Ser Arg
    130                 135                 140
```

<210> 2355
<211> 729
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(706)

<223> RXA01645

<400> 2355

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agagggcatc acctatgacc gcctgacaat ccgcgattac atctggcgct gggacaccga 60

ctggttctgg tgttcacgcg cattcggcac ccaaaacccc gtg gtg cgc aaa ctc   115
                                              Val Val Arg Lys Leu
                                                1               5

tgg ccc agg gat ctg ctg cgc tcg agt ttc tat tgg aag atc atc ggc   163
Trp Pro Arg Asp Leu Leu Arg Ser Ser Phe Tyr Trp Lys Ile Ile Gly
            10                  15                  20

tgg gat cga aaa tac tcc atc gct gat cgc ctg gaa gag cgc aaa ggc   211
Trp Asp Arg Lys Tyr Ser Ile Ala Asp Arg Leu Glu Glu Arg Lys Gly
        25                  30                  35

cgc ccg gct agg gaa cgg gtg gtc caa gac gtg gaa gtt acg att gat   259
Arg Pro Ala Arg Glu Arg Val Val Gln Asp Val Glu Val Thr Ile Asp
    40                  45                  50

aaa ctg cca gaa ttt ttg aaa tgg ttc ttt gaa agc agc gac atc gag   307
Lys Leu Pro Glu Phe Leu Lys Trp Phe Phe Glu Ser Ser Asp Ile Glu
55                  60                  65

ccg ctg tgg ctg tgc ccg atc aag ctt cgg gag gta cca ggt agt tcg   355
Pro Leu Trp Leu Cys Pro Ile Lys Leu Arg Glu Val Pro Gly Ser Ser
70                  75                  80                  85

gtt ggt gct gga gaa att ttg agc tcc gct gaa gca atc gac tcc ggt   403
Val Gly Ala Gly Glu Ile Leu Ser Ser Ala Glu Ala Ile Asp Ser Gly
                90                  95                  100

gct gct gaa cac cct tgg ccg ctg tat ccc ttg aag aag gac gtg ctg   451
Ala Ala Glu His Pro Trp Pro Leu Tyr Pro Leu Lys Lys Asp Val Leu
            105                 110                 115

tgg gtc aac atc gga ttc tgg tcc tca gtg ccg gtt gat ctg atg ggc   499
Trp Val Asn Ile Gly Phe Trp Ser Ser Val Pro Val Asp Leu Met Gly
        120                 125                 130

tcc gat gca cca gag gga gca ttt aac aga gaa atc gaa cgc gtc atg   547
Ser Asp Ala Pro Glu Gly Ala Phe Asn Arg Glu Ile Glu Arg Val Met
    135                 140                 145

gca gag cta ggc gga cat aaa tcg ctg tac tcc gaa gcg ttc tac acc   595
Ala Glu Leu Gly Gly His Lys Ser Leu Tyr Ser Glu Ala Phe Tyr Thr
150                 155                 160                 165

agg gaa gac ttt gaa aaa ctt tat ggc gga acc atc ccg gcg ctg cta   643
Arg Glu Asp Phe Glu Lys Leu Tyr Gly Gly Thr Ile Pro Ala Leu Leu
                170                 175                 180

aaa aag cag tgg gat ccc cac agc cga ttc ccc ggt ttg tat gaa aag   691
Lys Lys Gln Trp Asp Pro His Ser Arg Phe Pro Gly Leu Tyr Glu Lys
            185                 190                 195

aca gta aaa ggc gcc taggatcgct cactgtaggt aga                    729
Thr Val Lys Gly Ala
        200
```

<210> 2356
<211> 202
<212> PRT
<213> Corynebacterium glutamicum

<400> 2356
Val Val Arg Lys Leu Trp Pro Arg Asp Leu Leu Arg Ser Ser Phe Tyr
1 5 10 15

Trp Lys Ile Ile Gly Trp Asp Arg Lys Tyr Ser Ile Ala Asp Arg Leu
20 25 30

Glu Glu Arg Lys Gly Arg Pro Ala Arg Glu Arg Val Val Gln Asp Val
35 40 45

Glu Val Thr Ile Asp Lys Leu Pro Glu Phe Leu Lys Trp Phe Phe Glu
50 55 60

Ser Ser Asp Ile Glu Pro Leu Trp Leu Cys Pro Ile Lys Leu Arg Glu
65 70 75 80

Val Pro Gly Ser Ser Val Gly Ala Gly Glu Ile Leu Ser Ser Ala Glu
85 90 95

Ala Ile Asp Ser Gly Ala Ala Glu His Pro Trp Pro Leu Tyr Pro Leu
100 105 110

Lys Lys Asp Val Leu Trp Val Asn Ile Gly Phe Trp Ser Ser Val Pro
115 120 125

Val Asp Leu Met Gly Ser Asp Ala Pro Glu Gly Ala Phe Asn Arg Glu
130 135 140

Ile Glu Arg Val Met Ala Glu Leu Gly Gly His Lys Ser Leu Tyr Ser
145 150 155 160

Glu Ala Phe Tyr Thr Arg Glu Asp Phe Glu Lys Leu Tyr Gly Gly Thr
165 170 175

Ile Pro Ala Leu Leu Lys Lys Gln Trp Asp Pro His Ser Arg Phe Pro
180 185 190

Gly Leu Tyr Glu Lys Thr Val Lys Gly Ala
195 200

<210> 2357
<211> 942
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(919)
<223> RXA01646

<400> 2357
ggtcgtgccg tggagcgtgc tgcgattgtt gccgcaggga agtgaattag caaaagagac 60

agcgctcgcg cccacctatt aaggagtatg gtggccttac atg agc gga tta gtt 115

```
                                                    Met Ser Gly Leu Val
                                                      1               5

gac ccg gat agt act ttt tta aag acc atc gga aaa ctg agc aac agc   163
Asp Pro Asp Ser Thr Phe Leu Lys Thr Ile Gly Lys Leu Ser Asn Ser
                 10                  15                  20

ttg tcc att ggt cgt gga gta gat caa aaa gag gta atc ccc aaa ggc   211
Leu Ser Ile Gly Arg Gly Val Asp Gln Lys Glu Val Ile Pro Lys Gly
             25                  30                  35

tgg aac gcc cat tgg gag gca att aca aag ctt aag aga agc ttt gac   259
Trp Asn Ala His Trp Glu Ala Ile Thr Lys Leu Lys Arg Ser Phe Asp
         40                  45                  50

gcg att cct gct ggg gag cgg gtg cgt tta gct aag aaa acc tcc aac   307
Ala Ile Pro Ala Gly Glu Arg Val Arg Leu Ala Lys Lys Thr Ser Asn
     55                  60                  65

ctg ttc cgt gga cgc tcc gat gca ggt cac ggc cta gat gtg gca gcg   355
Leu Phe Arg Gly Arg Ser Asp Ala Gly His Gly Leu Asp Val Ala Ala
 70                  75                  80                  85

ctt ggg gga gtg att gcc att gat ccg gtc aat gcc acc gcc gat gta   403
Leu Gly Gly Val Ile Ala Ile Asp Pro Val Asn Ala Thr Ala Asp Val
                 90                  95                 100

cag ggc atg tgc acg tat gaa gac ctg gta gat gcc act tta agt tat   451
Gln Gly Met Cys Thr Tyr Glu Asp Leu Val Asp Ala Thr Leu Ser Tyr
             105                 110                 115

ggt ctg atg ccg ttg gtt gtg cct caa ctg aaa acc atc acg ctt ggt   499
Gly Leu Met Pro Leu Val Val Pro Gln Leu Lys Thr Ile Thr Leu Gly
         120                 125                 130

ggc gca gtg acc gga atg ggc gtg gaa tcc aca tcc ttc cgc aac ggt   547
Gly Ala Val Thr Gly Met Gly Val Glu Ser Thr Ser Phe Arg Asn Gly
     135                 140                 145

ttg cca cac gaa tca gtg ctg gag atg gat att ttt acc ggc act ggt   595
Leu Pro His Glu Ser Val Leu Glu Met Asp Ile Phe Thr Gly Thr Gly
150                 155                 160                 165

gag atc gtg act tgc tcg ccc aca gaa aat gtc gac ctt tac aga ggt   643
Glu Ile Val Thr Cys Ser Pro Thr Glu Asn Val Asp Leu Tyr Arg Gly
                 170                 175                 180

ttt ccc aac tct tat ggt tcg ctg gga tac gcg gtg cgg cta aaa att   691
Phe Pro Asn Ser Tyr Gly Ser Leu Gly Tyr Ala Val Arg Leu Lys Ile
             185                 190                 195

gag ctg gaa cca gtg caa gat tac gtc cag ctg cgc cac gtg cgc ttc   739
Glu Leu Glu Pro Val Gln Asp Tyr Val Gln Leu Arg His Val Arg Phe
         200                 205                 210

aac gat tta gag tct ttg acc aaa gcg att gag gaa gtc gcg tct tct   787
Asn Asp Leu Glu Ser Leu Thr Lys Ala Ile Glu Glu Val Ala Ser Ser
     215                 220                 225

ctg gag ttt gat aac caa ccc gtc gat tac ctt gac ggc gtg gtg ttt   835
Leu Glu Phe Asp Asn Gln Pro Val Asp Tyr Leu Asp Gly Val Val Phe
```

```
230                 235                 240                 245

tca ccc acg gaa gcc tac tta gtt ctt ggc acg caa acc tca caa cct   883
Ser Pro Thr Glu Ala Tyr Leu Val Leu Gly Thr Gln Thr Ser Gln Pro
                250                 255                 260

ggc ccc acc agc gat tac acc agg gat tta agc tac taacgctccc       929
Gly Pro Thr Ser Asp Tyr Thr Arg Asp Leu Ser Tyr
            265                 270

tgcaacaccc aga                                                   942


<210> 2358
<211> 273
<212> PRT
<213> Corynebacterium glutamicum

<400> 2358
Met Ser Gly Leu Val Asp Pro Asp Ser Thr Phe Leu Lys Thr Ile Gly
  1               5                  10                  15

Lys Leu Ser Asn Ser Leu Ser Ile Gly Arg Gly Val Asp Gln Lys Glu
             20                  25                  30

Val Ile Pro Lys Gly Trp Asn Ala His Trp Glu Ala Ile Thr Lys Leu
         35                  40                  45

Lys Arg Ser Phe Asp Ala Ile Pro Ala Gly Glu Arg Val Arg Leu Ala
     50                  55                  60

Lys Lys Thr Ser Asn Leu Phe Arg Gly Arg Ser Asp Ala Gly His Gly
 65                  70                  75                  80

Leu Asp Val Ala Ala Leu Gly Gly Val Ile Ala Ile Asp Pro Val Asn
                 85                  90                  95

Ala Thr Ala Asp Val Gln Gly Met Cys Thr Tyr Glu Asp Leu Val Asp
            100                 105                 110

Ala Thr Leu Ser Tyr Gly Leu Met Pro Leu Val Val Pro Gln Leu Lys
        115                 120                 125

Thr Ile Thr Leu Gly Gly Ala Val Thr Gly Met Gly Val Glu Ser Thr
    130                 135                 140

Ser Phe Arg Asn Gly Leu Pro His Glu Ser Val Leu Glu Met Asp Ile
145                 150                 155                 160

Phe Thr Gly Thr Gly Glu Ile Val Thr Cys Ser Pro Thr Glu Asn Val
                165                 170                 175

Asp Leu Tyr Arg Gly Phe Pro Asn Ser Tyr Gly Ser Leu Gly Tyr Ala
            180                 185                 190

Val Arg Leu Lys Ile Glu Leu Glu Pro Val Gln Asp Tyr Val Gln Leu
        195                 200                 205

Arg His Val Arg Phe Asn Asp Leu Glu Ser Leu Thr Lys Ala Ile Glu
    210                 215                 220
```

```
Glu Val Ala Ser Ser Leu Glu Phe Asp Asn Gln Pro Val Asp Tyr Leu
225                 230                 235                 240

Asp Gly Val Val Phe Ser Pro Thr Glu Ala Tyr Leu Val Leu Gly Thr
                245                 250                 255

Gln Thr Ser Gln Pro Gly Pro Thr Ser Asp Tyr Thr Arg Asp Leu Ser
            260                 265                 270

Tyr
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<210> 2359
<211> 1020
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(997)
<223> RXA01656

<400> 2359

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tcggcaagca tggcttcatc gtcctcaaaa aagtggtcta atgcaagtga ctgaaagtgg 60

atctaccgct agtccacttt gtggcgttgg atcatctgtc atg acc gaa act caa   115
                                            Met Thr Glu Thr Gln
                                              1               5

gaa act tac caa gca acc act cgt gtg aag cgc ggc ctt gcc gac atg   163
Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg Gly Leu Ala Asp Met
                10                  15                  20

ctc aag ggt ggt gtg atc atg gat gtg gtc acc cct gaa caa gcg cgc   211
Leu Lys Gly Gly Val Ile Met Asp Val Val Thr Pro Glu Gln Ala Arg
            25                  30                  35

atc gcc gaa gat gca ggt gcc agc gca gtt atg gca ctc gag cgc gtt   259
Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met Ala Leu Glu Arg Val
        40                  45                  50

ccc gcc gat atc cgt tct cag ggc ggc gtt gct cgc atg agt gat cct   307
Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala Arg Met Ser Asp Pro
    55                  60                  65

gac ctg atc gaa gga atc gtc aat gcg gtc tcc atc ccg gtc atg gcg   355
Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser Ile Pro Val Met Ala
70                  75                  80                  85

aaa gct cgc atc ggt cac ttc gtg gaa gct cag gtt ctg gaa gct ctc   403
Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln Val Leu Glu Ala Leu
                90                  95                  100

ggt gtt gat ttc atc gac gag tcc gaa gtt ctc agc cct gcc gac tac   451
Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu Ser Pro Ala Asp Tyr
            105                 110                 115

acg cac cac atc aac aag tgg aag ttc gac gtt cct ttc gtc tgt ggc   499
Thr His His Ile Asn Lys Trp Lys Phe Asp Val Pro Phe Val Cys Gly
        120                 125                 130
```

```
gcg acc aac ctc ggc gaa gct ttg cga cgc atc acc gaa ggc gct gca   547
Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile Thr Glu Gly Ala Ala
    135                 140                 145

atg atc cgt tcc aag ggc gaa gcc ggc acc ggc gat gtc tct gaa gct   595
Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly Asp Val Ser Glu Ala
150                 155                 160                 165

gtc cgt cac ctg cgc acc atc cgc ggc gac atc aat cgc ctg cgc tcc   643
Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile Asn Arg Leu Arg Ser
                170                 175                 180

ctg gat gag gat gaa ctc ttc gtc gcc gcc aag gaa ttc cag gca cca   691
Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys Glu Phe Gln Ala Pro
            185                 190                 195

tac gac ctg gtc cgc gaa gtc gcc tcc acc ggc aag ctc cct gtg gtc   739
Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly Lys Leu Pro Val Val
        200                 205                 210

acc ttc gtt gca ggt ggc gtc gca acc cca gcc gac gct gca ctc gtg   787
Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala Asp Ala Ala Leu Val
    215                 220                 225

cgc caa atg ggc gcc gaa ggc gtc ttt gtc ggc tcc ggc atc ttc aaa   835
Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly Ser Gly Ile Phe Lys
230                 235                 240                 245

tcc ggc aat cca gcc gcc cgc gcc gca gcg atc gtc aag gct gca acg   883
Ser Gly Asn Pro Ala Ala Arg Ala Ala Ala Ile Val Lys Ala Ala Thr
                250                 255                 260

ctt ttc gac gac ccc tcc gtc att gcc gac gta tcc cgc ggc ctg ggt   931
Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val Ser Arg Gly Leu Gly
            265                 270                 275

gaa gcc atg gtg ggc atc aac gta tcc gac gtt cca gca cca cac cga   979
Glu Ala Met Val Gly Ile Asn Val Ser Asp Val Pro Ala Pro His Arg
        280                 285                 290

ctc gcc gag cgc ggc tgg tgatcgttgg agttttagct ctc               1020
Leu Ala Glu Arg Gly Trp
    295
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Application Filed Electronically

<210> 2360
<211> 299
<212> PRT
<213> Corynebacterium glutamicum

<400> 2360

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Met Thr Glu Thr Gln Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg
  1               5                  10                  15

Gly Leu Ala Asp Met Leu Lys Gly Gly Val Ile Met Asp Val Val Thr
             20                  25                  30

Pro Glu Gln Ala Arg Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met
         35                  40                  45
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```
Ala Leu Glu Arg Val Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala
     50                  55                  60

Arg Met Ser Asp Pro Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser
 65                  70                  75                  80

Ile Pro Val Met Ala Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln
                 85                  90                  95

Val Leu Glu Ala Leu Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu
            100                 105                 110

Ser Pro Ala Asp Tyr Thr His His Ile Asn Lys Trp Lys Phe Asp Val
        115                 120                 125

Pro Phe Val Cys Gly Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile
    130                 135                 140

Thr Glu Gly Ala Ala Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly
145                 150                 155                 160

Asp Val Ser Glu Ala Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile
                165                 170                 175

Asn Arg Leu Arg Ser Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys
            180                 185                 190

Glu Phe Gln Ala Pro Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly
        195                 200                 205

Lys Leu Pro Val Val Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala
    210                 215                 220

Asp Ala Ala Leu Val Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly
225                 230                 235                 240

Ser Gly Ile Phe Lys Ser Gly Asn Pro Ala Ala Arg Ala Ala Ala Ile
                245                 250                 255

Val Lys Ala Ala Thr Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val
            260                 265                 270

Ser Arg Gly Leu Gly Glu Ala Met Val Gly Ile Asn Val Ser Asp Val
        275                 280                 285

Pro Ala Pro His Arg Leu Ala Glu Arg Gly Trp
    290                 295
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<210> 2361
<211> 843
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(820)
<223> RXA01665

<400> 2361
aggattggcg cccgtgacgc tactgaaaag gtggaggggc gcgtcgaaaa gcgttggccg 60

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gtgcttgagc gaaaacccgt gatgattagc atggtttgtt gtg aag atc gat gaa   115
                                              Val Lys Ile Asp Glu
                                                1               5

ttg att gct ctc gcc gcg gag caa ccc act cgc atc tcc agg cgt tcc   163
Leu Ile Ala Leu Ala Ala Glu Gln Pro Thr Arg Ile Ser Arg Arg Ser
               10                  15                  20

ggt gtc tcg cgc tcg acc ctg aag cgg gtc ggc gat ggc acc agc gag   211
Gly Val Ser Arg Ser Thr Leu Lys Arg Val Gly Asp Gly Thr Ser Glu
            25                  30                  35

ccc acc ctg tcg acg ctg cgt gag gtc gcg ttg gcg ctc ggg ctt gat   259
Pro Thr Leu Ser Thr Leu Arg Glu Val Ala Leu Ala Leu Gly Leu Asp
        40                  45                  50

att aag gtc gcc gcg cac cac gcc tgc gat ccc ttt gcg gcc gct gca   307
Ile Lys Val Ala Ala His His Ala Cys Asp Pro Phe Ala Ala Ala Ala
    55                  60                  65

gcg cgc acg ctt atc gac gcc tcc gtc ccc gaa aat ccc cac aac cag   355
Ala Arg Thr Leu Ile Asp Ala Ser Val Pro Glu Asn Pro His Asn Gln
70                  75                  80                  85

gaa att ctc gct tgg ttg cac cgt ttt gag cgg tgg aat atc aac gat   403
Glu Ile Leu Ala Trp Leu His Arg Phe Glu Arg Trp Asn Ile Asn Asp
               90                  95                 100

ccg ctc acc ctt gtc tct gaa gcc gga acg ctt cag ggc atc aca cat   451
Pro Leu Thr Leu Val Ser Glu Ala Gly Thr Leu Gln Gly Ile Thr His
            105                 110                 115

cgc cag gat gcg cag ttt gtg aaa ctc aat cca cgc ggc atc gct gag   499
Arg Gln Asp Ala Gln Phe Val Lys Leu Asn Pro Arg Gly Ile Ala Glu
        120                 125                 130

cta ccg gag ctt ttc caa cag cac aaa acc aaa tgg gcg ctg tcg ggc   547
Leu Pro Glu Leu Phe Gln Gln His Lys Thr Lys Trp Ala Leu Ser Gly
    135                 140                 145

gct gcg gct gcc acg gtg atc atg gga caa att gtg ctg ggg aat tcg   595
Ala Ala Ala Ala Thr Val Ile Met Gly Gln Ile Val Leu Gly Asn Ser
150                 155                 160                 165

att gtg tgg cac gaa cct gcc cac gat ctc gat gtc tca gcg ctg ggc   643
Ile Val Trp His Glu Pro Ala His Asp Leu Asp Val Ser Ala Leu Gly
               170                 175                 180

acc att gtt gat gtg gca gaa gac gcc gat cta att ctc ctg ccc gca   691
Thr Ile Val Asp Val Ala Glu Asp Ala Asp Leu Ile Leu Leu Pro Ala
            185                 190                 195

acg gtc acg gaa ctg gtg gga agt tac acc cag gac agg cta aat ttt   739
Thr Val Thr Glu Leu Val Gly Ser Tyr Thr Gln Asp Arg Leu Asn Phe
        200                 205                 210

gtg gca cct gtg caa tta gtt att gat cta cac agc ctc cac atg ttc   787
Val Ala Pro Val Gln Leu Val Ile Asp Leu His Ser Leu His Met Phe
    215                 220                 225
```

```
gag gaa gcc gat tac ctc acg agc ggt tgg cgc taaaatactt agcgtacgca 840
Glu Glu Ala Asp Tyr Leu Thr Ser Gly Trp Arg
230                 235                 240

ccc                                                               843
```

<210> 2362
<211> 240
<212> PRT
<213> Corynebacterium glutamicum

<400> 2362

```
Val Lys Ile Asp Glu Leu Ile Ala Leu Ala Ala Glu Gln Pro Thr Arg
  1               5                  10                  15

Ile Ser Arg Arg Ser Gly Val Ser Arg Ser Thr Leu Lys Arg Val Gly
             20                  25                  30

Asp Gly Thr Ser Glu Pro Thr Leu Ser Thr Leu Arg Glu Val Ala Leu
         35                  40                  45

Ala Leu Gly Leu Asp Ile Lys Val Ala Ala His His Ala Cys Asp Pro
     50                  55                  60

Phe Ala Ala Ala Ala Ala Arg Thr Leu Ile Asp Ala Ser Val Pro Glu
 65                  70                  75                  80

Asn Pro His Asn Gln Glu Ile Leu Ala Trp Leu His Arg Phe Glu Arg
                 85                  90                  95

Trp Asn Ile Asn Asp Pro Leu Thr Leu Val Ser Glu Ala Gly Thr Leu
            100                 105                 110

Gln Gly Ile Thr His Arg Gln Asp Ala Gln Phe Val Lys Leu Asn Pro
        115                 120                 125

Arg Gly Ile Ala Glu Leu Pro Glu Leu Phe Gln Gln His Lys Thr Lys
    130                 135                 140

Trp Ala Leu Ser Gly Ala Ala Ala Ala Thr Val Ile Met Gly Gln Ile
145                 150                 155                 160

Val Leu Gly Asn Ser Ile Val Trp His Glu Pro Ala His Asp Leu Asp
                165                 170                 175

Val Ser Ala Leu Gly Thr Ile Val Asp Val Ala Glu Asp Ala Asp Leu
            180                 185                 190

Ile Leu Leu Pro Ala Thr Val Thr Glu Leu Val Gly Ser Tyr Thr Gln
        195                 200                 205

Asp Arg Leu Asn Phe Val Ala Pro Val Gln Leu Val Ile Asp Leu His
    210                 215                 220

Ser Leu His Met Phe Glu Glu Ala Asp Tyr Leu Thr Ser Gly Trp Arg
225                 230                 235                 240
```

<210> 2363
<211> 738
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(715)
<223> RXA01671

<400> 2363
tctaaaaaca catttttaag ccctcccggc gcagctgaaa actcagtcgc cgggagggct 60

ttttgtacc cgaatttgta cccgaattta aggaatcgct atg aat cat gtt gtt 115
Met Asn His Val Val
1 5

aat ttt gct tca cat ttg gaa gac gca gcc ctg aag caa gcc gaa gct 163
Asn Phe Ala Ser His Leu Glu Asp Ala Ala Leu Lys Gln Ala Glu Ala
10 15 20

act gcc acc atg ccg ttt att tac ccg cat gtg gcg ttg atg cct gat 211
Thr Ala Thr Met Pro Phe Ile Tyr Pro His Val Ala Leu Met Pro Asp
25 30 35

gct cac ttt ggg ctg ggt tcg tcg gtg gga acg gtg ttc ggc acc aag 259
Ala His Phe Gly Leu Gly Ser Ser Val Gly Thr Val Phe Gly Thr Lys
40 45 50

ggt gcg atc att ccg gcg gct gtg ggt gtg gat ata ggt tgc gga atg 307
Gly Ala Ile Ile Pro Ala Ala Val Gly Val Asp Ile Gly Cys Gly Met
55 60 65

ata gga gtg tgt acc aat tac acg gcc tct gac ctg gag gga cgt gat 355
Ile Gly Val Cys Thr Asn Tyr Thr Ala Ser Asp Leu Glu Gly Arg Asp
70 75 80 85

ttg gtg acg ctt cgg gat tac atc gag cgg gtg att ccg ttg tct cct 403
Leu Val Thr Leu Arg Asp Tyr Ile Glu Arg Val Ile Pro Leu Ser Pro
90 95 100

gga aat tac aat tcc acc acc ttg aag gaa acc gcg aag gtg aag gtc 451
Gly Asn Tyr Asn Ser Thr Thr Leu Lys Glu Thr Ala Lys Val Lys Val
105 110 115

gcg gag ttg gag gaa ctc gcg gag cgc gat ggt gta gat ttg tcg cac 499
Ala Glu Leu Glu Glu Leu Ala Glu Arg Asp Gly Val Asp Leu Ser His
120 125 130

tct ccg acg tgg aag cgc cag ttg ggt tcg ctt ggt gga ggt aat cac 547
Ser Pro Thr Trp Lys Arg Gln Leu Gly Ser Leu Gly Gly Gly Asn His
135 140 145

ttc att gag ttg tgt ctt gat gag ttg gat cgg gtg tgg atg ttt ttg 595
Phe Ile Glu Leu Cys Leu Asp Glu Leu Asp Arg Val Trp Met Phe Leu
150 155 160 165

cac tct ggt tcc cgc ggt gtg ggt aac aag att gcc cat aag cac atc 643
His Ser Gly Ser Arg Gly Val Gly Asn Lys Ile Ala His Lys His Ile
170 175 180

```
aag aac gcg cag gcc cag tgt aag aat gag gag ctt ccc gat aag gat   691
Lys Asn Ala Gln Ala Gln Cys Lys Asn Glu Glu Leu Pro Asp Lys Asp
            185                 190                 195

ctt gcg tac ctt gac cga ggg gac tgaggagttt gagtcttaca tca         738
Leu Ala Tyr Leu Asp Arg Gly Asp
        200                 205
```

<210> 2364
<211> 205
<212> PRT
<213> Corynebacterium glutamicum

<400> 2364

```
Met Asn His Val Val Asn Phe Ala Ser His Leu Glu Asp Ala Ala Leu
  1               5                  10                  15

Lys Gln Ala Glu Ala Thr Ala Thr Met Pro Phe Ile Tyr Pro His Val
             20                  25                  30

Ala Leu Met Pro Asp Ala His Phe Gly Leu Gly Ser Ser Val Gly Thr
         35                  40                  45

Val Phe Gly Thr Lys Gly Ala Ile Ile Pro Ala Ala Val Gly Val Asp
     50                  55                  60

Ile Gly Cys Gly Met Ile Gly Val Cys Thr Asn Tyr Thr Ala Ser Asp
 65                  70                  75                  80

Leu Glu Gly Arg Asp Leu Val Thr Leu Arg Asp Tyr Ile Glu Arg Val
                 85                  90                  95

Ile Pro Leu Ser Pro Gly Asn Tyr Asn Ser Thr Thr Leu Lys Glu Thr
            100                 105                 110

Ala Lys Val Lys Val Ala Glu Leu Glu Glu Leu Ala Glu Arg Asp Gly
        115                 120                 125

Val Asp Leu Ser His Ser Pro Thr Trp Lys Arg Gln Leu Gly Ser Leu
    130                 135                 140

Gly Gly Gly Asn His Phe Ile Glu Leu Cys Leu Asp Glu Leu Asp Arg
145                 150                 155                 160

Val Trp Met Phe Leu His Ser Gly Ser Arg Gly Val Gly Asn Lys Ile
                165                 170                 175

Ala His Lys His Ile Lys Asn Ala Gln Ala Gln Cys Lys Asn Glu Glu
            180                 185                 190

Leu Pro Asp Lys Asp Leu Ala Tyr Leu Asp Arg Gly Asp
        195                 200                 205
```

<210> 2365
<211> 1158
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1135)
<223> RXA01673

<400> 2365
agtttgcagg ttcggccacc cattatccat atcaacatta tatgggtgga tatgaaagta 60

ccgtctaccg cgttcttttc aattagcgca accttgaagc atg tct aca aac ctt 115
Met Ser Thr Asn Leu
1 5

ctg gaa tcg acg ccg ccc ttt acc caa ctt cgc acc gga gtc ctc cag 163
Leu Glu Ser Thr Pro Pro Phe Thr Gln Leu Arg Thr Gly Val Leu Gln
10 15 20

aag tac acc ccg ggc ctg ctc tta tgc tcc att gcg gta ctc atc gct 211
Lys Tyr Thr Pro Gly Leu Leu Leu Cys Ser Ile Ala Val Leu Ile Ala
25 30 35

atg atc gtg aat cac ttt ttc tct ggt gtg agt ccg ctt atc gtc gcg 259
Met Ile Val Asn His Phe Phe Ser Gly Val Ser Pro Leu Ile Val Ala
40 45 50

atc att ctt ggc atc atc ctg acc aac ctg att cag ctc cca gca tcg 307
Ile Ile Leu Gly Ile Ile Leu Thr Asn Leu Ile Gln Leu Pro Ala Ser
55 60 65

acc tca ccc ggc atc acg ttg gcg tcg aaa aag ctt ttg cgg ctg gga 355
Thr Ser Pro Gly Ile Thr Leu Ala Ser Lys Lys Leu Leu Arg Leu Gly
70 75 80 85

atc gtc ttc ctt ggt ctg cag tta gtt ttc tca gat att ttg tca ctt 403
Ile Val Phe Leu Gly Leu Gln Leu Val Phe Ser Asp Ile Leu Ser Leu
90 95 100

ggt ttc ccc atg ctg gcg gtg att gtg tgc atc gtt gcc ggt ggt att 451
Gly Phe Pro Met Leu Ala Val Ile Val Cys Ile Val Ala Gly Gly Ile
105 110 115

ttt ggg acc atc ctc atg gga cac ctg ctc aga atg aaa cca acc caa 499
Phe Gly Thr Ile Leu Met Gly His Leu Leu Arg Met Lys Pro Thr Gln
120 125 130

gtt ctg ttg att gct tgt ggc ttt tct att tgt ggc gct gcg gcc gtg 547
Val Leu Leu Ile Ala Cys Gly Phe Ser Ile Cys Gly Ala Ala Ala Val
135 140 145

gca ggt gtt gaa gga gta act gat tcc gaa gaa gaa gag gtc gtt act 595
Ala Gly Val Glu Gly Val Thr Asp Ser Glu Glu Glu Glu Val Val Thr
150 155 160 165

gcg gtt gca ctt gtt gtt att ttc gga acg ctg atg att cct ttt atc 643
Ala Val Ala Leu Val Val Ile Phe Gly Thr Leu Met Ile Pro Phe Ile
170 175 180

cca ttc gca acc aaa gtc ttg ggg tta tcc cct gaa atc ggt ggg atg 691
Pro Phe Ala Thr Lys Val Leu Gly Leu Ser Pro Glu Ile Gly Gly Met
185 190 195

tgg gca ggc gga tcc atc cat gaa atc gcc caa gta gta gca gct gga 739

```
Trp Ala Gly Gly Ser Ile His Glu Ile Ala Gln Val Val Ala Ala Gly
        200                 205                 210

gga gtc att ggt ggt gga gca tta ggt gtt gca gtt gtg gtg aaa ctc   787
Gly Val Ile Gly Gly Gly Ala Leu Gly Val Ala Val Val Val Lys Leu
    215                 220                 225

gcc cga gta ctc cta ctt gca ccc att gct gcc att tta agt ttt cgc   835
Ala Arg Val Leu Leu Leu Ala Pro Ile Ala Ala Ile Leu Ser Phe Arg
230                 235                 240                 245

cag cgc cgc cag ggt tac acg tcc ccc gat gga aag aga cca ccg gtc   883
Gln Arg Arg Gln Gly Tyr Thr Ser Pro Asp Gly Lys Arg Pro Pro Val
                250                 255                 260

gtt ccc cta ttt atc ctt gga ttc ttg gcg atg gta gtt ttg cgc tcc   931
Val Pro Leu Phe Ile Leu Gly Phe Leu Ala Met Val Val Leu Arg Ser
            265                 270                 275

act gtt gcg ctc cca gac gag gta att gcg gct gga ggt ttc cta cag   979
Thr Val Ala Leu Pro Asp Glu Val Ile Ala Ala Gly Gly Phe Leu Gln
        280                 285                 290

aca gcc ttg ctc tct gca gca atg ttt ggt ctc ggg tgt ggc gta aaa   1027
Thr Ala Leu Leu Ser Ala Ala Met Phe Gly Leu Gly Cys Gly Val Lys
    295                 300                 305

atc cag aac ctg atc cat gtt ggg gtc aag cct ttc att ctg gct ttc   1075
Ile Gln Asn Leu Ile His Val Gly Val Lys Pro Phe Ile Leu Ala Phe
310                 315                 320                 325

gga tcc acg aca ctt gtc acc agt atc gca ctt gca ggc acc cta ctc   1123
Gly Ser Thr Thr Leu Val Thr Ser Ile Ala Leu Ala Gly Thr Leu Leu
                330                 335                 340

acc cac ctc gga tagaaccgaa gacccagttg tac                        1158
Thr His Leu Gly
            345
```

<210> 2366
<211> 345
<212> PRT
<213> Corynebacterium glutamicum

<400> 2366

```
Met Ser Thr Asn Leu Leu Glu Ser Thr Pro Pro Phe Thr Gln Leu Arg
  1               5                  10                  15

Thr Gly Val Leu Gln Lys Tyr Thr Pro Gly Leu Leu Leu Cys Ser Ile
             20                  25                  30

Ala Val Leu Ile Ala Met Ile Val Asn His Phe Phe Ser Gly Val Ser
         35                  40                  45

Pro Leu Ile Val Ala Ile Ile Leu Gly Ile Ile Leu Thr Asn Leu Ile
     50                  55                  60

Gln Leu Pro Ala Ser Thr Ser Pro Gly Ile Thr Leu Ala Ser Lys Lys
 65                  70                  75                  80
```

```
Leu Leu Arg Leu Gly Ile Val Phe Leu Gly Leu Gln Leu Val Phe Ser
                 85                  90                  95

Asp Ile Leu Ser Leu Gly Phe Pro Met Leu Ala Val Ile Val Cys Ile
            100                 105                 110

Val Ala Gly Gly Ile Phe Gly Thr Ile Leu Met Gly His Leu Leu Arg
        115                 120                 125

Met Lys Pro Thr Gln Val Leu Leu Ile Ala Cys Gly Phe Ser Ile Cys
    130                 135                 140

Gly Ala Ala Ala Val Ala Gly Val Glu Gly Val Thr Asp Ser Glu Glu
145                 150                 155                 160

Glu Glu Val Val Thr Ala Val Ala Leu Val Val Ile Phe Gly Thr Leu
                165                 170                 175

Met Ile Pro Phe Ile Pro Phe Ala Thr Lys Val Leu Gly Leu Ser Pro
            180                 185                 190

Glu Ile Gly Gly Met Trp Ala Gly Gly Ser Ile His Glu Ile Ala Gln
        195                 200                 205

Val Val Ala Ala Gly Gly Val Ile Gly Gly Gly Ala Leu Gly Val Ala
    210                 215                 220

Val Val Val Lys Leu Ala Arg Val Leu Leu Leu Ala Pro Ile Ala Ala
225                 230                 235                 240

Ile Leu Ser Phe Arg Gln Arg Arg Gln Gly Tyr Thr Ser Pro Asp Gly
                245                 250                 255

Lys Arg Pro Pro Val Val Pro Leu Phe Ile Leu Gly Phe Leu Ala Met
            260                 265                 270

Val Val Leu Arg Ser Thr Val Ala Leu Pro Asp Glu Val Ile Ala Ala
        275                 280                 285

Gly Gly Phe Leu Gln Thr Ala Leu Leu Ser Ala Ala Met Phe Gly Leu
    290                 295                 300

Gly Cys Gly Val Lys Ile Gln Asn Leu Ile His Val Gly Val Lys Pro
305                 310                 315                 320

Phe Ile Leu Ala Phe Gly Ser Thr Thr Leu Val Thr Ser Ile Ala Leu
                325                 330                 335

Ala Gly Thr Leu Leu Thr His Leu Gly
            340                 345
```

<210> 2367
<211> 534
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(511)
<223> RXA01675

<400> 2367
ttgccgattc tagcgggaga attagtgtcc atcgcatcga accacatctg attttgagcc 60

ctggctaacg gattgttttt gacagattgg aatgacaata atg aac gag att cca 115
Met Asn Glu Ile Pro
1 5

gaa tgg ttg act ctt gta tct gtt gaa gca gga aag aga ctt ggg cgg 163
Glu Trp Leu Thr Leu Val Ser Val Glu Ala Gly Lys Arg Leu Gly Arg
10 15 20

cct ggg cca ttg gtg ttt ccg ccg gag ttg gtc act ttg gca gtt gaa 211
Pro Gly Pro Leu Val Phe Pro Pro Glu Leu Val Thr Leu Ala Val Glu
25 30 35

ggg att gag ctt att gaa ctt gag cct tca tgg act tct gat ttg cct 259
Gly Ile Glu Leu Ile Glu Leu Glu Pro Ser Trp Thr Ser Asp Leu Pro
40 45 50

ctg ccg gaa ttc ggg ttc cta gct gcg gat atg gtt gat ttc tat gat 307
Leu Pro Glu Phe Gly Phe Leu Ala Ala Asp Met Val Asp Phe Tyr Asp
55 60 65

gat tat gag ttt agt gaa tgg att ccg ggt gcg tgg cct ctt gct tta 355
Asp Tyr Glu Phe Ser Glu Trp Ile Pro Gly Ala Trp Pro Leu Ala Leu
70 75 80 85

gat ggt gga gga ggt ttc ttt tgc ctt gat ctc cgt gct gcc aac gct 403
Asp Gly Gly Gly Gly Phe Phe Cys Leu Asp Leu Arg Ala Ala Asn Ala
90 95 100

gat gga gag att cct gtt gtg tgg gtg cat gcc agc aac ttg ggt tgg 451
Asp Gly Glu Ile Pro Val Val Trp Val His Ala Ser Asn Leu Gly Trp
105 110 115

ggt gat gat gag gca gta cgc gta gct gcc tcg ttg gca gat ttg ttg 499
Gly Asp Asp Glu Ala Val Arg Val Ala Ala Ser Leu Ala Asp Leu Leu
120 125 130

agt ccg tcg aaa tagaagaatt agcatttacc gga 534
Ser Pro Ser Lys
135

<210> 2368
<211> 137
<212> PRT
<213> Corynebacterium glutamicum

<400> 2368
Met Asn Glu Ile Pro Glu Trp Leu Thr Leu Val Ser Val Glu Ala Gly
1 5 10 15

Lys Arg Leu Gly Arg Pro Gly Pro Leu Val Phe Pro Pro Glu Leu Val
20 25 30

Thr Leu Ala Val Glu Gly Ile Glu Leu Ile Glu Leu Glu Pro Ser Trp
35 40 45

Thr Ser Asp Leu Pro Leu Pro Glu Phe Gly Phe Leu Ala Ala Asp Met

```
     50                  55                  60

Val Asp Phe Tyr Asp Asp Tyr Glu Phe Ser Glu Trp Ile Pro Gly Ala
 65                  70                  75                  80

Trp Pro Leu Ala Leu Asp Gly Gly Gly Gly Phe Phe Cys Leu Asp Leu
                85                  90                  95

Arg Ala Ala Asn Ala Asp Gly Glu Ile Pro Val Val Trp Val His Ala
            100                 105                 110

Ser Asn Leu Gly Trp Gly Asp Asp Glu Ala Val Arg Val Ala Ala Ser
        115                 120                 125

Leu Ala Asp Leu Leu Ser Pro Ser Lys
    130                 135


<210> 2369
<211> 879
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(856)
<223> RXA01676

<400> 2369
agttacagct tttctcggtg gcacactcgc gctacttagc ccttgtgccg cactcctttt 60

accagcattt tttgcatcct cagtgggtgc tggcccgcgc atg atc ctt cac ggt   115
                                            Met Ile Leu His Gly
                                              1               5

gtt gtg ttc tac gca gga ctt cta gta ctt ctc gtg cca ctt ggc ctt   163
Val Val Phe Tyr Ala Gly Leu Leu Val Leu Leu Val Pro Leu Gly Leu
                10                  15                  20

ggt gcg gga atc ctc ggc gag ctg ttt atc acc caa cgc cag acc atc   211
Gly Ala Gly Ile Leu Gly Glu Leu Phe Ile Thr Gln Arg Gln Thr Ile
            25                  30                  35

atc gtg gtt tca tcg atc gtg ctg att atc cta ggt ttt gtc cag atc   259
Ile Val Val Ser Ser Ile Val Leu Ile Ile Leu Gly Phe Val Gln Ile
        40                  45                  50

ttc ggc ggc gga ttc gac ttc gga aaa gca ctc cca gga tta gat cgt   307
Phe Gly Gly Gly Phe Asp Phe Gly Lys Ala Leu Pro Gly Leu Asp Arg
    55                  60                  65

ctg caa tct aag gcc act gtg acc tca ggt cta gga aag agc ttt tta   355
Leu Gln Ser Lys Ala Thr Val Thr Ser Gly Leu Gly Lys Ser Phe Leu
70                  75                  80                  85

cta gga atg acc agt agt att gcc ggt ttt tgt tcc gga cca atc ctc   403
Leu Gly Met Thr Ser Ser Ile Ala Gly Phe Cys Ser Gly Pro Ile Leu
                90                  95                  100

ggc gcc gtt ctt act ttg gct gcc acc agt gga aac tcc atc acc tca   451
Gly Ala Val Leu Thr Leu Ala Ala Thr Ser Gly Asn Ser Ile Thr Ser
```

```
            105                 110                 115

gca ctc att ttg agt gct tat ggt gcg gga atg gtg ctg ccc ctg atg   499
Ala Leu Ile Leu Ser Ala Tyr Gly Ala Gly Met Val Leu Pro Leu Met
        120                 125                 130

gct att gca gcg ctc tgg gcc aaa ctc gga cag cgt gga cag cag atg   547
Ala Ile Ala Ala Leu Trp Ala Lys Leu Gly Gln Arg Gly Gln Gln Met
    135                 140                 145

ctc cgc ggc cgg gaa ttc acc ttc ttg ggc agg cag tgg cac att gtt   595
Leu Arg Gly Arg Glu Phe Thr Phe Leu Gly Arg Gln Trp His Ile Val
150                 155                 160                 165

tct gtc att agc ggt gcc ctg atc atc gct gtc gga atc ctc ttt tgg   643
Ser Val Ile Ser Gly Ala Leu Ile Ile Ala Val Gly Ile Leu Phe Trp
                170                 175                 180

tcc acg aac ggc ctt gtc agc atg ccg gag ctc gtt cca atg gac acc   691
Ser Thr Asn Gly Leu Val Ser Met Pro Glu Leu Val Pro Met Asp Thr
            185                 190                 195

cag atc tgg cta cag gaa gcc aca ttc tca ctc ggg tca cca ctc ttt   739
Gln Ile Trp Leu Gln Glu Ala Thr Phe Ser Leu Gly Ser Pro Leu Phe
        200                 205                 210

gac atc gca ttg atc att gtc gcc gct ggc ttg ttc ttg tac ttc tgg   787
Asp Ile Ala Leu Ile Ile Val Ala Ala Gly Leu Phe Leu Tyr Phe Trp
    215                 220                 225

aac aaa cga caa aag cga aaa gaa gaa gct cag cga ccc aaa gaa agt   835
Asn Lys Arg Gln Lys Arg Lys Glu Glu Ala Gln Arg Pro Lys Glu Ser
230                 235                 240                 245

gga tgg gtt att aac cct cgc taattattag ttttggagcg agg            879
Gly Trp Val Ile Asn Pro Arg
                250
```

<210> 2370
<211> 252
<212> PRT
<213> Corynebacterium glutamicum

<400> 2370

```
Met Ile Leu His Gly Val Val Phe Tyr Ala Gly Leu Leu Val Leu Leu
  1               5                  10                  15

Val Pro Leu Gly Leu Gly Ala Gly Ile Leu Gly Glu Leu Phe Ile Thr
             20                  25                  30

Gln Arg Gln Thr Ile Ile Val Val Ser Ser Ile Val Leu Ile Ile Leu
         35                  40                  45

Gly Phe Val Gln Ile Phe Gly Gly Gly Phe Asp Phe Gly Lys Ala Leu
     50                  55                  60

Pro Gly Leu Asp Arg Leu Gln Ser Lys Ala Thr Val Thr Ser Gly Leu
 65                  70                  75                  80

Gly Lys Ser Phe Leu Leu Gly Met Thr Ser Ser Ile Ala Gly Phe Cys
```

```
                85                  90                  95

Ser Gly Pro Ile Leu Gly Ala Val Leu Thr Leu Ala Ala Thr Ser Gly
            100                 105                 110

Asn Ser Ile Thr Ser Ala Leu Ile Leu Ser Ala Tyr Gly Ala Gly Met
        115                 120                 125

Val Leu Pro Leu Met Ala Ile Ala Ala Leu Trp Ala Lys Leu Gly Gln
    130                 135                 140

Arg Gly Gln Gln Met Leu Arg Gly Arg Glu Phe Thr Phe Leu Gly Arg
145                 150                 155                 160

Gln Trp His Ile Val Ser Val Ile Ser Gly Ala Leu Ile Ile Ala Val
                165                 170                 175

Gly Ile Leu Phe Trp Ser Thr Asn Gly Leu Val Ser Met Pro Glu Leu
            180                 185                 190

Val Pro Met Asp Thr Gln Ile Trp Leu Gln Glu Ala Thr Phe Ser Leu
        195                 200                 205

Gly Ser Pro Leu Phe Asp Ile Ala Leu Ile Ile Val Ala Ala Gly Leu
    210                 215                 220

Phe Leu Tyr Phe Trp Asn Lys Arg Gln Lys Arg Lys Glu Glu Ala Gln
225                 230                 235                 240

Arg Pro Lys Glu Ser Gly Trp Val Ile Asn Pro Arg
                245                 250


<210> 2371
<211> 867
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(844)
<223> RXA01677

<400> 2371
gtcgccatag ttgagtttta ttcatggctt ttagctaggc gactttagtt gagggctttt 60

agttgagggc ttcccagcag ggatggttaa ggagaattca gtg aac caa cag agt   115
                                            Val Asn Gln Gln Ser
                                              1               5

aaa aag tgg ctc gta ccg aca ctg gtc gtc atc att gca gtg ctc ctc   163
Lys Lys Trp Leu Val Pro Thr Leu Val Val Ile Ile Ala Val Leu Leu
                  10                  15                  20

atc gca gtt gtt ctg ttg atg tac cga gga aat gcg agt gat acg gcc   211
Ile Ala Val Val Leu Leu Met Tyr Arg Gly Asn Ala Ser Asp Thr Ala
              25                  30                  35

gag ggc gtt tca gcc gct gcg act tcg gac tcg gct gct gct tcg act   259
Glu Gly Val Ser Ala Ala Ala Thr Ser Asp Ser Ala Ala Ala Ser Thr
          40                  45                  50
```

```
gct gct tcg ggt tcc gct tct ggt gct gcg gac tcc gat ctg acc agc   307
Ala Ala Ser Gly Ser Ala Ser Gly Ala Ala Asp Ser Asp Leu Thr Ser
     55                  60                  65

gtg gaa gca cgc gac cct tcc gac cct gtt gcg gtg gga gac gtt gat   355
Val Glu Ala Arg Asp Pro Ser Asp Pro Val Ala Val Gly Asp Val Asp
 70                  75                  80                  85

gca cct gtt ggg tta gtg gtg ttt tcc gac tac caa tgc ccg ttc tgt   403
Ala Pro Val Gly Leu Val Val Phe Ser Asp Tyr Gln Cys Pro Phe Cys
                90                  95                 100

gca aag tgg agc gat gaa acc ctg cca cag atg atg aag cat gtg gaa   451
Ala Lys Trp Ser Asp Glu Thr Leu Pro Gln Met Met Lys His Val Glu
            105                 110                 115

gat gga aac ctc cgc att gaa tgg cgt gaa gtg aac atc ttt gga gaa   499
Asp Gly Asn Leu Arg Ile Glu Trp Arg Glu Val Asn Ile Phe Gly Glu
        120                 125                 130

cca tct gag cgt gga gct cgc gcg gca tac gct gcg ggt ttg cag gac   547
Pro Ser Glu Arg Gly Ala Arg Ala Ala Tyr Ala Ala Gly Leu Gln Asp
    135                 140                 145

gca tac ttg gaa tac cac aac gca ctc ttt gcc aac ggt gaa aaa ccc   595
Ala Tyr Leu Glu Tyr His Asn Ala Leu Phe Ala Asn Gly Glu Lys Pro
150                 155                 160                 165

agc gaa gac ctg ctc agc gaa gag gga ctt att aag ctt gct ggt gac   643
Ser Glu Asp Leu Leu Ser Glu Glu Gly Leu Ile Lys Leu Ala Gly Asp
                170                 175                 180

ctt gga cta gac gaa tcg aaa ttc act gcc gat ttc caa tcc cct gaa   691
Leu Gly Leu Asp Glu Ser Lys Phe Thr Ala Asp Phe Gln Ser Pro Glu
            185                 190                 195

act gca gtc gca att gcg caa cat caa cag ctg gga atc gat ctt ggc   739
Thr Ala Val Ala Ile Ala Gln His Gln Gln Leu Gly Ile Asp Leu Gly
        200                 205                 210

gcc tac tcc acc cca gct ttc ctc cta ggt ggc cag cca atc atg ggc   787
Ala Tyr Ser Thr Pro Ala Phe Leu Leu Gly Gly Gln Pro Ile Met Gly
    215                 220                 225

gct cag cct gct tct gta ttt gaa gcc gcc ttc gag caa gca ctg gca   835
Ala Gln Pro Ala Ser Val Phe Glu Ala Ala Phe Glu Gln Ala Leu Ala
230                 235                 240                 245

gcg aaa gaa taaaccgtgg atgtcggcct agt                             867
Ala Lys Glu
```

<210> 2372
<211> 248
<212> PRT
<213> Corynebacterium glutamicum

<400> 2372
Val Asn Gln Gln Ser Lys Lys Trp Leu Val Pro Thr Leu Val Val Ile

```
  1               5                  10                  15

Ile Ala Val Leu Leu Ile Ala Val Val Leu Leu Met Tyr Arg Gly Asn
            20                  25                  30

Ala Ser Asp Thr Ala Glu Gly Val Ser Ala Ala Ala Thr Ser Asp Ser
        35                  40                  45

Ala Ala Ala Ser Thr Ala Ala Ser Gly Ser Ala Ser Gly Ala Ala Asp
    50                  55                  60

Ser Asp Leu Thr Ser Val Glu Ala Arg Asp Pro Ser Asp Pro Val Ala
65                  70                  75                  80

Val Gly Asp Val Asp Ala Pro Val Gly Leu Val Val Phe Ser Asp Tyr
                85                  90                  95

Gln Cys Pro Phe Cys Ala Lys Trp Ser Asp Glu Thr Leu Pro Gln Met
            100                 105                 110

Met Lys His Val Glu Asp Gly Asn Leu Arg Ile Glu Trp Arg Glu Val
        115                 120                 125

Asn Ile Phe Gly Glu Pro Ser Glu Arg Gly Ala Arg Ala Ala Tyr Ala
    130                 135                 140

Ala Gly Leu Gln Asp Ala Tyr Leu Glu Tyr His Asn Ala Leu Phe Ala
145                 150                 155                 160

Asn Gly Glu Lys Pro Ser Glu Asp Leu Leu Ser Glu Glu Gly Leu Ile
                165                 170                 175

Lys Leu Ala Gly Asp Leu Gly Leu Asp Glu Ser Lys Phe Thr Ala Asp
            180                 185                 190

Phe Gln Ser Pro Glu Thr Ala Val Ala Ile Ala Gln His Gln Gln Leu
        195                 200                 205

Gly Ile Asp Leu Gly Ala Tyr Ser Thr Pro Ala Phe Leu Leu Gly Gly
    210                 215                 220

Gln Pro Ile Met Gly Ala Gln Pro Ala Ser Val Phe Glu Ala Ala Phe
225                 230                 235                 240

Glu Gln Ala Leu Ala Ala Lys Glu
                245
```

<210> 2373
<211> 756
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(733)
<223> RXA01681

<400> 2373
ctttaacgaa agacttgtcg ttactttagt aattagacca acatggtggt gagtggttga 60

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aatcttgcca tcaaaattat cgagtgagtt gaagcattcc gtg gaa gta cta cta   115
                                            Val Glu Val Leu Leu
                                              1               5

ctt atc gca atc gtc gtt ggt ggt ggc gtt ttt gtc gcc tca aag atg   163
Leu Ile Ala Ile Val Val Gly Gly Gly Val Phe Val Ala Ser Lys Met
                 10                  15                  20

gga tcc aat aac aat aag aag caa gaa gaa gcc aag ttt gct gac gca   211
Gly Ser Asn Asn Asn Lys Lys Gln Glu Glu Ala Lys Phe Ala Asp Ala
             25                  30                  35

cag gca gat gcg cgt cgg tgg att gag cgt ctt ggt tcc cag gtt ttg   259
Gln Ala Asp Ala Arg Arg Trp Ile Glu Arg Leu Gly Ser Gln Val Leu
         40                  45                  50

acc atc gca ggt aca gat gct gcg tcg acc cag gct att gct gac gcc   307
Thr Ile Ala Gly Thr Asp Ala Ala Ser Thr Gln Ala Ile Ala Asp Ala
     55                  60                  65

tca gag cgc tat acc gct gcg tct tct cag att tct tct gcc act act   355
Ser Glu Arg Tyr Thr Ala Ala Ser Ser Gln Ile Ser Ser Ala Thr Thr
 70                  75                  80                  85

cct cgt cag gca gag ttg gct cga gaa tct gca cta gag ggt ctg cat   403
Pro Arg Gln Ala Glu Leu Ala Arg Glu Ser Ala Leu Glu Gly Leu His
                 90                  95                 100

tat atg aac gcg gct cgt gag atc atg ggt atg act gct ggc cct gag   451
Tyr Met Asn Ala Ala Arg Glu Ile Met Gly Met Thr Ala Gly Pro Glu
             105                 110                 115

ctg cct cct ctg gaa ggt cag cgc aat gct ggt cgc gtt aca gaa aag   499
Leu Pro Pro Leu Glu Gly Gln Arg Asn Ala Gly Arg Val Thr Glu Lys
         120                 125                 130

cgc acc att gag cag gag ggt cgc cag atc act gct tcc ccc gtc gca   547
Arg Thr Ile Glu Gln Glu Gly Arg Gln Ile Thr Ala Ser Pro Val Ala
     135                 140                 145

aca gat gaa act ccg aac tac tac cct ggc ggt aac gtt gcg ggt cgc   595
Thr Asp Glu Thr Pro Asn Tyr Tyr Pro Gly Gly Asn Val Ala Gly Arg
150                 155                 160                 165

cca gtc cct gct ggt tgg tac tcc gag cct tgg tgg gca agc gca ttg   643
Pro Val Pro Ala Gly Trp Tyr Ser Glu Pro Trp Trp Ala Ser Ala Leu
                 170                 175                 180

cgt tcc ggt ctg tgg act gca ggt tcg gtc atg atg ttc tca gca atg   691
Arg Ser Gly Leu Trp Thr Ala Gly Ser Val Met Met Phe Ser Ala Met
             185                 190                 195

ttt aac ggc atg gct ggt gtc ggc tac tcc gct gca gac ctt           733
Phe Asn Gly Met Ala Gly Val Gly Tyr Ser Ala Ala Asp Leu
         200                 205                 210

tgaaaaatgg ctatggcgag ggc                                        756
```

<210> 2374
<211> 211

<212> PRT
<213> Corynebacterium glutamicum

<400> 2374

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Val Glu Val Leu Leu Leu Ile Ala Ile Val Val Gly Gly Gly Val Phe
  1               5                  10                  15

Val Ala Ser Lys Met Gly Ser Asn Asn Asn Lys Lys Gln Glu Glu Ala
             20                  25                  30

Lys Phe Ala Asp Ala Gln Ala Asp Ala Arg Arg Trp Ile Glu Arg Leu
         35                  40                  45

Gly Ser Gln Val Leu Thr Ile Ala Gly Thr Asp Ala Ala Ser Thr Gln
     50                  55                  60

Ala Ile Ala Asp Ala Ser Glu Arg Tyr Thr Ala Ala Ser Ser Gln Ile
 65                  70                  75                  80

Ser Ser Ala Thr Thr Pro Arg Gln Ala Glu Leu Ala Arg Glu Ser Ala
                 85                  90                  95

Leu Glu Gly Leu His Tyr Met Asn Ala Ala Arg Glu Ile Met Gly Met
            100                 105                 110

Thr Ala Gly Pro Glu Leu Pro Pro Leu Glu Gly Gln Arg Asn Ala Gly
        115                 120                 125

Arg Val Thr Glu Lys Arg Thr Ile Glu Gln Glu Gly Arg Gln Ile Thr
    130                 135                 140

Ala Ser Pro Val Ala Thr Asp Glu Thr Pro Asn Tyr Tyr Pro Gly Gly
145                 150                 155                 160

Asn Val Ala Gly Arg Pro Val Pro Ala Gly Trp Tyr Ser Glu Pro Trp
                165                 170                 175

Trp Ala Ser Ala Leu Arg Ser Gly Leu Trp Thr Ala Gly Ser Val Met
            180                 185                 190

Met Phe Ser Ala Met Phe Asn Gly Met Ala Gly Val Gly Tyr Ser Ala
        195                 200                 205

Ala Asp Leu
    210
```

<210> 2375
<211> 702
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(679)
<223> RXA01685

<400> 2375
caataattag gtgagcaacc ctaataagaa acctttagat cccgcacaaa gattctccct 60

ccccaccaga tgggcgatgt tctttgtcgg gatctttatt atg tcc ttc gcc atc 115

```
                                                    Met Ser Phe Ala Ile
                                                      1               5

ggc atc acc gtc cac gca gga cta gga acc acc aca att tca tca ctt   163
Gly Ile Thr Val His Ala Gly Leu Gly Thr Thr Thr Ile Ser Ser Leu
                 10                  15                  20

ccc gtg gtg tgg act gct gcc agc gga tta tcc ctg ggc tgg acc aca   211
Pro Val Val Trp Thr Ala Ala Ser Gly Leu Ser Leu Gly Trp Thr Thr
             25                  30                  35

att tac ttc aat ggc ttc atg att ctg tgc caa ata att gtg ctg cgt   259
Ile Tyr Phe Asn Gly Phe Met Ile Leu Cys Gln Ile Ile Val Leu Arg
         40                  45                  50

tcc cag ttc aaa cca caa atg tta gtc caa atc ctg tgg gca ttc ctc   307
Ser Gln Phe Lys Pro Gln Met Leu Val Gln Ile Leu Trp Ala Phe Leu
     55                  60                  65

ttt ggg ttt ctt tgt gat tta agc ctg caa cta acc acc tgg gcg caa   355
Phe Gly Phe Leu Cys Asp Leu Ser Leu Gln Leu Thr Thr Trp Ala Gln
 70                  75                  80                  85

act gac aat tat ttt gtg gcc tgg atc tgg gtt att gtg tcc acc att   403
Thr Asp Asn Tyr Phe Val Ala Trp Ile Trp Val Ile Val Ser Thr Ile
                 90                  95                 100

ttg atg tcg atc gga gtt ttt att caa gta ctc ccc aac atc act ttc   451
Leu Met Ser Ile Gly Val Phe Ile Gln Val Leu Pro Asn Ile Thr Phe
            105                 110                 115

atc gct ggt gaa ggc att gtc tct gcg ctg gtg aag aaa ttt ccc aac   499
Ile Ala Gly Glu Gly Ile Val Ser Ala Leu Val Lys Lys Phe Pro Asn
        120                 125                 130

gtg gaa ttt ggc acc atg aaa caa atc gtc gac tgg act ttc gtc tcc   547
Val Glu Phe Gly Thr Met Lys Gln Ile Val Asp Trp Thr Phe Val Ser
    135                 140                 145

gtc gct gcc att ttg tcc tgg atc acc atg ggt gga ctt att ggc gtg   595
Val Ala Ala Ile Leu Ser Trp Ile Thr Met Gly Gly Leu Ile Gly Val
150                 155                 160                 165

cgc gaa gga aca gtg ttc gcg gcg ttt ttc atc gga ttc ttc gtc cgc   643
Arg Glu Gly Thr Val Phe Ala Ala Phe Phe Ile Gly Phe Phe Val Arg
                170                 175                 180

cag tgg cgc aaa ctc tac ctc cgc tcc atc ggt cac taaagagctt        689
Gln Trp Arg Lys Leu Tyr Leu Arg Ser Ile Gly His
            185                 190

gttccaggaa gag                                                   702
```

<210> 2376
<211> 193
<212> PRT
<213> Corynebacterium glutamicum

<400> 2376
Met Ser Phe Ala Ile Gly Ile Thr Val His Ala Gly Leu Gly Thr Thr

```
  1               5                  10                  15

Thr Ile Ser Ser Leu Pro Val Val Trp Thr Ala Ala Ser Gly Leu Ser
            20                  25                  30

Leu Gly Trp Thr Thr Ile Tyr Phe Asn Gly Phe Met Ile Leu Cys Gln
        35                  40                  45

Ile Ile Val Leu Arg Ser Gln Phe Lys Pro Gln Met Leu Val Gln Ile
    50                  55                  60

Leu Trp Ala Phe Leu Phe Gly Phe Leu Cys Asp Leu Ser Leu Gln Leu
65                  70                  75                  80

Thr Thr Trp Ala Gln Thr Asp Asn Tyr Phe Val Ala Trp Ile Trp Val
                85                  90                  95

Ile Val Ser Thr Ile Leu Met Ser Ile Gly Val Phe Ile Gln Val Leu
            100                 105                 110

Pro Asn Ile Thr Phe Ile Ala Gly Glu Gly Ile Val Ser Ala Leu Val
        115                 120                 125

Lys Lys Phe Pro Asn Val Glu Phe Gly Thr Met Lys Gln Ile Val Asp
    130                 135                 140

Trp Thr Phe Val Ser Val Ala Ala Ile Leu Ser Trp Ile Thr Met Gly
145                 150                 155                 160

Gly Leu Ile Gly Val Arg Glu Gly Thr Val Phe Ala Ala Phe Phe Ile
                165                 170                 175

Gly Phe Phe Val Arg Gln Trp Arg Lys Leu Tyr Leu Arg Ser Ile Gly
            180                 185                 190

His
```

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<210> 2377
<211> 564
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(541)
<223> RXA01686

<400> 2377
ggaggaaggg ttgcaacgct ttttcaagag aatgaccgtg cgtccgctta aacgaagcgt 60

cgaacgccgg tcttttctca tttcacttaa gatgtagaac atg act tca ctc agg 115
Met Thr Ser Leu Arg
1 5

gac tta ctt gtt tcc acc aat gcc gac gca gca att gca gat atg tca 163
Asp Leu Leu Val Ser Thr Asn Ala Asp Ala Ala Ile Ala Asp Met Ser
10 15 20

gca ttt atc gaa gaa acc gtg ggc aag caa tcc ggc atc agc ggc atc 211

```
Ala Phe Ile Glu Glu Thr Val Gly Lys Gln Ser Gly Ile Ser Gly Ile
            25                  30                  35

gca ctc aaa ggc gca atg ggt gct gca acc aag atc gac tcc gac atc   259
Ala Leu Lys Gly Ala Met Gly Ala Ala Thr Lys Ile Asp Ser Asp Ile
        40                  45                  50

gta gcc aaa ggc tcc agg cgc ctc ctc ccg gaa atc gct gac tcc ctc   307
Val Ala Lys Gly Ser Arg Arg Leu Leu Pro Glu Ile Ala Asp Ser Leu
    55                  60                  65

gac gga ctc tgg cag gaa tac caa aat ggt ggc acc gcc gca gat ttc   355
Asp Gly Leu Trp Gln Glu Tyr Gln Asn Gly Gly Thr Ala Ala Asp Phe
70                  75                  80                  85

ggc gcc cac ctc gag gcc aac agc tcc acc gca ctc gac gcg att ctc   403
Gly Ala His Leu Glu Ala Asn Ser Ser Thr Ala Leu Asp Ala Ile Leu
                90                  95                  100

agc gtt gct gac aaa aac gca gag agc atc aac gtt cca gga ctt ggc   451
Ser Val Ala Asp Lys Asn Ala Glu Ser Ile Asn Val Pro Gly Leu Gly
            105                 110                 115

aag gtc tac aag ggc gtg cgc ggc aag gct gcc aaa gta atc gag cag   499
Lys Val Tyr Lys Gly Val Arg Gly Lys Ala Ala Lys Val Ile Glu Gln
        120                 125                 130

gaa ctt cct gca att ggc cag ttg atc gaa aag aac gca caa           541
Glu Leu Pro Ala Ile Gly Gln Leu Ile Glu Lys Asn Ala Gln
    135                 140                 145

taattaggtg agcaacccta ata                                        564


<210> 2378
<211> 147
<212> PRT
<213> Corynebacterium glutamicum

<400> 2378
Met Thr Ser Leu Arg Asp Leu Leu Val Ser Thr Asn Ala Asp Ala Ala
  1               5                  10                  15

Ile Ala Asp Met Ser Ala Phe Ile Glu Glu Thr Val Gly Lys Gln Ser
            20                  25                  30

Gly Ile Ser Gly Ile Ala Leu Lys Gly Ala Met Gly Ala Ala Thr Lys
        35                  40                  45

Ile Asp Ser Asp Ile Val Ala Lys Gly Ser Arg Arg Leu Leu Pro Glu
    50                  55                  60

Ile Ala Asp Ser Leu Asp Gly Leu Trp Gln Glu Tyr Gln Asn Gly Gly
65                  70                  75                  80

Thr Ala Ala Asp Phe Gly Ala His Leu Glu Ala Asn Ser Ser Thr Ala
                85                  90                  95

Leu Asp Ala Ile Leu Ser Val Ala Asp Lys Asn Ala Glu Ser Ile Asn
            100                 105                 110
```

```
Val Pro Gly Leu Gly Lys Val Tyr Lys Gly Val Arg Gly Lys Ala Ala
        115                 120                 125

Lys Val Ile Glu Gln Glu Leu Pro Ala Ile Gly Gln Leu Ile Glu Lys
    130                 135                 140

Asn Ala Gln
145
```

<210> 2379
<211> 1545
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1522)
<223> RXA01693

<400> 2379

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aggagactgg ctggattatt ggctggtttt cttgggaaat cgtcatgggc attaatccta 60

gtcccaacaa ttgccagaac ccgaacacta ggcttgaacc atg aat act gca cct   115
                                          Met Asn Thr Ala Pro
                                            1               5

ttc aaa ctc gaa gct gac ttc gca tca gcc ctg ccc acc atg gca gcc   163
Phe Lys Leu Glu Ala Asp Phe Ala Ser Ala Leu Pro Thr Met Ala Ala
                10                  15                  20

ccc tgg caa ggt gag gaa gcc ccc aac cct gag ctc gtg att tta aat   211
Pro Trp Gln Gly Glu Glu Ala Pro Asn Pro Glu Leu Val Ile Leu Asn
            25                  30                  35

gac gac ctc gcc tac agc ctc ggg ctt gat ccg aca tgg ctt cgc aca   259
Asp Asp Leu Ala Tyr Ser Leu Gly Leu Asp Pro Thr Trp Leu Arg Thr
        40                  45                  50

cct gag ggc gtt caa ttt ctt ctc gga ctc aac ccc gag ccc tta aca   307
Pro Glu Gly Val Gln Phe Leu Leu Gly Leu Asn Pro Glu Pro Leu Thr
    55                  60                  65

aaa gca gtt gcg cag gcc tat tcc ggc cac caa ttc gga cag ttt gtg   355
Lys Ala Val Ala Gln Ala Tyr Ser Gly His Gln Phe Gly Gln Phe Val
70                  75                  80                  85

gca agc ctt ggt gat ggc cga gcg ctt ctt ctc ggc gaa gcc cgc tca   403
Ala Ser Leu Gly Asp Gly Arg Ala Leu Leu Leu Gly Glu Ala Arg Ser
                90                  95                  100

gct gac ggc gta ctg cat gat atc cac ctc aaa gga tct gga cga acc   451
Ala Asp Gly Val Leu His Asp Ile His Leu Lys Gly Ser Gly Arg Thr
            105                 110                 115

caa ttc tcc cga gga gcc gat gga cgc gcc gtc ctt ggc ccc gtc tta   499
Gln Phe Ser Arg Gly Ala Asp Gly Arg Ala Val Leu Gly Pro Val Leu
        120                 125                 130

cgc gaa tac atc atc tcc gaa gcg atg cat gca ctt ggt gtt ccc acc   547
Arg Glu Tyr Ile Ile Ser Glu Ala Met His Ala Leu Gly Val Pro Thr
```

```
    135                 140                 145

acc agg tca ctt gca gta att agc acc ggt agg aaa atc caa cga gga   595
Thr Arg Ser Leu Ala Val Ile Ser Thr Gly Arg Lys Ile Gln Arg Gly
150                 155                 160                 165

agc gta gcc cca ggc gca gtc ctt gtt cga gta gca acc agc ctc att   643
Ser Val Ala Pro Gly Ala Val Leu Val Arg Val Ala Thr Ser Leu Ile
                170                 175                 180

cga gtc gga tcc ttc caa tac tcc aac atc tct ggt ggc atc gaa cta   691
Arg Val Gly Ser Phe Gln Tyr Ser Asn Ile Ser Gly Gly Ile Glu Leu
            185                 190                 195

tct caa cac ctg gcg aac tat acg atc acc agg cat ttc cct tcg ttg   739
Ser Gln His Leu Ala Asn Tyr Thr Ile Thr Arg His Phe Pro Ser Leu
        200                 205                 210

gta gct gaa cta tcc gca cca acc ccc gca act tat gta tca ctg ttt   787
Val Ala Glu Leu Ser Ala Pro Thr Pro Ala Thr Tyr Val Ser Leu Phe
    215                 220                 225

aaa gcg att ctt cag cgc caa gca gac acc gtt gga aaa tgg acc agg   835
Lys Ala Ile Leu Gln Arg Gln Ala Asp Thr Val Gly Lys Trp Thr Arg
230                 235                 240                 245

ctg ggt ttc gtt cac gga gcc ctc aac aca gac aac acg ttg ata tcc   883
Leu Gly Phe Val His Gly Ala Leu Asn Thr Asp Asn Thr Leu Ile Ser
                250                 255                 260

gga gaa act gtt gac tac ggc cca tgc gct ttc atg gag cgc tac cgt   931
Gly Glu Thr Val Asp Tyr Gly Pro Cys Ala Phe Met Glu Arg Tyr Arg
            265                 270                 275

ggc gac gcg aaa ttt agc tcc atc gac act tat ggt cgc tac aaa ttt   979
Gly Asp Ala Lys Phe Ser Ser Ile Asp Thr Tyr Gly Arg Tyr Lys Phe
        280                 285                 290

gaa aac caa cct atg atc ctc gga tgg aac atg gcc cgc ctc gta gaa   1027
Glu Asn Gln Pro Met Ile Leu Gly Trp Asn Met Ala Arg Leu Val Glu
    295                 300                 305

acc ctc ctc cca ctc ctg ggc gcc aca cca gac gaa ggc atg aca gca   1075
Thr Leu Leu Pro Leu Leu Gly Ala Thr Pro Asp Glu Gly Met Thr Ala
310                 315                 320                 325

gcc caa gaa gct ctc gta gaa ttc gat gac ctc tgc gaa caa gca atc   1123
Ala Gln Glu Ala Leu Val Glu Phe Asp Asp Leu Cys Glu Gln Ala Ile
                330                 335                 340

cga aaa gaa ttc gcc act gca ctg ggc ctt gac gag tca gac acc ggc   1171
Arg Lys Glu Phe Ala Thr Ala Leu Gly Leu Asp Glu Ser Asp Thr Gly
            345                 350                 355

acg gta gag cag ttc cgt gaa ctg ctc tac ctc cat aac ccc gac atc   1219
Thr Val Glu Gln Phe Arg Glu Leu Leu Tyr Leu His Asn Pro Asp Ile
        360                 365                 370

acc acg ctg ctg cgc gca ctc acc gac aac acc gca cca ccg agt ggc   1267
Thr Thr Leu Leu Arg Ala Leu Thr Asp Asn Thr Ala Pro Pro Ser Gly
    375                 380                 385
```

```
ttt gaa gca ttc gtt cac gac tgg aaa acc caa gac cca gat atc gaa   1315
Phe Glu Ala Phe Val His Asp Trp Lys Thr Gln Asp Pro Asp Ile Glu
390                 395                 400                 405

gca atg cga gca gta aat cca ctt ttc att cca cgc aat cac ctc gtg   1363
Ala Met Arg Ala Val Asn Pro Leu Phe Ile Pro Arg Asn His Leu Val
                410                 415                 420

gaa gct gct ctc gca gac gca gtt gaa ggg aat cta gaa aag ttc cac   1411
Glu Ala Ala Leu Ala Asp Ala Val Glu Gly Asn Leu Glu Lys Phe His
            425                 430                 435

gaa ctc ctc gct gct gtc acc aat cct ttt gat cca act gcg ggc ccc   1459
Glu Leu Leu Ala Ala Val Thr Asn Pro Phe Asp Pro Thr Ala Gly Pro
        440                 445                 450

gat gaa cta cgc ctg cca agc gaa gaa gga ttt gaa gaa gac tac atg   1507
Asp Glu Leu Arg Leu Pro Ser Glu Glu Gly Phe Glu Glu Asp Tyr Met
    455                 460                 465

acc ttc tgc ggt acc taggacagat ggtggggcag acg                    1545
Thr Phe Cys Gly Thr
470
```

<210> 2380
<211> 474
<212> PRT
<213> Corynebacterium glutamicum

<400> 2380

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Met Asn Thr Ala Pro Phe Lys Leu Glu Ala Asp Phe Ala Ser Ala Leu
  1               5                  10                  15

Pro Thr Met Ala Ala Pro Trp Gln Gly Glu Glu Ala Pro Asn Pro Glu
             20                  25                  30

Leu Val Ile Leu Asn Asp Asp Leu Ala Tyr Ser Leu Gly Leu Asp Pro
         35                  40                  45

Thr Trp Leu Arg Thr Pro Glu Gly Val Gln Phe Leu Leu Gly Leu Asn
     50                  55                  60

Pro Glu Pro Leu Thr Lys Ala Val Ala Gln Ala Tyr Ser Gly His Gln
 65                  70                  75                  80

Phe Gly Gln Phe Val Ala Ser Leu Gly Asp Gly Arg Ala Leu Leu Leu
                 85                  90                  95

Gly Glu Ala Arg Ser Ala Asp Gly Val Leu His Asp Ile His Leu Lys
            100                 105                 110

Gly Ser Gly Arg Thr Gln Phe Ser Arg Gly Ala Asp Gly Arg Ala Val
        115                 120                 125

Leu Gly Pro Val Leu Arg Glu Tyr Ile Ile Ser Glu Ala Met His Ala
    130                 135                 140

Leu Gly Val Pro Thr Thr Arg Ser Leu Ala Val Ile Ser Thr Gly Arg
145                 150                 155                 160
```

Lys Ile Gln Arg Gly Ser Val Ala Pro Gly Ala Val Leu Val Arg Val
165 170 175

Ala Thr Ser Leu Ile Arg Val Gly Ser Phe Gln Tyr Ser Asn Ile Ser
180 185 190

Gly Gly Ile Glu Leu Ser Gln His Leu Ala Asn Tyr Thr Ile Thr Arg
195 200 205

His Phe Pro Ser Leu Val Ala Glu Leu Ser Ala Pro Thr Pro Ala Thr
210 215 220

Tyr Val Ser Leu Phe Lys Ala Ile Leu Gln Arg Gln Ala Asp Thr Val
225 230 235 240

Gly Lys Trp Thr Arg Leu Gly Phe Val His Gly Ala Leu Asn Thr Asp
245 250 255

Asn Thr Leu Ile Ser Gly Glu Thr Val Asp Tyr Gly Pro Cys Ala Phe
260 265 270

Met Glu Arg Tyr Arg Gly Asp Ala Lys Phe Ser Ser Ile Asp Thr Tyr
275 280 285

Gly Arg Tyr Lys Phe Glu Asn Gln Pro Met Ile Leu Gly Trp Asn Met
290 295 300

Ala Arg Leu Val Glu Thr Leu Leu Pro Leu Leu Gly Ala Thr Pro Asp
305 310 315 320

Glu Gly Met Thr Ala Ala Gln Glu Ala Leu Val Glu Phe Asp Asp Leu
325 330 335

Cys Glu Gln Ala Ile Arg Lys Glu Phe Ala Thr Ala Leu Gly Leu Asp
340 345 350

Glu Ser Asp Thr Gly Thr Val Glu Gln Phe Arg Glu Leu Leu Tyr Leu
355 360 365

His Asn Pro Asp Ile Thr Thr Leu Leu Arg Ala Leu Thr Asp Asn Thr
370 375 380

Ala Pro Pro Ser Gly Phe Glu Ala Phe Val His Asp Trp Lys Thr Gln
385 390 395 400

Asp Pro Asp Ile Glu Ala Met Arg Ala Val Asn Pro Leu Phe Ile Pro
405 410 415

Arg Asn His Leu Val Glu Ala Ala Leu Ala Asp Ala Val Glu Gly Asn
420 425 430

Leu Glu Lys Phe His Glu Leu Leu Ala Ala Val Thr Asn Pro Phe Asp
435 440 445

Pro Thr Ala Gly Pro Asp Glu Leu Arg Leu Pro Ser Glu Glu Gly Phe
450 455 460

Glu Glu Asp Tyr Met Thr Phe Cys Gly Thr
465 470

<210> 2381
<211> 738
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(715)
<223> RXA01714

<400> 2381
cattggataa ttagcaggag tgaagttgca tcaaaggaca aacataaaat aaacggcgcg 60

cctccccaga gttaccccaa taattagtaa attgcagatt gtg atc gat tcc gaa 115
Val Ile Asp Ser Glu
1 5

gcg acc tct cag cac aag acc tca gct acc ccg gca gag agc act ccc 163
Ala Thr Ser Gln His Lys Thr Ser Ala Thr Pro Ala Glu Ser Thr Pro
10 15 20

gcg gag ttt tcc gaa gcg gtt gag tct atg cac aga gcg cgc ctg cgc 211
Ala Glu Phe Ser Glu Ala Val Glu Ser Met His Arg Ala Arg Leu Arg
25 30 35

cca gaa ctt act ttg ggc acg att agg ccg cct cag cgc ctg gcg ccg 259
Pro Glu Leu Thr Leu Gly Thr Ile Arg Pro Pro Gln Arg Leu Ala Pro
40 45 50

ttt tcg cac gcc att gga ctc gaa gtc gga aat caa gaa gag tca gac 307
Phe Ser His Ala Ile Gly Leu Glu Val Gly Asn Gln Glu Glu Ser Asp
55 60 65

gat gtc tcc acc aac agc gaa ggt gat tcc ttt ggt cgt ttg att ctg 355
Asp Val Ser Thr Asn Ser Glu Gly Asp Ser Phe Gly Arg Leu Ile Leu
70 75 80 85

ctc cac gat ccg ggt gcc gaa gaa acc tgg gaa gga gca atg cgc ctt 403
Leu His Asp Pro Gly Ala Glu Glu Thr Trp Glu Gly Ala Met Arg Leu
90 95 100

gtc gcc tat att caa gct gac atg gat cac gct gtt gct tcc gac ccg 451
Val Ala Tyr Ile Gln Ala Asp Met Asp His Ala Val Ala Ser Asp Pro
105 110 115

cta ttg ccg gaa gta gcg tgg caa tgg ctt aac gaa ggt ttg gaa caa 499
Leu Leu Pro Glu Val Ala Trp Gln Trp Leu Asn Glu Gly Leu Glu Gln
120 125 130

gcc ggc gca gga ttt acc aac cta ggc gga acc gta acc tcc aca acc 547
Ala Gly Ala Gly Phe Thr Asn Leu Gly Gly Thr Val Thr Ser Thr Thr
135 140 145

tcg gtg cgc ttt ggt gaa atc ggt gga ccg cca agt gcc tac caa gtg 595
Ser Val Arg Phe Gly Glu Ile Gly Gly Pro Pro Ser Ala Tyr Gln Val
150 155 160 165

gaa atg cgt gcg tcc tgg acc gcg act ggc acc gac ctc acc gcg cat 643
Glu Met Arg Ala Ser Trp Thr Ala Thr Gly Thr Asp Leu Thr Ala His
170 175 180

```
gtt gaa gcg ttc gca gca gtg ctt gcc tct gtt gct gga ctt ccc cca   691
Val Glu Ala Phe Ala Ala Val Leu Ala Ser Val Ala Gly Leu Pro Pro
            185                 190                 195

gag ggc gtc acc gaa cta cga agg tagattggac accatggttt ccg        738
Glu Gly Val Thr Glu Leu Arg Arg
        200                 205
```

<210> 2382
<211> 205
<212> PRT
<213> Corynebacterium glutamicum

<400> 2382

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Val Ile Asp Ser Glu Ala Thr Ser Gln His Lys Thr Ser Ala Thr Pro
  1               5                  10                  15

Ala Glu Ser Thr Pro Ala Glu Phe Ser Glu Ala Val Glu Ser Met His
             20                  25                  30

Arg Ala Arg Leu Arg Pro Glu Leu Thr Leu Gly Thr Ile Arg Pro Pro
         35                  40                  45

Gln Arg Leu Ala Pro Phe Ser His Ala Ile Gly Leu Glu Val Gly Asn
     50                  55                  60

Gln Glu Glu Ser Asp Asp Val Ser Thr Asn Ser Glu Gly Asp Ser Phe
 65                  70                  75                  80

Gly Arg Leu Ile Leu Leu His Asp Pro Gly Ala Glu Glu Thr Trp Glu
                 85                  90                  95

Gly Ala Met Arg Leu Val Ala Tyr Ile Gln Ala Asp Met Asp His Ala
            100                 105                 110

Val Ala Ser Asp Pro Leu Leu Pro Glu Val Ala Trp Gln Trp Leu Asn
        115                 120                 125

Glu Gly Leu Glu Gln Ala Gly Ala Gly Phe Thr Asn Leu Gly Gly Thr
    130                 135                 140

Val Thr Ser Thr Thr Ser Val Arg Phe Gly Glu Ile Gly Gly Pro Pro
145                 150                 155                 160

Ser Ala Tyr Gln Val Glu Met Arg Ala Ser Trp Thr Ala Thr Gly Thr
                165                 170                 175

Asp Leu Thr Ala His Val Glu Ala Phe Ala Ala Val Leu Ala Ser Val
            180                 185                 190

Ala Gly Leu Pro Pro Glu Gly Val Thr Glu Leu Arg Arg
        195                 200                 205
```

<210> 2383
<211> 819
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(796)
<223> RXA01715

<400> 2383
acatgttgtt ggaacatgcc ggcagagccg acactacgat tcattcgcta aagggtctgg 60

ccactgacac tggcaaagat ccacgaaagg aagttaccct gtg agc gag ctc gat 115
Val Ser Glu Leu Asp
1 5

att aaa cag ctc aac aaa ctg cag cgc tac tct cag tgg gcg gtg ttc 163
Ile Lys Gln Leu Asn Lys Leu Gln Arg Tyr Ser Gln Trp Ala Val Phe
10 15 20

cgt gct att cct gga gcg ctc gat gat gat cgc aca gaa gtc act gac 211
Arg Ala Ile Pro Gly Ala Leu Asp Asp Asp Arg Thr Glu Val Thr Asp
25 30 35

caa gca gcc aag ttc ttt gcc gac ctt gaa gca gaa ggc aaa gtc act 259
Gln Ala Ala Lys Phe Phe Ala Asp Leu Glu Ala Glu Gly Lys Val Thr
40 45 50

gtc cgt ggc att tac aac gcc tcc ggc ctg cgc gca gac gct gac tac 307
Val Arg Gly Ile Tyr Asn Ala Ser Gly Leu Arg Ala Asp Ala Asp Tyr
55 60 65

atg atc tgg tgg cac gca gaa gaa ttc gaa gac att cag aag gcc ttc 355
Met Ile Trp Trp His Ala Glu Glu Phe Glu Asp Ile Gln Lys Ala Phe
70 75 80 85

gct gat ttc cgc cgc acc acc att ttg ggt cag gtt tct gag gtc ttc 403
Ala Asp Phe Arg Arg Thr Thr Ile Leu Gly Gln Val Ser Glu Val Phe
90 95 100

tgg atc gga aac gct ctc cac cgt cca tct gag ttc aac aag gct cac 451
Trp Ile Gly Asn Ala Leu His Arg Pro Ser Glu Phe Asn Lys Ala His
105 110 115

ttg cct tca ttc atc atg ggt gaa gaa gca aag gac tgg atc act gtt 499
Leu Pro Ser Phe Ile Met Gly Glu Glu Ala Lys Asp Trp Ile Thr Val
120 125 130

tac ccg ttc gtg cgc agc tac gac tgg tac atc atg gag ccc ttg aag 547
Tyr Pro Phe Val Arg Ser Tyr Asp Trp Tyr Ile Met Glu Pro Leu Lys
135 140 145

cgt tcc cgc att ctc cgc gag cac gga caa gct gct gtg gaa ttc cca 595
Arg Ser Arg Ile Leu Arg Glu His Gly Gln Ala Ala Val Glu Phe Pro
150 155 160 165

gat gtt cgt gcc aac act gtg ccg gct ttc gca ctg ggt gac tac gaa 643
Asp Val Arg Ala Asn Thr Val Pro Ala Phe Ala Leu Gly Asp Tyr Glu
170 175 180

tgg gtg ctg gct ttc gag gct gat gag ttg cac cgc att gtc gat ttg 691
Trp Val Leu Ala Phe Glu Ala Asp Glu Leu His Arg Ile Val Asp Leu
185 190 195

atg cac aag atg cgt tac acc gag gct cgc ctc cac gtc cgt gag gag 739

```
Met His Lys Met Arg Tyr Thr Glu Ala Arg Leu His Val Arg Glu Glu
        200                 205                 210

ctg cca ttt att tct gga cag cgc gtc gac att gca gat ctg att aag   787
Leu Pro Phe Ile Ser Gly Gln Arg Val Asp Ile Ala Asp Leu Ile Lys
    215                 220                 225

gtt ctt cct taaaagctgc ttttctaaac gat                             819
Val Leu Pro
230
```

<210> 2384
<211> 232
<212> PRT
<213> Corynebacterium glutamicum

<400> 2384

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Val Ser Glu Leu Asp Ile Lys Gln Leu Asn Lys Leu Gln Arg Tyr Ser
  1               5                  10                  15

Gln Trp Ala Val Phe Arg Ala Ile Pro Gly Ala Leu Asp Asp Asp Arg
             20                  25                  30

Thr Glu Val Thr Asp Gln Ala Ala Lys Phe Phe Ala Asp Leu Glu Ala
         35                  40                  45

Glu Gly Lys Val Thr Val Arg Gly Ile Tyr Asn Ala Ser Gly Leu Arg
     50                  55                  60

Ala Asp Ala Asp Tyr Met Ile Trp Trp His Ala Glu Glu Phe Glu Asp
 65                  70                  75                  80

Ile Gln Lys Ala Phe Ala Asp Phe Arg Arg Thr Thr Ile Leu Gly Gln
                 85                  90                  95

Val Ser Glu Val Phe Trp Ile Gly Asn Ala Leu His Arg Pro Ser Glu
            100                 105                 110

Phe Asn Lys Ala His Leu Pro Ser Phe Ile Met Gly Glu Glu Ala Lys
        115                 120                 125

Asp Trp Ile Thr Val Tyr Pro Phe Val Arg Ser Tyr Asp Trp Tyr Ile
    130                 135                 140

Met Glu Pro Leu Lys Arg Ser Arg Ile Leu Arg Glu His Gly Gln Ala
145                 150                 155                 160

Ala Val Glu Phe Pro Asp Val Arg Ala Asn Thr Val Pro Ala Phe Ala
                165                 170                 175

Leu Gly Asp Tyr Glu Trp Val Leu Ala Phe Glu Ala Asp Glu Leu His
            180                 185                 190

Arg Ile Val Asp Leu Met His Lys Met Arg Tyr Thr Glu Ala Arg Leu
        195                 200                 205

His Val Arg Glu Glu Leu Pro Phe Ile Ser Gly Gln Arg Val Asp Ile
    210                 215                 220

Ala Asp Leu Ile Lys Val Leu Pro
```

225 230

<210> 2385
<211> 642
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(619)
<223> RXA01729

<400> 2385
tcaaggtccg gcgattcttc aattcttcga gttcaggaaa tcgcatactc tctaggctag 60

taaacttttc tacgaaccta ttactaagaa ggagcccgaa gtg aag ttg agg aca 115
Val Lys Leu Arg Thr
1 5

atc cca gcc ctg tta gcc gtc gca ctt ctt gca ggc tgt tcg ggt gaa 163
Ile Pro Ala Leu Leu Ala Val Ala Leu Leu Ala Gly Cys Ser Gly Glu
10 15 20

agt gct gat agc caa gcc gtt tcc gct gag gaa acc atg gaa gta acc 211
Ser Ala Asp Ser Gln Ala Val Ser Ala Glu Glu Thr Met Glu Val Thr
25 30 35

act acc tca acc ccg gtg ttc gaa gcc aaa gag gta agc cca atc aca 259
Thr Thr Ser Thr Pro Val Phe Glu Ala Lys Glu Val Ser Pro Ile Thr
40 45 50

gtc cca agc ggc gat atc agg gtt gaa gac cca ggt ctc aat gtt gaa 307
Val Pro Ser Gly Asp Ile Arg Val Glu Asp Pro Gly Leu Asn Val Glu
55 60 65

ttt atc ttc cga ggc acc cgc tac ggc acc aac ggt ggc tca att att 355
Phe Ile Phe Arg Gly Thr Arg Tyr Gly Thr Asn Gly Gly Ser Ile Ile
70 75 80 85

cac atc gcg gtg aaa aac cta aac gac gta gcc ctg cca gcc gac gcc 403
His Ile Ala Val Lys Asn Leu Asn Asp Val Ala Leu Pro Ala Asp Ala
90 95 100

atc gat cca ccc acc ctg gac atc gaa gac tac aac ggc aac aaa acc 451
Ile Asp Pro Pro Thr Leu Asp Ile Glu Asp Tyr Asn Gly Asn Lys Thr
105 110 115

aac atc gaa acc ctc tcc ggc gac gac aac atc cca ctc gac cta cca 499
Asn Ile Glu Thr Leu Ser Gly Asp Asp Asn Ile Pro Leu Asp Leu Pro
120 125 130

ctg ggt gcc ggc gcg aca acg aac ctg caa tac gcg ttc aac acc tca 547
Leu Gly Ala Gly Ala Thr Thr Asn Leu Gln Tyr Ala Phe Asn Thr Ser
135 140 145

aac ggc tca ttg tcg aat gct aaa ttc cag atc gga aac gtc atc tac 595
Asn Gly Ser Leu Ser Asn Ala Lys Phe Gln Ile Gly Asn Val Ile Tyr
150 155 160 165

tca ggc aat ttg aac agc ttg gcg taagttcaaa aaataatttg aat 642

```
Ser Gly Asn Leu Asn Ser Leu Ala
                170


<210> 2386
<211> 173
<212> PRT
<213> Corynebacterium glutamicum

<400> 2386
Val Lys Leu Arg Thr Ile Pro Ala Leu Leu Ala Val Ala Leu Leu Ala
  1               5                  10                  15

Gly Cys Ser Gly Glu Ser Ala Asp Ser Gln Ala Val Ser Ala Glu Glu
             20                  25                  30

Thr Met Glu Val Thr Thr Thr Ser Thr Pro Val Phe Glu Ala Lys Glu
         35                  40                  45

Val Ser Pro Ile Thr Val Pro Ser Gly Asp Ile Arg Val Glu Asp Pro
     50                  55                  60

Gly Leu Asn Val Glu Phe Ile Phe Arg Gly Thr Arg Tyr Gly Thr Asn
 65                  70                  75                  80

Gly Gly Ser Ile Ile His Ile Ala Val Lys Asn Leu Asn Asp Val Ala
                 85                  90                  95

Leu Pro Ala Asp Ala Ile Asp Pro Pro Thr Leu Asp Ile Glu Asp Tyr
            100                 105                 110

Asn Gly Asn Lys Thr Asn Ile Glu Thr Leu Ser Gly Asp Asp Asn Ile
        115                 120                 125

Pro Leu Asp Leu Pro Leu Gly Ala Gly Ala Thr Thr Asn Leu Gln Tyr
    130                 135                 140

Ala Phe Asn Thr Ser Asn Gly Ser Leu Ser Asn Ala Lys Phe Gln Ile
145                 150                 155                 160

Gly Asn Val Ile Tyr Ser Gly Asn Leu Asn Ser Leu Ala
                165                 170


<210> 2387
<211> 822
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(799)
<223> RXA01731

<400> 2387
gcttttgcag ctgtggggtt gggctggggg caagtgttca tgtaggtgtc attgatcgtt 60

cactcaaggt tggacgttgt gttcatgaat aacttttatg atg aac gca tcg tcc   115
                                        Met Asn Ala Ser Ser
                                          1               5
```

```
att tct tcc cga ttc aag gat ctt ttt gtg aca ccc agt att gtt ttt   163
Ile Ser Ser Arg Phe Lys Asp Leu Phe Val Thr Pro Ser Ile Val Phe
                 10                  15                  20

gat ttc gat ggc acg ctt gcc att ggc cat ggc cct gtc ctt gcg tat   211
Asp Phe Asp Gly Thr Leu Ala Ile Gly His Gly Pro Val Leu Ala Tyr
             25                  30                  35

gca ttg tgt gtt gca ccg gag ggt tcc aag gac ttt ctg gag cgt gtg   259
Ala Leu Cys Val Ala Pro Glu Gly Ser Lys Asp Phe Leu Glu Arg Val
         40                  45                  50

cgc agg gag ctt cgg cgc tat gac gat ggt cag agt att tac cgt gat   307
Arg Arg Glu Leu Arg Arg Tyr Asp Asp Gly Gln Ser Ile Tyr Arg Asp
     55                  60                  65

ggg tat gac att gtg gct aag ttg gcg tcg gaa ttg ggg att gat gat   355
Gly Tyr Asp Ile Val Ala Lys Leu Ala Ser Glu Leu Gly Ile Asp Asp
 70                  75                  80                  85

ggc acg atg tct gtc gct tat ggc gag agc cgg aag ttg ctt ggt tcg   403
Gly Thr Met Ser Val Ala Tyr Gly Glu Ser Arg Lys Leu Leu Gly Ser
                 90                  95                 100

gat tta gcg cct gtt gag cat gtg cgg ggt att aag gat att ttg tcc   451
Asp Leu Ala Pro Val Glu His Val Arg Gly Ile Lys Asp Ile Leu Ser
            105                 110                 115

tcg ttg aaa ggt cat gct cgg ttg gtt tta gct acc aat gcc ccg gaa   499
Ser Leu Lys Gly His Ala Arg Leu Val Leu Ala Thr Asn Ala Pro Glu
        120                 125                 130

aat ggc gtg cat gat ttg ctg cgt cag tgg ggt gtt gct gat ttg ttt   547
Asn Gly Val His Asp Leu Leu Arg Gln Trp Gly Val Ala Asp Leu Phe
    135                 140                 145

gat cag ttg cat ttt gtg gtg ggt aag cct gca ggg ttg att tcg atc   595
Asp Gln Leu His Phe Val Val Gly Lys Pro Ala Gly Leu Ile Ser Ile
150                 155                 160                 165

att tct gat ttg cag ctt gat ggt ccg gtg ctt gcg gtg ggc gat att   643
Ile Ser Asp Leu Gln Leu Asp Gly Pro Val Leu Ala Val Gly Asp Ile
                170                 175                 180

tat gaa ttc gat ctg agt cct gca gcg cag tta ggt gca gat acg gct   691
Tyr Glu Phe Asp Leu Ser Pro Ala Ala Gln Leu Gly Ala Asp Thr Ala
            185                 190                 195

ctg gtt gga gct aca gca acc att tct gaa gcg aag gtc tcc atg cgt   739
Leu Val Gly Ala Thr Ala Thr Ile Ser Glu Ala Lys Val Ser Met Arg
        200                 205                 210

gga gat tct atc gct gat ctc cct ctc ctt gcc tgg gtt tgt tcc cgg   787
Gly Asp Ser Ile Ala Asp Leu Pro Leu Leu Ala Trp Val Cys Ser Arg
    215                 220                 225

gtc tcc tct tct taactttctt gtctcatgtc gct                        822
Val Ser Ser Ser
230
```

<210> 2388
<211> 233
<212> PRT
<213> Corynebacterium glutamicum

<400> 2388
Met Asn Ala Ser Ser Ile Ser Ser Arg Phe Lys Asp Leu Phe Val Thr
1 5 10 15

Pro Ser Ile Val Phe Asp Phe Asp Gly Thr Leu Ala Ile Gly His Gly
20 25 30

Pro Val Leu Ala Tyr Ala Leu Cys Val Ala Pro Glu Gly Ser Lys Asp
35 40 45

Phe Leu Glu Arg Val Arg Arg Glu Leu Arg Arg Tyr Asp Asp Gly Gln
50 55 60

Ser Ile Tyr Arg Asp Gly Tyr Asp Ile Val Ala Lys Leu Ala Ser Glu
65 70 75 80

Leu Gly Ile Asp Asp Gly Thr Met Ser Val Ala Tyr Gly Glu Ser Arg
85 90 95

Lys Leu Leu Gly Ser Asp Leu Ala Pro Val Glu His Val Arg Gly Ile
100 105 110

Lys Asp Ile Leu Ser Ser Leu Lys Gly His Ala Arg Leu Val Leu Ala
115 120 125

Thr Asn Ala Pro Glu Asn Gly Val His Asp Leu Leu Arg Gln Trp Gly
130 135 140

Val Ala Asp Leu Phe Asp Gln Leu His Phe Val Val Gly Lys Pro Ala
145 150 155 160

Gly Leu Ile Ser Ile Ile Ser Asp Leu Gln Leu Asp Gly Pro Val Leu
165 170 175

Ala Val Gly Asp Ile Tyr Glu Phe Asp Leu Ser Pro Ala Ala Gln Leu
180 185 190

Gly Ala Asp Thr Ala Leu Val Gly Ala Thr Ala Thr Ile Ser Glu Ala
195 200 205

Lys Val Ser Met Arg Gly Asp Ser Ile Ala Asp Leu Pro Leu Leu Ala
210 215 220

Trp Val Cys Ser Arg Val Ser Ser Ser
225 230

<210> 2389
<211> 837
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(814)
<223> RXA01738

<400> 2389
gtgagctcta ccgcatcgac tccccagaag cagaaactgt agagcccggc gatcgtctcc 60

tttacgttcg ccgagtattt agcgaggagg taaatgacaa atg aga att ctt ccc 115
Met Arg Ile Leu Pro
1 5

atc ggc ccc cac gat gaa atc gcc gtc aac gga tca ata gtc ctt cta 163
Ile Gly Pro His Asp Glu Ile Ala Val Asn Gly Ser Ile Val Leu Leu
10 15 20

tcc gag cac gac gga gac atc gta tcg gtc ggc ccc gac ctc ggc acg 211
Ser Glu His Asp Gly Asp Ile Val Ser Val Gly Pro Asp Leu Gly Thr
25 30 35

gtg cga gtt acc ctt gaa gag atc gaa agt tta ggt aca ccg acg gca 259
Val Arg Val Thr Leu Glu Glu Ile Glu Ser Leu Gly Thr Pro Thr Ala
40 45 50

ccc cgc gat ctg ggt tct cgg gaa gtc gac gca tgc gta tcg ttg ctc 307
Pro Arg Asp Leu Gly Ser Arg Glu Val Asp Ala Cys Val Ser Leu Leu
55 60 65

cgc aac cgc gag tta gtg cga ttc gat ccc cac gat ggc agt gaa tta 355
Arg Asn Arg Glu Leu Val Arg Phe Asp Pro His Asp Gly Ser Glu Leu
70 75 80 85

acc tat cgg gaa cat agc gtt gct tac ggt gcg agt ggc aag cca ttg 403
Thr Tyr Arg Glu His Ser Val Ala Tyr Gly Ala Ser Gly Lys Pro Leu
90 95 100

ttt ccc cga ttg gat cca gcg gtg atc ggc att gtg gag ctg cga ggt 451
Phe Pro Arg Leu Asp Pro Ala Val Ile Gly Ile Val Glu Leu Arg Gly
105 110 115

gag gat cgt ttg ctt ctg ggc atg aat gcg cag aaa cgc caa cgc tat 499
Glu Asp Arg Leu Leu Leu Gly Met Asn Ala Gln Lys Arg Gln Arg Tyr
120 125 130

tca tta atc gca ggt tat gtt tcg cat ggt gag tcg ctg gaa gac gca 547
Ser Leu Ile Ala Gly Tyr Val Ser His Gly Glu Ser Leu Glu Asp Ala
135 140 145

ttc acc aga gaa gtg ttc gag gaa gcg gcg cgc cgg gta tct gag att 595
Phe Thr Arg Glu Val Phe Glu Glu Ala Ala Arg Arg Val Ser Glu Ile
150 155 160 165

tcc tat gtg tcg tct caa cca tgg ccg atc tct ggt tcg ctg atg ctg 643
Ser Tyr Val Ser Ser Gln Pro Trp Pro Ile Ser Gly Ser Leu Met Leu
170 175 180

ggt atg aag ggc ttc acg gaa gat gag ttg cct caa ggc gaa act gat 691
Gly Met Lys Gly Phe Thr Glu Asp Glu Leu Pro Gln Gly Glu Thr Asp
185 190 195

ggt gaa tta gcg gag aca atc tgg gct tcg cca cta gac att atc gat 739
Gly Glu Leu Ala Glu Thr Ile Trp Ala Ser Pro Leu Asp Ile Ile Asp
200 205 210

cgt aag att ccg atc gcc cca ccc gga tcg att gcc tac gac atg atc 787

```
Arg Lys Ile Pro Ile Ala Pro Pro Gly Ser Ile Ala Tyr Asp Met Ile
    215                 220                 225

aac gcc tgg gcg cga gat aaa caa aac taagggagct ttttacagtg        834
Asn Ala Trp Ala Arg Asp Lys Gln Asn
230                 235

atc                                                              837


<210> 2390
<211> 238
<212> PRT
<213> Corynebacterium glutamicum

<400> 2390
Met Arg Ile Leu Pro Ile Gly Pro His Asp Glu Ile Ala Val Asn Gly
  1               5                  10                  15

Ser Ile Val Leu Leu Ser Glu His Asp Gly Asp Ile Val Ser Val Gly
             20                  25                  30

Pro Asp Leu Gly Thr Val Arg Val Thr Leu Glu Glu Ile Glu Ser Leu
         35                  40                  45

Gly Thr Pro Thr Ala Pro Arg Asp Leu Gly Ser Arg Glu Val Asp Ala
     50                  55                  60

Cys Val Ser Leu Leu Arg Asn Arg Glu Leu Val Arg Phe Asp Pro His
 65                  70                  75                  80

Asp Gly Ser Glu Leu Thr Tyr Arg Glu His Ser Val Ala Tyr Gly Ala
                 85                  90                  95

Ser Gly Lys Pro Leu Phe Pro Arg Leu Asp Pro Ala Val Ile Gly Ile
            100                 105                 110

Val Glu Leu Arg Gly Glu Asp Arg Leu Leu Leu Gly Met Asn Ala Gln
        115                 120                 125

Lys Arg Gln Arg Tyr Ser Leu Ile Ala Gly Tyr Val Ser His Gly Glu
    130                 135                 140

Ser Leu Glu Asp Ala Phe Thr Arg Glu Val Phe Glu Glu Ala Ala Arg
145                 150                 155                 160

Arg Val Ser Glu Ile Ser Tyr Val Ser Ser Gln Pro Trp Pro Ile Ser
                165                 170                 175

Gly Ser Leu Met Leu Gly Met Lys Gly Phe Thr Glu Asp Glu Leu Pro
            180                 185                 190

Gln Gly Glu Thr Asp Gly Glu Leu Ala Glu Thr Ile Trp Ala Ser Pro
        195                 200                 205

Leu Asp Ile Ile Asp Arg Lys Ile Pro Ile Ala Pro Pro Gly Ser Ile
    210                 215                 220

Ala Tyr Asp Met Ile Asn Ala Trp Ala Arg Asp Lys Gln Asn
225                 230                 235
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<210> 2391
<211> 921
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(898)
<223> RXA01741

<400> 2391
gcatctctgg cttttcctgc atgacagatg attgtaactg tgatgaaata aggccagatg 60

aagtaactgt gtcgattaag ttttgggggga aatttttcag atg aca cac atc gct 115
Met Thr His Ile Ala
1 5

tta gcc aac tct gcc caa gtt ctg atc cgc ccg gat tct gcg att caa 163
Leu Ala Asn Ser Ala Gln Val Leu Ile Arg Pro Asp Ser Ala Ile Gln
10 15 20

ttc ggc atc gac gcc acc cgc gct ggc gtc tta aat atc gat cca tcg 211
Phe Gly Ile Asp Ala Thr Arg Ala Gly Val Leu Asn Ile Asp Pro Ser
25 30 35

ctg tcg tcg cga gtc gtc ccg gtg ctg cgg aat ctg cgg acc gcc cga 259
Leu Ser Ser Arg Val Val Pro Val Leu Arg Asn Leu Arg Thr Ala Arg
40 45 50

ccg atc gtt gat gtc atc gcc gac ctc acg act gca ggc ctc gca ccc 307
Pro Ile Val Asp Val Ile Ala Asp Leu Thr Thr Ala Gly Leu Ala Pro
55 60 65

acc gct gcg agc agt ttg ctc gag gac ctt tta gaa ttc ggt gtg gtc 355
Thr Ala Ala Ser Ser Leu Leu Glu Asp Leu Leu Glu Phe Gly Val Val
70 75 80 85

cgc gaa tcg gcg gcg gcg cag gtg ttg ctg ttc ggg gac ggt tcg ctt 403
Arg Glu Ser Ala Ala Ala Gln Val Leu Leu Phe Gly Asp Gly Ser Leu
90 95 100

gtc gac gtc acc tcc ttc ctt ttg gaa acc tcc ggc ttt gtt ccc aga 451
Val Asp Val Thr Ser Phe Leu Leu Glu Thr Ser Gly Phe Val Pro Arg
105 110 115

ccc cag atc atc gat gag tcg cct cga gag ttt ttc gag ctt ccc tcc 499
Pro Gln Ile Ile Asp Glu Ser Pro Arg Glu Phe Phe Glu Leu Pro Ser
120 125 130

agc cac att ttg gtt ctc aac aag ctc gca cat tcc caa cgt cta tcc 547
Ser His Ile Leu Val Leu Asn Lys Leu Ala His Ser Gln Arg Leu Ser
135 140 145

ccg ctg ctt cac aaa tat gcg ccg acg tat ctg tgc gcc gcg atc gtc 595
Pro Leu Leu His Lys Tyr Ala Pro Thr Tyr Leu Cys Ala Ala Ile Val
150 155 160 165

gat aat cgt ggc atc atc ggc ccg ggc cgg aga tca cga tcg ggg ccg 643
Asp Asn Arg Gly Ile Ile Gly Pro Gly Arg Arg Ser Arg Ser Gly Pro
170 175 180

```
tgt ttg atg tgt gtg gat ctg cat cgc tgc gat atc gat ccg cat tgg   691
Cys Leu Met Cys Val Asp Leu His Arg Cys Asp Ile Asp Pro His Trp
            185                 190                 195

ctc tct att atc aat cag caa ccc aac ggt ccc acc ttt cct gat ccc   739
Leu Ser Ile Ile Asn Gln Gln Pro Asn Gly Pro Thr Phe Pro Asp Pro
        200                 205                 210

gtc acg gag atg gcg acg gct gcc cga ctc gtc gcc tgg gtc act gcc   787
Val Thr Glu Met Ala Thr Ala Ala Arg Leu Val Ala Trp Val Thr Ala
    215                 220                 225

gat aca tgg ttg ccc ggc gtt gtg gag gaa gta aac ccc cac gat cga   835
Asp Thr Trp Leu Pro Gly Val Val Glu Glu Val Asn Pro His Asp Arg
230                 235                 240                 245

aca aac tcg gta cgc acc ctc cct gtg cat cca aaa tgt ccg atg tgt   883
Thr Asn Ser Val Arg Thr Leu Pro Val His Pro Lys Cys Pro Met Cys
                250                 255                 260

tgg agt tta ggt tcc taaagtgctc ccaaaatcgc gag                    921
Trp Ser Leu Gly Ser
            265
```

<210> 2392
<211> 266
<212> PRT
<213> Corynebacterium glutamicum

<400> 2392

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Met Thr His Ile Ala Leu Ala Asn Ser Ala Gln Val Leu Ile Arg Pro
  1               5                  10                  15

Asp Ser Ala Ile Gln Phe Gly Ile Asp Ala Thr Arg Ala Gly Val Leu
             20                  25                  30

Asn Ile Asp Pro Ser Leu Ser Ser Arg Val Val Pro Val Leu Arg Asn
         35                  40                  45

Leu Arg Thr Ala Arg Pro Ile Val Asp Val Ile Ala Asp Leu Thr Thr
     50                  55                  60

Ala Gly Leu Ala Pro Thr Ala Ala Ser Ser Leu Leu Glu Asp Leu Leu
 65                  70                  75                  80

Glu Phe Gly Val Val Arg Glu Ser Ala Ala Ala Gln Val Leu Leu Phe
                 85                  90                  95

Gly Asp Gly Ser Leu Val Asp Val Thr Ser Phe Leu Leu Glu Thr Ser
            100                 105                 110

Gly Phe Val Pro Arg Pro Gln Ile Ile Asp Glu Ser Pro Arg Glu Phe
        115                 120                 125

Phe Glu Leu Pro Ser Ser His Ile Leu Val Leu Asn Lys Leu Ala His
    130                 135                 140

Ser Gln Arg Leu Ser Pro Leu Leu His Lys Tyr Ala Pro Thr Tyr Leu
145                 150                 155                 160
```

```
Cys Ala Ala Ile Val Asp Asn Arg Gly Ile Ile Gly Pro Gly Arg Arg
                165                 170                 175

Ser Arg Ser Gly Pro Cys Leu Met Cys Val Asp Leu His Arg Cys Asp
            180                 185                 190

Ile Asp Pro His Trp Leu Ser Ile Ile Asn Gln Gln Pro Asn Gly Pro
        195                 200                 205

Thr Phe Pro Asp Pro Val Thr Glu Met Ala Thr Ala Ala Arg Leu Val
    210                 215                 220

Ala Trp Val Thr Ala Asp Thr Trp Leu Pro Gly Val Val Glu Glu Val
225                 230                 235                 240

Asn Pro His Asp Arg Thr Asn Ser Val Arg Thr Leu Pro Val His Pro
                245                 250                 255

Lys Cys Pro Met Cys Trp Ser Leu Gly Ser
            260                 265
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Sequence Listing Free Text

<210> 2393
<211> 903
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(880)
<223> RXA01748

<400> 2393

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atcaccaaat gtggcggttt tgcgtcgaaa agcgtgctct ttctacacct ctttgaggtt 60

cattttcgcg gtttcctcac aatcgcctat tgttaagtac atg gca gac gcg aaa   115
                                            Met Ala Asp Ala Lys
                                              1               5

aag cag gcg gat aaa gcc gcc aag aag cag gta aga gca gcc aag aag   163
Lys Gln Ala Asp Lys Ala Ala Lys Lys Gln Val Arg Ala Ala Lys Lys
                10                  15                  20

gca cag cgc aag gag act cgc tca caa atg tgg cag gtc ttc aac atg   211
Ala Gln Arg Lys Glu Thr Arg Ser Gln Met Trp Gln Val Phe Asn Met
            25                  30                  35

caa cgc aag cag gat aag gct ctt att ccg ctt ctg ttg ctc gct att   259
Gln Arg Lys Gln Asp Lys Ala Leu Ile Pro Leu Leu Leu Leu Ala Ile
        40                  45                  50

ctt ggt atc ccg ctg gtc ctt ttc ctc atc ggt ttg att tgg ggt ggt   307
Leu Gly Ile Pro Leu Val Leu Phe Leu Ile Gly Leu Ile Trp Gly Gly
    55                  60                  65

cag tgg tgg atg ctt ccg atc ggc att gct gca ggt gtt gta gct gca   355
Gln Trp Trp Met Leu Pro Ile Gly Ile Ala Ala Gly Val Val Ala Ala
70                  75                  80                  85

atg ttt att ttc acc cgt cgc gtt gag cgt gac gtg tac aag cgc gcc   403
```

```
Met Phe Ile Phe Thr Arg Arg Val Glu Arg Asp Val Tyr Lys Arg Ala
                 90                  95                 100

gaa ggt cag cag ggt gct gct ggt tgg gct gtg gag aac ctc cgc tct   451
Glu Gly Gln Gln Gly Ala Ala Gly Trp Ala Val Glu Asn Leu Arg Ser
            105                 110                 115

ggc gtg ggc atg acc tgg cgc acc aag acc gct gtt gca gtg acc act   499
Gly Val Gly Met Thr Trp Arg Thr Lys Thr Ala Val Ala Val Thr Thr
        120                 125                 130

cag atg gat gca gtg cac cgc gtc att ggt ctg tgt ggt gtt gtg ctg   547
Gln Met Asp Ala Val His Arg Val Ile Gly Leu Cys Gly Val Val Leu
    135                 140                 145

gtc ggc gag ggc tcc cct cac cgc ctg aag cca atg ctt gcg cag caa   595
Val Gly Glu Gly Ser Pro His Arg Leu Lys Pro Met Leu Ala Gln Gln
150                 155                 160                 165

aag aag cgc ctg aac cgc gtg gca cct ggt gtt cca gtg tat gaa atc   643
Lys Lys Arg Leu Asn Arg Val Ala Pro Gly Val Pro Val Tyr Glu Ile
                170                 175                 180

atc acg ggc aac ggc gaa ggc cag acc cct atc gcg aag ctg cag cgt   691
Ile Thr Gly Asn Gly Glu Gly Gln Thr Pro Ile Ala Lys Leu Gln Arg
            185                 190                 195

gaa ctg gtc aag ctg cct cgc aac tac aag aag aac gac gtc gct gcc   739
Glu Leu Val Lys Leu Pro Arg Asn Tyr Lys Lys Asn Asp Val Ala Ala
        200                 205                 210

ctg gcc gct cgc att gag gct atg gac aat gtc gga aac gct cct ggc   787
Leu Ala Ala Arg Ile Glu Ala Met Asp Asn Val Gly Asn Ala Pro Gly
    215                 220                 225

gga tct ttg cct aag ggt cca ttg cca aag ggc gca agc atg tcc ggt   835
Gly Ser Leu Pro Lys Gly Pro Leu Pro Lys Gly Ala Ser Met Ser Gly
230                 235                 240                 245

atg aac cgc cgc gct cgc cga cag gct gaa cgc aag ggc gag gct       880
Met Asn Arg Arg Ala Arg Arg Gln Ala Glu Arg Lys Gly Glu Ala
                250                 255                 260

taaagccttt tcgctttcgc gtc                                        903


<210> 2394
<211> 260
<212> PRT
<213> Corynebacterium glutamicum

<400> 2394
Met Ala Asp Ala Lys Lys Gln Ala Asp Lys Ala Ala Lys Lys Gln Val
  1               5                  10                  15

Arg Ala Ala Lys Lys Ala Gln Arg Lys Glu Thr Arg Ser Gln Met Trp
             20                  25                  30

Gln Val Phe Asn Met Gln Arg Lys Gln Asp Lys Ala Leu Ile Pro Leu
         35                  40                  45
```

```
Leu Leu Leu Ala Ile Leu Gly Ile Pro Leu Val Leu Phe Leu Ile Gly
     50                  55                  60

Leu Ile Trp Gly Gly Gln Trp Trp Met Leu Pro Ile Gly Ile Ala Ala
 65                  70                  75                  80

Gly Val Val Ala Ala Met Phe Ile Phe Thr Arg Arg Val Glu Arg Asp
                 85                  90                  95

Val Tyr Lys Arg Ala Glu Gly Gln Gln Gly Ala Ala Gly Trp Ala Val
            100                 105                 110

Glu Asn Leu Arg Ser Gly Val Gly Met Thr Trp Arg Thr Lys Thr Ala
        115                 120                 125

Val Ala Val Thr Thr Gln Met Asp Ala Val His Arg Val Ile Gly Leu
    130                 135                 140

Cys Gly Val Val Leu Val Gly Glu Gly Ser Pro His Arg Leu Lys Pro
145                 150                 155                 160

Met Leu Ala Gln Gln Lys Lys Arg Leu Asn Arg Val Ala Pro Gly Val
                165                 170                 175

Pro Val Tyr Glu Ile Ile Thr Gly Asn Gly Glu Gly Gln Thr Pro Ile
            180                 185                 190

Ala Lys Leu Gln Arg Glu Leu Val Lys Leu Pro Arg Asn Tyr Lys Lys
        195                 200                 205

Asn Asp Val Ala Ala Leu Ala Ala Arg Ile Glu Ala Met Asp Asn Val
    210                 215                 220

Gly Asn Ala Pro Gly Gly Ser Leu Pro Lys Gly Pro Leu Pro Lys Gly
225                 230                 235                 240

Ala Ser Met Ser Gly Met Asn Arg Arg Ala Arg Arg Gln Ala Glu Arg
                245                 250                 255

Lys Gly Glu Ala
            260
```

<210> 2395
<211> 1740
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1717)
<223> RXA01749

<400> 2395

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ggtttttgcg tgctctggtt tagggactgg ttttgggaac gtgcccagtt ccacatcaaa 60

taacgctgag gtcgtactta atccatgaga tcatgaatgg gtg agc ttc ctt gta   115
                                              Val Ser Phe Leu Val
                                                1               5

gaa aat caa tta ctc gcg ttg gtt gtc atc atg acg gtc gga cta ttg   163
```

```
Glu Asn Gln Leu Leu Ala Leu Val Val Ile Met Thr Val Gly Leu Leu
                10                  15                  20

ctc ggc cgc atc aaa att ttc ggg ttc cgt ctc ggc gtc gcc gct gta   211
Leu Gly Arg Ile Lys Ile Phe Gly Phe Arg Leu Gly Val Ala Ala Val
            25                  30                  35

ctg ttt gta ggt cta gcg cta tcc acc att gag ccg gat att tcc gtc   259
Leu Phe Val Gly Leu Ala Leu Ser Thr Ile Glu Pro Asp Ile Ser Val
        40                  45                  50

cca tcc ctc att tac gtg gtt gga ctg tcg ctt ttt gtc tac acg atc   307
Pro Ser Leu Ile Tyr Val Val Gly Leu Ser Leu Phe Val Tyr Thr Ile
    55                  60                  65

ggt ctg gaa gcc ggc cct gga ttc ttc acc tcc atg aaa acc act ggt   355
Gly Leu Glu Ala Gly Pro Gly Phe Phe Thr Ser Met Lys Thr Thr Gly
70                  75                  80                  85

ctg cgc aac aac gca ctg acc ttg ggc gcc atc atc gcc acc acg gca   403
Leu Arg Asn Asn Ala Leu Thr Leu Gly Ala Ile Ile Ala Thr Thr Ala
                90                  95                  100

ctc gca tgg gca ctc atc aca gtt ttg aac atc gat gcc gcc tcc ggc   451
Leu Ala Trp Ala Leu Ile Thr Val Leu Asn Ile Asp Ala Ala Ser Gly
            105                 110                 115

gcc ggc atg ctc acc ggc gcg ctc acc aac acc cca gcc atg gcc gca   499
Ala Gly Met Leu Thr Gly Ala Leu Thr Asn Thr Pro Ala Met Ala Ala
        120                 125                 130

gtt gtt gac gca ctt cct tcg ctt atc gac gac acc ggc cag ctt cac   547
Val Val Asp Ala Leu Pro Ser Leu Ile Asp Asp Thr Gly Gln Leu His
    135                 140                 145

ctc atc gcc gag ctg ccc gtc gtc gca tat tcc ttg gca tac ccc ctc   595
Leu Ile Ala Glu Leu Pro Val Val Ala Tyr Ser Leu Ala Tyr Pro Leu
150                 155                 160                 165

ggt gtg ctc atc gtt att ctc tcc atc gcc atc ttc agc tct gtg ttc   643
Gly Val Leu Ile Val Ile Leu Ser Ile Ala Ile Phe Ser Ser Val Phe
                170                 175                 180

aaa gtc gac cac aac aaa gaa gcc gaa gaa gcg ggc gtt gcg gtc cag   691
Lys Val Asp His Asn Lys Glu Ala Glu Glu Ala Gly Val Ala Val Gln
            185                 190                 195

gaa ctc aaa ggc cgt cgc atc cgc gtc acc gtc gct gat ctt cca gcc   739
Glu Leu Lys Gly Arg Arg Ile Arg Val Thr Val Ala Asp Leu Pro Ala
        200                 205                 210

ctg gag aac atc cca gag ctg ctc aac ctc cac gtc att gtg tcc cga   787
Leu Glu Asn Ile Pro Glu Leu Leu Asn Leu His Val Ile Val Ser Arg
    215                 220                 225

gtg gaa cga gac ggt gag caa ttc atc ccg ctt tat ggc gaa cac gca   835
Val Glu Arg Asp Gly Glu Gln Phe Ile Pro Leu Tyr Gly Glu His Ala
230                 235                 240                 245

cgc atc ggc gat gtc tta aca gtg gtg ggt gcc gat gaa gaa ctc aac   883
Arg Ile Gly Asp Val Leu Thr Val Val Gly Ala Asp Glu Glu Leu Asn
```

```
                  250                 255                 260

cgc gcg gaa aaa gcc atc ggt gaa ctc att gac ggc gac ccc tac agc   931
Arg Ala Glu Lys Ala Ile Gly Glu Leu Ile Asp Gly Asp Pro Tyr Ser
            265                 270                 275

aat gtg gaa ctt gat tac cga cgc atc ttc gtc tca aac aca gca gtc   979
Asn Val Glu Leu Asp Tyr Arg Arg Ile Phe Val Ser Asn Thr Ala Val
        280                 285                 290

gtg ggc act ccc cta tcc aag ctc cag cca ctg ttt aaa gac atg ctg   1027
Val Gly Thr Pro Leu Ser Lys Leu Gln Pro Leu Phe Lys Asp Met Leu
    295                 300                 305

atc acc cgc atc agg cgc ggc gac aca gat ttg gtg gcc tcc tcc gac   1075
Ile Thr Arg Ile Arg Arg Gly Asp Thr Asp Leu Val Ala Ser Ser Asp
310                 315                 320                 325

atg act ttg cag ctc ggt gac cgt gtc cgc gtt gtc gca cca gca gaa   1123
Met Thr Leu Gln Leu Gly Asp Arg Val Arg Val Val Ala Pro Ala Glu
                330                 335                 340

aaa ctc cgc gaa gca acc caa ttg ctc ggc gat tcc tac aag aaa ctc   1171
Lys Leu Arg Glu Ala Thr Gln Leu Leu Gly Asp Ser Tyr Lys Lys Leu
            345                 350                 355

tcc gat ttc aac ctg ctc cca ctc gct gcc ggc ctc atg atc ggt gtg   1219
Ser Asp Phe Asn Leu Leu Pro Leu Ala Ala Gly Leu Met Ile Gly Val
        360                 365                 370

ctt gtc ggc atg gtg gag ttc cca cta cca ggt gga agc tcc ctg aaa   1267
Leu Val Gly Met Val Glu Phe Pro Leu Pro Gly Gly Ser Ser Leu Lys
    375                 380                 385

ctg ggt aac gca ggt gga ccg cta gtt gtt gcg ctg ctg ctc ggc atg   1315
Leu Gly Asn Ala Gly Gly Pro Leu Val Val Ala Leu Leu Leu Gly Met
390                 395                 400                 405

atc aat cgc aca ggc aag ttc gtc tgg caa atc ccc tac gga gca aac   1363
Ile Asn Arg Thr Gly Lys Phe Val Trp Gln Ile Pro Tyr Gly Ala Asn
                410                 415                 420

ctt gcc ctt cgc caa ctg ggc atc aca cta ttt ttg gct gcc atc ggt   1411
Leu Ala Leu Arg Gln Leu Gly Ile Thr Leu Phe Leu Ala Ala Ile Gly
            425                 430                 435

acc tca gcg ggc gca gga ttt cga tca gcg atc agc gac ccc caa tca   1459
Thr Ser Ala Gly Ala Gly Phe Arg Ser Ala Ile Ser Asp Pro Gln Ser
        440                 445                 450

ctc acc atc atc ggc ttc ggt gcg ctg ctc act ttg ttc atc tcc atc   1507
Leu Thr Ile Ile Gly Phe Gly Ala Leu Leu Thr Leu Phe Ile Ser Ile
    455                 460                 465

acg gtg ctg ttc gtt ggc cac aaa ctg atg aaa atc ccc ttc ggt gaa   1555
Thr Val Leu Phe Val Gly His Lys Leu Met Lys Ile Pro Phe Gly Glu
470                 475                 480                 485

acc gct ggc atc ctc gcc ggt acg caa acc cac cct gct gtg ctg agt   1603
Thr Ala Gly Ile Leu Ala Gly Thr Gln Thr His Pro Ala Val Leu Ser
                490                 495                 500
```

```
tat gtg tca gat gcc tcc cgc aac gag ctc cct gcc atg ggt tat acc   1651
Tyr Val Ser Asp Ala Ser Arg Asn Glu Leu Pro Ala Met Gly Tyr Thr
            505                 510                 515

tct gtg tat ccg ctg gcg atg atc gca aag atc ctg gcc gcc caa acg   1699
Ser Val Tyr Pro Leu Ala Met Ile Ala Lys Ile Leu Ala Ala Gln Thr
        520                 525                 530

ttg ttg ttc cta ctt atc tagcattgac cccttaagcg cag                 1740
Leu Leu Phe Leu Leu Ile
    535
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<210> 2396
<211> 539
<212> PRT
<213> Corynebacterium glutamicum

<400> 2396

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Val Ser Phe Leu Val Glu Asn Gln Leu Leu Ala Leu Val Val Ile Met
  1               5                  10                  15

Thr Val Gly Leu Leu Leu Gly Arg Ile Lys Ile Phe Gly Phe Arg Leu
             20                  25                  30

Gly Val Ala Ala Val Leu Phe Val Gly Leu Ala Leu Ser Thr Ile Glu
         35                  40                  45

Pro Asp Ile Ser Val Pro Ser Leu Ile Tyr Val Val Gly Leu Ser Leu
     50                  55                  60

Phe Val Tyr Thr Ile Gly Leu Glu Ala Gly Pro Gly Phe Phe Thr Ser
 65                  70                  75                  80

Met Lys Thr Thr Gly Leu Arg Asn Asn Ala Leu Thr Leu Gly Ala Ile
                 85                  90                  95

Ile Ala Thr Thr Ala Leu Ala Trp Ala Leu Ile Thr Val Leu Asn Ile
            100                 105                 110

Asp Ala Ala Ser Gly Ala Gly Met Leu Thr Gly Ala Leu Thr Asn Thr
        115                 120                 125

Pro Ala Met Ala Ala Val Val Asp Ala Leu Pro Ser Leu Ile Asp Asp
    130                 135                 140

Thr Gly Gln Leu His Leu Ile Ala Glu Leu Pro Val Val Ala Tyr Ser
145                 150                 155                 160

Leu Ala Tyr Pro Leu Gly Val Leu Ile Val Ile Leu Ser Ile Ala Ile
                165                 170                 175

Phe Ser Ser Val Phe Lys Val Asp His Asn Lys Glu Ala Glu Glu Ala
            180                 185                 190

Gly Val Ala Val Gln Glu Leu Lys Gly Arg Arg Ile Arg Val Thr Val
        195                 200                 205

Ala Asp Leu Pro Ala Leu Glu Asn Ile Pro Glu Leu Leu Asn Leu His
    210                 215                 220
```

```
Val Ile Val Ser Arg Val Glu Arg Asp Gly Glu Gln Phe Ile Pro Leu
225                 230                 235                 240

Tyr Gly Glu His Ala Arg Ile Gly Asp Val Leu Thr Val Val Gly Ala
                245                 250                 255

Asp Glu Glu Leu Asn Arg Ala Glu Lys Ala Ile Gly Glu Leu Ile Asp
            260                 265                 270

Gly Asp Pro Tyr Ser Asn Val Glu Leu Asp Tyr Arg Arg Ile Phe Val
        275                 280                 285

Ser Asn Thr Ala Val Val Gly Thr Pro Leu Ser Lys Leu Gln Pro Leu
    290                 295                 300

Phe Lys Asp Met Leu Ile Thr Arg Ile Arg Arg Gly Asp Thr Asp Leu
305                 310                 315                 320

Val Ala Ser Ser Asp Met Thr Leu Gln Leu Gly Asp Arg Val Arg Val
                325                 330                 335

Val Ala Pro Ala Glu Lys Leu Arg Glu Ala Thr Gln Leu Leu Gly Asp
            340                 345                 350

Ser Tyr Lys Lys Leu Ser Asp Phe Asn Leu Leu Pro Leu Ala Ala Gly
        355                 360                 365

Leu Met Ile Gly Val Leu Val Gly Met Val Glu Phe Pro Leu Pro Gly
    370                 375                 380

Gly Ser Ser Leu Lys Leu Gly Asn Ala Gly Gly Pro Leu Val Val Ala
385                 390                 395                 400

Leu Leu Leu Gly Met Ile Asn Arg Thr Gly Lys Phe Val Trp Gln Ile
                405                 410                 415

Pro Tyr Gly Ala Asn Leu Ala Leu Arg Gln Leu Gly Ile Thr Leu Phe
            420                 425                 430

Leu Ala Ala Ile Gly Thr Ser Ala Gly Ala Gly Phe Arg Ser Ala Ile
        435                 440                 445

Ser Asp Pro Gln Ser Leu Thr Ile Ile Gly Phe Gly Ala Leu Leu Thr
    450                 455                 460

Leu Phe Ile Ser Ile Thr Val Leu Phe Val Gly His Lys Leu Met Lys
465                 470                 475                 480

Ile Pro Phe Gly Glu Thr Ala Gly Ile Leu Ala Gly Thr Gln Thr His
                485                 490                 495

Pro Ala Val Leu Ser Tyr Val Ser Asp Ala Ser Arg Asn Glu Leu Pro
            500                 505                 510

Ala Met Gly Tyr Thr Ser Val Tyr Pro Leu Ala Met Ile Ala Lys Ile
        515                 520                 525

Leu Ala Ala Gln Thr Leu Leu Phe Leu Leu Ile
    530                 535
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<210> 2397
<211> 1764
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1741)
<223> RXA01750

<400> 2397
tcgcccccga ggattgtgtt gcgaacagtc ctgaagatca tgtcagacct acattgagcc 60

aatgatcgac atgtggacga gggaaactcg accgaacaat atg tgt atc aac gac 115
Met Cys Ile Asn Asp
1 5

cct aaa ggc gag ttg ctg aag aaa aat tat gtt cgg atg tct aag cgc 163
Pro Lys Gly Glu Leu Leu Lys Lys Asn Tyr Val Arg Met Ser Lys Arg
10 15 20

ggt ttt cag gtt gtt cag ttt aac ctg att aac aac ctg aaa act gat 211
Gly Phe Gln Val Val Gln Phe Asn Leu Ile Asn Asn Leu Lys Thr Asp
25 30 35

att tat aac ccg ttg gga tta gca gcc gaa gca gct cgc gaa ggt aac 259
Ile Tyr Asn Pro Leu Gly Leu Ala Ala Glu Ala Ala Arg Glu Gly Asn
40 45 50

ggg atg aag tgc gca acc tat gtg gaa aat atc gca gag gtg ttc ttt 307
Gly Met Lys Cys Ala Thr Tyr Val Glu Asn Ile Ala Glu Val Phe Phe
55 60 65

ccg gtg gac ggt gcc gat gat ccg gta tgg ccg aat gcg gcc aac aat 355
Pro Val Asp Gly Ala Asp Asp Pro Val Trp Pro Asn Ala Ala Asn Asn
70 75 80 85

gcc ttc aag cgt gca gcc tat ggt ctt atc gac ttc tat ttg gaa gag 403
Ala Phe Lys Arg Ala Ala Tyr Gly Leu Ile Asp Phe Tyr Leu Glu Glu
90 95 100

gag cgc gag atg cgc aag cag gct gca gct gag aat tgg gat gcc aag 451
Glu Arg Glu Met Arg Lys Gln Ala Ala Ala Glu Asn Trp Asp Ala Lys
105 110 115

gtg ctt gat aca cgt att gat cag atg tgg ggt aag gtc acg ctc tac 499
Val Leu Asp Thr Arg Ile Asp Gln Met Trp Gly Lys Val Thr Leu Tyr
120 125 130

aac tgc tac cag ctc ttt gtg cag ctt tcg gca aag aag ctg aag aat 547
Asn Cys Tyr Gln Leu Phe Val Gln Leu Ser Ala Lys Lys Leu Lys Asn
135 140 145

ccc gtt gag cga ctc aat gaa cgt gca cgt gcc ggt gaa ttc ggt aac 595
Pro Val Glu Arg Leu Asn Glu Arg Ala Arg Ala Gly Glu Phe Gly Asn
150 155 160 165

tta gag act gat gaa aat gca gcc atg atg ttc cag gat gct gtg aca 643
Leu Glu Thr Asp Glu Asn Ala Ala Met Met Phe Gln Asp Ala Val Thr
170 175 180

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gag gcc gaa gag aac gaa atg ttt ctg tgg gag ggt gag aaa gaa aaa   691
Glu Ala Glu Glu Asn Glu Met Phe Leu Trp Glu Gly Glu Lys Glu Lys
            185                 190                 195

gac atg ctc acc ttg ttc ttt agt gcc aca gac ggt ctg cca aag tcc   739
Asp Met Leu Thr Leu Phe Phe Ser Ala Thr Asp Gly Leu Pro Lys Ser
        200                 205                 210

agt gtt cgt act ctg gtg ggc aac gca gat aag gcc ctg aaa gca atg   787
Ser Val Arg Thr Leu Val Gly Asn Ala Asp Lys Ala Leu Lys Ala Met
    215                 220                 225

ggt ggc gct gaa aaa atg atg gcg tcg gtc tac ggt atc gcg att aca   835
Gly Gly Ala Glu Lys Met Met Ala Ser Val Tyr Gly Ile Ala Ile Thr
230                 235                 240                 245

gcg atg tcc ttc ttt aca gac ccc aca att tca acg tta acc tca ggc   883
Ala Met Ser Phe Phe Thr Asp Pro Thr Ile Ser Thr Leu Thr Ser Gly
                250                 255                 260

aca cta agt cag aac gtt gac ttg gcc gga ttg tcg ttt cca cgg cgc   931
Thr Leu Ser Gln Asn Val Asp Leu Ala Gly Leu Ser Phe Pro Arg Arg
            265                 270                 275

atg ggt gtt cgt ttt gcg gcc ccc tat gtg aag cgc tac aac ctg gtt   979
Met Gly Val Arg Phe Ala Ala Pro Tyr Val Lys Arg Tyr Asn Leu Val
        280                 285                 290

gga tca cag gtg aaa tgg gat gcg tat agt gac gcc aag ttc acc aag   1027
Gly Ser Gln Val Lys Trp Asp Ala Tyr Ser Asp Ala Lys Phe Thr Lys
    295                 300                 305

ccg ttg ggt aag aat ttt gtt cat gat gac acg ctg tcg gtt gag ggt   1075
Pro Leu Gly Lys Asn Phe Val His Asp Asp Thr Leu Ser Val Glu Gly
310                 315                 320                 325

tgg gcg cgg ttc tat att aaa gac tcg ttc ccg agt aat act gcg tac   1123
Trp Ala Arg Phe Tyr Ile Lys Asp Ser Phe Pro Ser Asn Thr Ala Tyr
                330                 335                 340

ctg cgt ttg cgg att ctc aat ggt act tct ggc acg ttg atc aag act   1171
Leu Arg Leu Arg Ile Leu Asn Gly Thr Ser Gly Thr Leu Ile Lys Thr
            345                 350                 355

ctg tac ttc aag ttc acc aag ggc tac caa acg aac ctt aaa ggc cgt   1219
Leu Tyr Phe Lys Phe Thr Lys Gly Tyr Gln Thr Asn Leu Lys Gly Arg
        360                 365                 370

gcg ttt att act gat ccg gtg acc gat gag aag atc att aag aat ggt   1267
Ala Phe Ile Thr Asp Pro Val Thr Asp Glu Lys Ile Ile Lys Asn Gly
    375                 380                 385

ctg ctg atc gag ctg gtg aaa aac gat gct ggt gac ttt gtt cca ggt   1315
Leu Leu Ile Glu Leu Val Lys Asn Asp Ala Gly Asp Phe Val Pro Gly
390                 395                 400                 405

cat gtg cag ttt aag acg aag aaa ctg aat ctt gac caa ctc acg cag   1363
His Val Gln Phe Lys Thr Lys Lys Leu Asn Leu Asp Gln Leu Thr Gln
                410                 415                 420
```

```
gaa cag atc aat atg ccg ggt cat gac atg atc aag cag gtt gat gcg   1411
Glu Gln Ile Asn Met Pro Gly His Asp Met Ile Lys Gln Val Asp Ala
            425                 430                 435

atg gtt gat gcg gtg tcg gct ctg aat gtg cgg tat tcg gag aag cct   1459
Met Val Asp Ala Val Ser Ala Leu Asn Val Arg Tyr Ser Glu Lys Pro
        440                 445                 450

aag gca gtg ttc ttc gta acg cct ccg cat ctt atg aaa tat gcg aag   1507
Lys Ala Val Phe Phe Val Thr Pro Pro His Leu Met Lys Tyr Ala Lys
    455                 460                 465

ttg att ttg att ctc atc aaa cag ctt gtg gat ctg aac ttc gat tcc   1555
Leu Ile Leu Ile Leu Ile Lys Gln Leu Val Asp Leu Asn Phe Asp Ser
470                 475                 480                 485

tcg tat atg acg cgt gag aat cag aag ccg gat tat aag act cgt ttc   1603
Ser Tyr Met Thr Arg Glu Asn Gln Lys Pro Asp Tyr Lys Thr Arg Phe
                490                 495                 500

atg ttg gac gag ttg gga aac ctt cag agt gag ggt cat ggt att gcg   1651
Met Leu Asp Glu Leu Gly Asn Leu Gln Ser Glu Gly His Gly Ile Ala
            505                 510                 515

gga ttt gaa acc atg ctc tcg atc ggt ctg gga caa gaa caa caa ttt   1699
Gly Phe Glu Thr Met Leu Ser Ile Gly Leu Gly Gln Glu Gln Gln Phe
        520                 525                 530

agt gcg acc agt tgc gta gcg aaa aac tac gct ctt gca gct           1741
Ser Ala Thr Ser Cys Val Ala Lys Asn Tyr Ala Leu Ala Ala
    535                 540                 545

taaagttgca agaaactgtt tca                                        1764
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<210> 2398
<211> 547
<212> PRT
<213> Corynebacterium glutamicum

<400> 2398

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Met Cys Ile Asn Asp Pro Lys Gly Glu Leu Leu Lys Lys Asn Tyr Val
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Arg Met Ser Lys Arg Gly Phe Gln Val Val Gln Phe Asn Leu Ile Asn
             20                  25                  30

Asn Leu Lys Thr Asp Ile Tyr Asn Pro Leu Gly Leu Ala Ala Glu Ala
         35                  40                  45

Ala Arg Glu Gly Asn Gly Met Lys Cys Ala Thr Tyr Val Glu Asn Ile
     50                  55                  60

Ala Glu Val Phe Phe Pro Val Asp Gly Ala Asp Asp Pro Val Trp Pro
 65                  70                  75                  80

Asn Ala Ala Asn Asn Ala Phe Lys Arg Ala Ala Tyr Gly Leu Ile Asp
                 85                  90                  95

Phe Tyr Leu Glu Glu Glu Arg Glu Met Arg Lys Gln Ala Ala Ala Glu
            100                 105                 110
```

```
Asn Trp Asp Ala Lys Val Leu Asp Thr Arg Ile Asp Gln Met Trp Gly
        115                 120                 125

Lys Val Thr Leu Tyr Asn Cys Tyr Gln Leu Phe Val Gln Leu Ser Ala
    130                 135                 140

Lys Lys Leu Lys Asn Pro Val Glu Arg Leu Asn Glu Arg Ala Arg Ala
145                 150                 155                 160

Gly Glu Phe Gly Asn Leu Glu Thr Asp Glu Asn Ala Ala Met Met Phe
                165                 170                 175

Gln Asp Ala Val Thr Glu Ala Glu Glu Asn Glu Met Phe Leu Trp Glu
            180                 185                 190

Gly Glu Lys Glu Lys Asp Met Leu Thr Leu Phe Phe Ser Ala Thr Asp
        195                 200                 205

Gly Leu Pro Lys Ser Ser Val Arg Thr Leu Val Gly Asn Ala Asp Lys
    210                 215                 220

Ala Leu Lys Ala Met Gly Gly Ala Glu Lys Met Met Ala Ser Val Tyr
225                 230                 235                 240

Gly Ile Ala Ile Thr Ala Met Ser Phe Phe Thr Asp Pro Thr Ile Ser
                245                 250                 255

Thr Leu Thr Ser Gly Thr Leu Ser Gln Asn Val Asp Leu Ala Gly Leu
            260                 265                 270

Ser Phe Pro Arg Arg Met Gly Val Arg Phe Ala Ala Pro Tyr Val Lys
        275                 280                 285

Arg Tyr Asn Leu Val Gly Ser Gln Val Lys Trp Asp Ala Tyr Ser Asp
    290                 295                 300

Ala Lys Phe Thr Lys Pro Leu Gly Lys Asn Phe Val His Asp Asp Thr
305                 310                 315                 320

Leu Ser Val Glu Gly Trp Ala Arg Phe Tyr Ile Lys Asp Ser Phe Pro
                325                 330                 335

Ser Asn Thr Ala Tyr Leu Arg Leu Arg Ile Leu Asn Gly Thr Ser Gly
            340                 345                 350

Thr Leu Ile Lys Thr Leu Tyr Phe Lys Phe Thr Lys Gly Tyr Gln Thr
        355                 360                 365

Asn Leu Lys Gly Arg Ala Phe Ile Thr Asp Pro Val Thr Asp Glu Lys
    370                 375                 380

Ile Ile Lys Asn Gly Leu Leu Ile Glu Leu Val Lys Asn Asp Ala Gly
385                 390                 395                 400

Asp Phe Val Pro Gly His Val Gln Phe Lys Thr Lys Lys Leu Asn Leu
                405                 410                 415

Asp Gln Leu Thr Gln Glu Gln Ile Asn Met Pro Gly His Asp Met Ile
            420                 425                 430
```

```
Lys Gln Val Asp Ala Met Val Asp Ala Val Ser Ala Leu Asn Val Arg
        435                 440                 445

Tyr Ser Glu Lys Pro Lys Ala Val Phe Phe Val Thr Pro Pro His Leu
    450                 455                 460

Met Lys Tyr Ala Lys Leu Ile Leu Ile Leu Ile Lys Gln Leu Val Asp
465                 470                 475                 480

Leu Asn Phe Asp Ser Ser Tyr Met Thr Arg Glu Asn Gln Lys Pro Asp
                485                 490                 495

Tyr Lys Thr Arg Phe Met Leu Asp Glu Leu Gly Asn Leu Gln Ser Glu
            500                 505                 510

Gly His Gly Ile Ala Gly Phe Glu Thr Met Leu Ser Ile Gly Leu Gly
        515                 520                 525

Gln Glu Gln Gln Phe Ser Ala Thr Ser Cys Val Ala Lys Asn Tyr Ala
    530                 535                 540

Leu Ala Ala
545
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<210> 2399
<211> 652
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(652)
<223> RXA01752

<400> 2399

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gaaatgacgt gaccatcgat accaataccc aattgaaaga tcttgacctg gtcagccaag 60

ttggccgtca gatcgtggca gaacaacagg tggggaggtc atg atg gaa caa gat   115
                                              Met Met Glu Gln Asp
                                                1               5

ctc agc tac cgt gaa att ctt ccc ctc aac gcg agt gag gag aag aaa   163
Leu Ser Tyr Arg Glu Ile Leu Pro Leu Asn Ala Ser Glu Glu Lys Lys
                10                  15                  20

aag gct gca ctg att gat gcc att gaa ggg tta agg gtg cgc gat ccg   211
Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu Arg Val Arg Asp Pro
            25                  30                  35

cta ctc tct gcc tcg att gca ttt act aga ggg cag aaa gtc gcc ttc   259
Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly Gln Lys Val Ala Phe
        40                  45                  50

att gct gtg gtg gtg ggc ttt atc ttg atg ctc att ttt gct cgg caa   307
Ile Ala Val Val Val Gly Phe Ile Leu Met Leu Ile Phe Ala Arg Gln
    55                  60                  65

gca gca ctt att gga ctg tca gca acg tgt acg ttc atg tac ctc att   355
Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr Phe Met Tyr Leu Ile
70                  75                  80                  85
```

```
aca ttg ttg gac aga ttt atc atg ttt tcc aga ggt atc cgc gcg gaa   403
Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg Gly Ile Arg Ala Glu
                 90                  95                 100

tcc atc atc cag gta tcg gat gaa gat gcg ctg gct ttc cct gag gac   451
Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu Ala Phe Pro Glu Asp
            105                 110                 115

aag ctg aaa acc tac acg gtg ttg gtg ccc gcc tat ggc gaa cct gag   499
Lys Leu Lys Thr Tyr Thr Val Leu Val Pro Ala Tyr Gly Glu Pro Glu
        120                 125                 130

gtg att gcg cag ctg ctg gca tcc atg cac gct ttt gat tac ccc aag   547
Val Ile Ala Gln Leu Leu Ala Ser Met His Ala Phe Asp Tyr Pro Lys
    135                 140                 145

cat ctt ctg cag gta ttg ctc atg ttg gag gaa gat gat ctg ccc acg   595
His Leu Leu Gln Val Leu Leu Met Leu Glu Glu Asp Asp Leu Pro Thr
150                 155                 160                 165

atc gcc gcg gca gag gca gcg gga gtg gat cag gtg gca acg atc att   643
Ile Ala Ala Ala Glu Ala Ala Gly Val Asp Gln Val Ala Thr Ile Ile
                170                 175                 180

aag gtg ccg                                                      652
Lys Val Pro
```

<210> 2400
<211> 184
<212> PRT
<213> Corynebacterium glutamicum

<400> 2400

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Met Met Glu Gln Asp Leu Ser Tyr Arg Glu Ile Leu Pro Leu Asn Ala
  1               5                  10                  15

Ser Glu Glu Lys Lys Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu
             20                  25                  30

Arg Val Arg Asp Pro Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly
         35                  40                  45

Gln Lys Val Ala Phe Ile Ala Val Val Val Gly Phe Ile Leu Met Leu
     50                  55                  60

Ile Phe Ala Arg Gln Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr
 65                  70                  75                  80

Phe Met Tyr Leu Ile Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg
                 85                  90                  95

Gly Ile Arg Ala Glu Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu
            100                 105                 110

Ala Phe Pro Glu Asp Lys Leu Lys Thr Tyr Thr Val Leu Val Pro Ala
        115                 120                 125

Tyr Gly Glu Pro Glu Val Ile Ala Gln Leu Leu Ala Ser Met His Ala
```

```
    130                 135                 140

Phe Asp Tyr Pro Lys His Leu Leu Gln Val Leu Leu Met Leu Glu Glu
145                 150                 155                 160

Asp Asp Leu Pro Thr Ile Ala Ala Ala Glu Ala Ala Gly Val Asp Gln
                165                 170                 175

Val Ala Thr Ile Ile Lys Val Pro
            180
```

<210> 2401
<211> 1662
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1639)
<223> RXA01753

<400> 2401

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ctgattgtcg cagccgtggt gtcagtgtcc aggcgttcgc aaaaaggata caaatgattt 60

cttctttacc cagtagaacg caggggagga ggttgggtcc atg agt aac ccg tcg   115
                                            Met Ser Asn Pro Ser
                                              1               5

cta gaa cct cta gaa ccg atc gag ctt tct gac ggt act gaa att gaa   163
Leu Glu Pro Leu Glu Pro Ile Glu Leu Ser Asp Gly Thr Glu Ile Glu
                10                  15                  20

gtt tca gac gtt gat cca gaa ccg caa gct ggc aat gcg cag atg gaa   211
Val Ser Asp Val Asp Pro Glu Pro Gln Ala Gly Asn Ala Gln Met Glu
            25                  30                  35

gta ccc agc tta cgg aca tat gtt ttt cgc gga atc att gcc att gcc   259
Val Pro Ser Leu Arg Thr Tyr Val Phe Arg Gly Ile Ile Ala Ile Ala
        40                  45                  50

tgt ttg atc att ggt ttt tat gag agc ttt gtg ctg atg tgg caa aac   307
Cys Leu Ile Ile Gly Phe Tyr Glu Ser Phe Val Leu Met Trp Gln Asn
    55                  60                  65

ctc cga atc ggc gtg gcc aac tac tca cta ctt gtg gtg ctc atg gcg   355
Leu Arg Ile Gly Val Ala Asn Tyr Ser Leu Leu Val Val Leu Met Ala
70                  75                  80                  85

atc gtg ttg ttt atc gga ctg gac cgc aag cgt gct cgt gca ttg aac   403
Ile Val Leu Phe Ile Gly Leu Asp Arg Lys Arg Ala Arg Ala Leu Asn
                90                  95                  100

att cac gac cgc gaa gtc gac tac atc att ggt ggc att gtc gta ctg   451
Ile His Asp Arg Glu Val Asp Tyr Ile Ile Gly Gly Ile Val Val Leu
            105                 110                 115

ata gcc atc acg att aag agc cag ctt ctg cca cgt ttt gtg gac tgg   499
Ile Ala Ile Thr Ile Lys Ser Gln Leu Leu Pro Arg Phe Val Asp Trp
        120                 125                 130
```

```
gaa act ctg ctg cgc ttg gat atg ttc gca ctg tta ttc ttt gcg ttt   547
Glu Thr Leu Leu Arg Leu Asp Met Phe Ala Leu Leu Phe Phe Ala Phe
    135                 140                 145

ggt att tcc ggc ctg gtg ttt ggc atg cgc tct acc ttt tct ttt gca   595
Gly Ile Ser Gly Leu Val Phe Gly Met Arg Ser Thr Phe Ser Phe Ala
150                 155                 160                 165

ccc ggc tgg att ttg ctg ttt ggc tac aac gcg gtg gca cac ctg atc   643
Pro Gly Trp Ile Leu Leu Phe Gly Tyr Asn Ala Val Ala His Leu Ile
                170                 175                 180

atc tcg gtg att ttc ggt ggt ggc ttt tgg ggc ccg gtg atg gca aac   691
Ile Ser Val Ile Phe Gly Gly Gly Phe Trp Gly Pro Val Met Ala Asn
            185                 190                 195

atc att gga ctg tct ctt gcg gtg ttg gtg tcc tcc aac agg gac ctg   739
Ile Ile Gly Leu Ser Leu Ala Val Leu Val Ser Ser Asn Arg Asp Leu
        200                 205                 210

gtt cag gcc acc tat ttg gca ctg atg acg gtg ttg ttt ggc gtc att   787
Val Gln Ala Thr Tyr Leu Ala Leu Met Thr Val Leu Phe Gly Val Ile
    215                 220                 225

att gcc atc atc gtg tgg gcg ctg acc gat ggc agt aag ttc ctc acc   835
Ile Ala Ile Ile Val Trp Ala Leu Thr Asp Gly Ser Lys Phe Leu Thr
230                 235                 240                 245

ttg gtc cca gca gtg ctg gca acc atc act gtg gtg ttg gtg tct tcg   883
Leu Val Pro Ala Val Leu Ala Thr Ile Thr Val Val Leu Val Ser Ser
                250                 255                 260

cgt tgg agg ctt ggt cag tgg aaa att cgt cgt aga caa ccc acg gtg   931
Arg Trp Arg Leu Gly Gln Trp Lys Ile Arg Arg Arg Gln Pro Thr Val
            265                 270                 275

gaa aaa gcc gga ccc gcg ctt atc gcg gtc gtg gtt gcg aca gca ctc   979
Glu Lys Ala Gly Pro Ala Leu Ile Ala Val Val Val Ala Thr Ala Leu
        280                 285                 290

ttg gcg tgg att cct act cct tat gtg gag cgc gtc aac aac ctc ccc   1027
Leu Ala Trp Ile Pro Thr Pro Tyr Val Glu Arg Val Asn Asn Leu Pro
    295                 300                 305

ggg ctt caa atg ctg gca aag cct gcc cca ggt gtt atc gca cct att   1075
Gly Leu Gln Met Leu Ala Lys Pro Ala Pro Gly Val Ile Ala Pro Ile
310                 315                 320                 325

ggt tgg cac atc gac gat gtg cag tat tac aac tgg gct tcg cgc tac   1123
Gly Trp His Ile Asp Asp Val Gln Tyr Tyr Asn Trp Ala Ser Arg Tyr
                330                 335                 340

ttc ggc ccc ggt tcc tct ctg ctt agg cag acg atg acg gca gat cat   1171
Phe Gly Pro Gly Ser Ser Leu Leu Arg Gln Thr Met Thr Ala Asp His
            345                 350                 355

tac aac gag gcg tgg gat cca gat gga ctc gac cga act gtt gtg gtg   1219
Tyr Asn Glu Ala Trp Asp Pro Asp Gly Leu Asp Arg Thr Val Val Val
        360                 365                 370

gat acc ctc caa tcg gcg gaa cgg ttc cag cag cgt gcc ttt ggt gac   1267
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```
Asp Thr Leu Gln Ser Ala Glu Arg Phe Gln Gln Arg Ala Phe Gly Asp
    375                 380                 385

gag acg ctg tat tcc act ctg aga ggt cga aag tca gat acc gtc cag   1315
Glu Thr Leu Tyr Ser Thr Leu Arg Gly Arg Lys Ser Asp Thr Val Gln
390                 395                 400                 405

gtg gat ctg gga tac ggc gtg gac gga cgc gcc tac acg gtg ctc gat   1363
Val Asp Leu Gly Tyr Gly Val Asp Gly Arg Ala Tyr Thr Val Leu Asp
                410                 415                 420

gaa act gac ttc ttg acg tac acc aag ctg gtt ttt gaa tgg cag acc   1411
Glu Thr Asp Phe Leu Thr Tyr Thr Lys Leu Val Phe Glu Trp Gln Thr
            425                 430                 435

acc aac aac acc gtg gag aag atc tcc gtc atc gcg gtg gat gat cac   1459
Thr Asn Asn Thr Val Glu Lys Ile Ser Val Ile Ala Val Asp Asp His
        440                 445                 450

cgc gca gaa gcg aag ttc ccg gag ctt gca cca tcg gtt acc aga atg   1507
Arg Ala Glu Ala Lys Phe Pro Glu Leu Ala Pro Ser Val Thr Arg Met
    455                 460                 465

ttt atc cag gtg gct acc att ttg ttc cgt gga aat gac gtg acc atc   1555
Phe Ile Gln Val Ala Thr Ile Leu Phe Arg Gly Asn Asp Val Thr Ile
470                 475                 480                 485

gat acc aat acc caa ttg aaa gat ctt gac ctg gtc agc caa gtt ggc   1603
Asp Thr Asn Thr Gln Leu Lys Asp Leu Asp Leu Val Ser Gln Val Gly
                490                 495                 500

cgt cag atc gtg gca gaa caa cag gtg ggg agg tca tgatggaaca        1649
Arg Gln Ile Val Ala Glu Gln Gln Val Gly Arg Ser
            505                 510

agatctcagc tac                                                   1662


<210> 2402
<211> 513
<212> PRT
<213> Corynebacterium glutamicum

<400> 2402
Met Ser Asn Pro Ser Leu Glu Pro Leu Glu Pro Ile Glu Leu Ser Asp
  1               5                  10                  15

Gly Thr Glu Ile Glu Val Ser Asp Val Asp Pro Glu Pro Gln Ala Gly
             20                  25                  30

Asn Ala Gln Met Glu Val Pro Ser Leu Arg Thr Tyr Val Phe Arg Gly
         35                  40                  45

Ile Ile Ala Ile Ala Cys Leu Ile Ile Gly Phe Tyr Glu Ser Phe Val
     50                  55                  60

Leu Met Trp Gln Asn Leu Arg Ile Gly Val Ala Asn Tyr Ser Leu Leu
 65                  70                  75                  80

Val Val Leu Met Ala Ile Val Leu Phe Ile Gly Leu Asp Arg Lys Arg
                 85                  90                  95
```

```
Ala Arg Ala Leu Asn Ile His Asp Arg Glu Val Asp Tyr Ile Ile Gly
            100                 105                 110

Gly Ile Val Val Leu Ile Ala Ile Thr Ile Lys Ser Gln Leu Leu Pro
        115                 120                 125

Arg Phe Val Asp Trp Glu Thr Leu Leu Arg Leu Asp Met Phe Ala Leu
    130                 135                 140

Leu Phe Phe Ala Phe Gly Ile Ser Gly Leu Val Phe Gly Met Arg Ser
145                 150                 155                 160

Thr Phe Ser Phe Ala Pro Gly Trp Ile Leu Leu Phe Gly Tyr Asn Ala
                165                 170                 175

Val Ala His Leu Ile Ile Ser Val Ile Phe Gly Gly Gly Phe Trp Gly
            180                 185                 190

Pro Val Met Ala Asn Ile Ile Gly Leu Ser Leu Ala Val Leu Val Ser
        195                 200                 205

Ser Asn Arg Asp Leu Val Gln Ala Thr Tyr Leu Ala Leu Met Thr Val
    210                 215                 220

Leu Phe Gly Val Ile Ile Ala Ile Ile Val Trp Ala Leu Thr Asp Gly
225                 230                 235                 240

Ser Lys Phe Leu Thr Leu Val Pro Ala Val Leu Ala Thr Ile Thr Val
                245                 250                 255

Val Leu Val Ser Ser Arg Trp Arg Leu Gly Gln Trp Lys Ile Arg Arg
            260                 265                 270

Arg Gln Pro Thr Val Glu Lys Ala Gly Pro Ala Leu Ile Ala Val Val
        275                 280                 285

Val Ala Thr Ala Leu Leu Ala Trp Ile Pro Thr Pro Tyr Val Glu Arg
    290                 295                 300

Val Asn Asn Leu Pro Gly Leu Gln Met Leu Ala Lys Pro Ala Pro Gly
305                 310                 315                 320

Val Ile Ala Pro Ile Gly Trp His Ile Asp Asp Val Gln Tyr Tyr Asn
                325                 330                 335

Trp Ala Ser Arg Tyr Phe Gly Pro Gly Ser Ser Leu Leu Arg Gln Thr
            340                 345                 350

Met Thr Ala Asp His Tyr Asn Glu Ala Trp Asp Pro Asp Gly Leu Asp
        355                 360                 365

Arg Thr Val Val Val Asp Thr Leu Gln Ser Ala Glu Arg Phe Gln Gln
    370                 375                 380

Arg Ala Phe Gly Asp Glu Thr Leu Tyr Ser Thr Leu Arg Gly Arg Lys
385                 390                 395                 400

Ser Asp Thr Val Gln Val Asp Leu Gly Tyr Gly Val Asp Gly Arg Ala
                405                 410                 415
```

```
Tyr Thr Val Leu Asp Glu Thr Asp Phe Leu Thr Tyr Thr Lys Leu Val
            420                 425                 430

Phe Glu Trp Gln Thr Thr Asn Asn Thr Val Glu Lys Ile Ser Val Ile
        435                 440                 445

Ala Val Asp Asp His Arg Ala Glu Ala Lys Phe Pro Glu Leu Ala Pro
    450                 455                 460

Ser Val Thr Arg Met Phe Ile Gln Val Ala Thr Ile Leu Phe Arg Gly
465                 470                 475                 480

Asn Asp Val Thr Ile Asp Thr Asn Thr Gln Leu Lys Asp Leu Asp Leu
                485                 490                 495

Val Ser Gln Val Gly Arg Gln Ile Val Ala Glu Gln Gln Val Gly Arg
            500                 505                 510

Ser
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<210> 2403
<211> 405
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(382)
<223> RXA01760

<400> 2403

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acctactcaa actttcctct gcgccataac gtgaagtgag tgccggggca gtcccggcag 60

cacccaaaag cgcatttttg atacgaaagt gagtcatacg atg gca gca ttt cta   115
                                               Met Ala Ala Phe Leu
                                                 1               5

gag atc acc ttg aaa atc aat gac gaa ggc cgc cca tca gca gct ggc   163
Glu Ile Thr Leu Lys Ile Asn Asp Glu Gly Arg Pro Ser Ala Ala Gly
                10                  15                  20

gtc tac cag gaa tac aag caa cca ttc ctc agc tca att gct ggc gct   211
Val Tyr Gln Glu Tyr Lys Gln Pro Phe Leu Ser Ser Ile Ala Gly Ala
            25                  30                  35

aca agc aaa gaa ctc ctc atc cga gaa gaa gac gtg cag gtg ctc cac   259
Thr Ser Lys Glu Leu Leu Ile Arg Glu Glu Asp Val Gln Val Leu His
        40                  45                  50

ggc tgt gac acc gta gct aat gct gaa gat tat ctt gtc agc gaa ctg   307
Gly Cys Asp Thr Val Ala Asn Ala Glu Asp Tyr Leu Val Ser Glu Leu
    55                  60                  65

ttc acg gcc gat gtt gtc ggt ggt cta gct cca cta ttg cag gct gat   355
Phe Thr Ala Asp Val Val Gly Gly Leu Ala Pro Leu Leu Gln Ala Asp
70                  75                  80                  85

cca gag att cgt att tac cag gtc gcg taactgctgt ggcaggctca         402
Pro Glu Ile Arg Ile Tyr Gln Val Ala
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90

tcg 405

<210> 2404
<211> 94
<212> PRT
<213> Corynebacterium glutamicum

<400> 2404
Met Ala Ala Phe Leu Glu Ile Thr Leu Lys Ile Asn Asp Glu Gly Arg
1 5 10 15

Pro Ser Ala Ala Gly Val Tyr Gln Glu Tyr Lys Gln Pro Phe Leu Ser
20 25 30

Ser Ile Ala Gly Ala Thr Ser Lys Glu Leu Leu Ile Arg Glu Glu Asp
35 40 45

Val Gln Val Leu His Gly Cys Asp Thr Val Ala Asn Ala Glu Asp Tyr
50 55 60

Leu Val Ser Glu Leu Phe Thr Ala Asp Val Val Gly Gly Leu Ala Pro
65 70 75 80

Leu Leu Gln Ala Asp Pro Glu Ile Arg Ile Tyr Gln Val Ala
85 90

<210> 2405
<211> 501
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(478)
<223> RXA01768

<400> 2405
gacaacgaac acaacaccca gatcctgcac tggtccggcg ttaatcgcta cctcatgcag 60

gcactctccc gtactcattt ctagaaaggt ttttcccgtc atg tct gaa tct act 115
Met Ser Glu Ser Thr
1 5

tct tct gct aac tcc acc acc atc ctc aac gac acc ttc aac ccg aag 163
Ser Ser Ala Asn Ser Thr Thr Ile Leu Asn Asp Thr Phe Asn Pro Lys
10 15 20

cct ggc gta cct tat gca cgc gtc gat aat ctc gaa ttt gcc aca cgt 211
Pro Gly Val Pro Tyr Ala Arg Val Asp Asn Leu Glu Phe Ala Thr Arg
25 30 35

gac gaa ttc cgc gct tgg gct acc gca gag atg gag gcc ggt aac gtt 259
Asp Glu Phe Arg Ala Trp Ala Thr Ala Glu Met Glu Ala Gly Asn Val
40 45 50

atc tct gca acc atc gcc aat gcc cca cgc gaa gac cgc atc aag tct 307
Ile Ser Ala Thr Ile Ala Asn Ala Pro Arg Glu Asp Arg Ile Lys Ser

```
     55                  60                  65

ttt gtc atg gat ctt gtt cga gac ggt att gac gac gct gct gag gaa   355
Phe Val Met Asp Leu Val Arg Asp Gly Ile Asp Asp Ala Ala Glu Glu
 70                  75                  80                  85

atc gtc tca cgc att gat agc ggt gac ttc act atg aag gaa gct ctc   403
Ile Val Ser Arg Ile Asp Ser Gly Asp Phe Thr Met Lys Glu Ala Leu
                 90                  95                 100

acc gcg atc gcg gca tca atc aac gac ctc gat gct gac gat gta gtc   451
Thr Ala Ile Ala Ala Ser Ile Asn Asp Leu Asp Ala Asp Asp Val Val
            105                 110                 115

agc gac atc gtt gaa aac cac ttc aac tagtcaacac accagccctc         498
Ser Asp Ile Val Glu Asn His Phe Asn
        120                 125

cac                                                               501


<210> 2406
<211> 126
<212> PRT
<213> Corynebacterium glutamicum

<400> 2406
Met Ser Glu Ser Thr Ser Ser Ala Asn Ser Thr Thr Ile Leu Asn Asp
  1               5                  10                  15

Thr Phe Asn Pro Lys Pro Gly Val Pro Tyr Ala Arg Val Asp Asn Leu
             20                  25                  30

Glu Phe Ala Thr Arg Asp Glu Phe Arg Ala Trp Ala Thr Ala Glu Met
         35                  40                  45

Glu Ala Gly Asn Val Ile Ser Ala Thr Ile Ala Asn Ala Pro Arg Glu
     50                  55                  60

Asp Arg Ile Lys Ser Phe Val Met Asp Leu Val Arg Asp Gly Ile Asp
 65                  70                  75                  80

Asp Ala Ala Glu Glu Ile Val Ser Arg Ile Asp Ser Gly Asp Phe Thr
                 85                  90                  95

Met Lys Glu Ala Leu Thr Ala Ile Ala Ala Ser Ile Asn Asp Leu Asp
            100                 105                 110

Ala Asp Asp Val Val Ser Asp Ile Val Glu Asn His Phe Asn
        115                 120                 125


<210> 2407
<211> 3888
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(3865)
<223> RXA01770
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<400> 2407
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acacctccac tttttctact tttaagaaag ccacattctc atg cca att atc att 115
Met Pro Ile Ile Ile
1 5

gat aac ctc aat tct gac gac gac tcc acc atc ggc act gcc acc gaa 163
Asp Asn Leu Asn Ser Asp Asp Asp Ser Thr Ile Gly Thr Ala Thr Glu
10 15 20

tac aac cct gac act gac gcc gat tta ctt gat gct att aac gct gat 211
Tyr Asn Pro Asp Thr Asp Ala Asp Leu Leu Asp Ala Ile Asn Ala Asp
25 30 35

gct gac ctt gat ggc gac gcc acc atc agc act aac gcg aca gaa gaa 259
Ala Asp Leu Asp Gly Asp Ala Thr Ile Ser Thr Asn Ala Thr Glu Glu
40 45 50

ggt gta gac gca gca gct gaa aaa cct aag aaa aag cgt aaa gcc cct 307
Gly Val Asp Ala Ala Ala Glu Lys Pro Lys Lys Lys Arg Lys Ala Pro
55 60 65

gct ctg aag cct aaa gga ctc acg gca aag ttc ttc cac cgt gat ctt 355
Ala Leu Lys Pro Lys Gly Leu Thr Ala Lys Phe Phe His Arg Asp Leu
70 75 80 85

act ggc gta ggt ggt agg acc ggt cgc ctc aac aag aac gta cac ccg 403
Thr Gly Val Gly Gly Arg Thr Gly Arg Leu Asn Lys Asn Val His Pro
90 95 100

acc aac cca gat ctg tcc tac cag cca gtc tct gat gtc tac acc cca 451
Thr Asn Pro Asp Leu Ser Tyr Gln Pro Val Ser Asp Val Tyr Thr Pro
105 110 115

caa tca gca gat cac aag ggt att aag acc cgc tac atc ctt acc cat 499
Gln Ser Ala Asp His Lys Gly Ile Lys Thr Arg Tyr Ile Leu Thr His
120 125 130

cca acc ccc gct gtt gtt ctc agt gag tcc atc agc aac gcg ttt cat 547
Pro Thr Pro Ala Val Val Leu Ser Glu Ser Ile Ser Asn Ala Phe His
135 140 145

gtc tct acc ctg cgt cgc aac aat aat gtc aac aac tct gat tcg gaa 595
Val Ser Thr Leu Arg Arg Asn Asn Asn Val Asn Asn Ser Asp Ser Glu
150 155 160 165

ttg gct gcc tgg ccg tac ctc tac caa ctc gat att ccg cag ctg gac 643
Leu Ala Ala Trp Pro Tyr Leu Tyr Gln Leu Asp Ile Pro Gln Leu Asp
170 175 180

cag atg att aat gtc gct gac atc tgt gat tac cat ttc cac gga tat 691
Gln Met Ile Asn Val Ala Asp Ile Cys Asp Tyr His Phe His Gly Tyr
185 190 195

aac ctg tgg gtg gat ttt acc ccg cag act atc gct cta cga tcc ggt 739
Asn Leu Trp Val Asp Phe Thr Pro Gln Thr Ile Ala Leu Arg Ser Gly
200 205 210

aag acg gta ctc gat gac ggt acc acc gcc tct gat aac acc act cat 787

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Lys Thr Val Leu Asp Asp Gly Thr Thr Ala Ser Asp Asn Thr Thr His
    215                 220                 225

gtc tat tac cgc gtc acc gtt cac gtt att gcc ggt caa gat cat gga   835
Val Tyr Tyr Arg Val Thr Val His Val Ile Ala Gly Gln Asp His Gly
230                 235                 240                 245

tct act ctg ctt gat gac cag ggc aac cag gtg ctt gat agg gat gat   883
Ser Thr Leu Leu Asp Asp Gln Gly Asn Gln Val Leu Asp Arg Asp Asp
                250                 255                 260

aat cct att tct acc cca agt atc aag cgt att ggc gct gtc act gat   931
Asn Pro Ile Ser Thr Pro Ser Ile Lys Arg Ile Gly Ala Val Thr Asp
            265                 270                 275

ctt ttc gat cac aat cct ttt ggc ttc gct agt gta aac tct ttc gca   979
Leu Phe Asp His Asn Pro Phe Gly Phe Ala Ser Val Asn Ser Phe Ala
        280                 285                 290

ttt gtc gat ttc tca tgg gac cca gcc acc acc ttg gtc gat atg ctc   1027
Phe Val Asp Phe Ser Trp Asp Pro Ala Thr Thr Leu Val Asp Met Leu
    295                 300                 305

aac aac ctt gat tca tat ctc tct aat cac atc aat att gcc agc tcc   1075
Asn Asn Leu Asp Ser Tyr Leu Ser Asn His Ile Asn Ile Ala Ser Ser
310                 315                 320                 325

cca acc ccc att gcc ctc gat atg gtt gtg ctc aat gaa tgg tct gaa   1123
Pro Thr Pro Ile Ala Leu Asp Met Val Val Leu Asn Glu Trp Ser Glu
                330                 335                 340

aag tcc tat cag ctg tgc gaa cgc gtt gtt gca cag gca aag ctc atc   1171
Lys Ser Tyr Gln Leu Cys Glu Arg Val Val Ala Gln Ala Lys Leu Ile
            345                 350                 355

aac agc aac aag atc acc gca cat gtg agt gat gtc atc aag caa aat   1219
Asn Ser Asn Lys Ile Thr Ala His Val Ser Asp Val Ile Lys Gln Asn
        360                 365                 370

gcc cac aat atc ttg tgg ttt acc gaa cag atg aac cct ggc acc acc   1267
Ala His Asn Ile Leu Trp Phe Thr Glu Gln Met Asn Pro Gly Thr Thr
    375                 380                 385

aac ctc agc gag gta cct atc tcc aag aag tct atg ctg ccg atg tct   1315
Asn Leu Ser Glu Val Pro Ile Ser Lys Lys Ser Met Leu Pro Met Ser
390                 395                 400                 405

cgc cag cta cgt att ttg gag cac tac gat gta cca ctg acc gcg tac   1363
Arg Gln Leu Arg Ile Leu Glu His Tyr Asp Val Pro Leu Thr Ala Tyr
                410                 415                 420

tct gct ctt ttc tgg act gtc agc gcc att aag aat gaa tct atg gtg   1411
Ser Ala Leu Phe Trp Thr Val Ser Ala Ile Lys Asn Glu Ser Met Val
            425                 430                 435

cag tac ctt gtg cga cag aat atg cag ctc acc ttg agc tca aat ctg   1459
Gln Tyr Leu Val Arg Gln Asn Met Gln Leu Thr Leu Ser Ser Asn Leu
        440                 445                 450

gat gca ctc aac tcc att gtc tcc cag ctc cct gta cca gat aag gac   1507
Asp Ala Leu Asn Ser Ile Val Ser Gln Leu Pro Val Pro Asp Lys Asp
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    455                 460                 465

gtt gtg gct gct tct ggc tac cag att cag cca cac ttc tcc acg cag   1555
Val Val Ala Ala Ser Gly Tyr Gln Ile Gln Pro His Phe Ser Thr Gln
470                 475                 480                 485

cag cgt gaa gca atc acc act gat aat cct ctc gcg att att cag gcc   1603
Gln Arg Glu Ala Ile Thr Thr Asp Asn Pro Leu Ala Ile Ile Gln Ala
                490                 495                 500

ggt gct ggt acc ggt aaa tcc acc gtg att ctg gaa cgc att gag tac   1651
Gly Ala Gly Thr Gly Lys Ser Thr Val Ile Leu Glu Arg Ile Glu Tyr
            505                 510                 515

ttg tgc gct gca ggc acc aac cct gaa gag att gct gtg ctg tct ttt   1699
Leu Cys Ala Ala Gly Thr Asn Pro Glu Glu Ile Ala Val Leu Ser Phe
        520                 525                 530

act aat gct gcc gcc gat aac atc aca gca aaa aat gac aag gtg acc   1747
Thr Asn Ala Ala Ala Asp Asn Ile Thr Ala Lys Asn Asp Lys Val Thr
    535                 540                 545

tct atg acc atc tcc aag atg gtt cat gag att tac gca cac aat ttc   1795
Ser Met Thr Ile Ser Lys Met Val His Glu Ile Tyr Ala His Asn Phe
550                 555                 560                 565

cct gat cat gag atc tcc acc atc gac acc att atc aat acg ctt gat   1843
Pro Asp His Glu Ile Ser Thr Ile Asp Thr Ile Ile Asn Thr Leu Asp
                570                 575                 580

att gaa tac ggc gat caa atg gtg acc tcc gat tac atg att cag ctc   1891
Ile Glu Tyr Gly Asp Gln Met Val Thr Ser Asp Tyr Met Ile Gln Leu
            585                 590                 595

cgt gac ctg ctc tat aag gtc atg acg cag ggt ggc aac gcc aac ctg   1939
Arg Asp Leu Leu Tyr Lys Val Met Thr Gln Gly Gly Asn Ala Asn Leu
        600                 605                 610

aca gcg ttg agc atc ttc atg gaa tcc cat atc gag gcg ttc atc tcg   1987
Thr Ala Leu Ser Ile Phe Met Glu Ser His Ile Glu Ala Phe Ile Ser
    615                 620                 625

gtg ttg gat cag atc aag cag act tct ctt gag ctg gaa atc atc atc   2035
Val Leu Asp Gln Ile Lys Gln Thr Ser Leu Glu Leu Glu Ile Ile Ile
630                 635                 640                 645

tgc tac ctg ctc ttg gat aag ctg atc gag cct cat gca tcg ccg aag   2083
Cys Tyr Leu Leu Leu Asp Lys Leu Ile Glu Pro His Ala Ser Pro Lys
                650                 655                 660

tac ctc att att gat gag gtg cag gac aac tcg gtc ttc gag ttc gtc   2131
Tyr Leu Ile Ile Asp Glu Val Gln Asp Asn Ser Val Phe Glu Phe Val
            665                 670                 675

ttt gca ctt cgt ttt gcg gca aag cac aat acg agt ctg tac ttg gtg   2179
Phe Ala Leu Arg Phe Ala Ala Lys His Asn Thr Ser Leu Tyr Leu Val
        680                 685                 690

ggt gac tcg tca cag acc ttg tat gag ttc cgt tct gct aac cct aag   2227
Gly Asp Ser Ser Gln Thr Leu Tyr Glu Phe Arg Ser Ala Asn Pro Lys
    695                 700                 705
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gct ctg aac tcc ctg gaa gca tct ggt gtt ttc ggt acc tac cgt ttg   2275
Ala Leu Asn Ser Leu Glu Ala Ser Gly Val Phe Gly Thr Tyr Arg Leu
710                 715                 720                 725

acc acc aat tac cgt tcc aac cag gaa att ctt gac ttc gct aat atc   2323
Thr Thr Asn Tyr Arg Ser Asn Gln Glu Ile Leu Asp Phe Ala Asn Ile
                730                 735                 740

cac ctc tcg gat att gaa gct aac cag ttc gca ggt att cag ctc tac   2371
His Leu Ser Asp Ile Glu Ala Asn Gln Phe Ala Gly Ile Gln Leu Tyr
            745                 750                 755

gcc aac tct ttt gat gca cct act gcg gac agc ttc aaa gaa aag gtt   2419
Ala Asn Ser Phe Asp Ala Pro Thr Ala Asp Ser Phe Lys Glu Lys Val
        760                 765                 770

gaa ctg gac atg cac cat gtg tct aag cag tct gag ttt acc gac agc   2467
Glu Leu Asp Met His His Val Ser Lys Gln Ser Glu Phe Thr Asp Ser
    775                 780                 785

att cct tat ttc atg gag tcc aat aaa gct cgc ttt gat gct gcg atc   2515
Ile Pro Tyr Phe Met Glu Ser Asn Lys Ala Arg Phe Asp Ala Ala Ile
790                 795                 800                 805

ttg aac aat gag caa acc att gtg ctt gct cat tct ggt cgt gaa att   2563
Leu Asn Asn Glu Gln Thr Ile Val Leu Ala His Ser Gly Arg Glu Ile
                810                 815                 820

cgt gca gcg cag caa gcg cta gcc gag atg tac ccc agc atc acg gtg   2611
Arg Ala Ala Gln Gln Ala Leu Ala Glu Met Tyr Pro Ser Ile Thr Val
            825                 830                 835

cgt aac ttg cag tcc gat aag ggt ttc aac aac acg gta ttt tcg acc   2659
Arg Asn Leu Gln Ser Asp Lys Gly Phe Asn Asn Thr Val Phe Ser Thr
        840                 845                 850

ttt att aag gat ttc tgg ttt gag gtc acc gct gta gac cca gct cat   2707
Phe Ile Lys Asp Phe Trp Phe Glu Val Thr Ala Val Asp Pro Ala His
    855                 860                 865

gcc gca ttt acc ttt acc agc caa gtc acc gct cat cta gat aag ttg   2755
Ala Ala Phe Thr Phe Thr Ser Gln Val Thr Ala His Leu Asp Lys Leu
870                 875                 880                 885

gta cgc gga aag cgt gag cag atg gag gat cgc gtt atc cgg tct atg   2803
Val Arg Gly Lys Arg Glu Gln Met Glu Asp Arg Val Ile Arg Ser Met
                890                 895                 900

gct gca tgg tgg cgt gaa aat gag cgt gac atc cag ggt tgg gtg cag   2851
Ala Ala Trp Trp Arg Glu Asn Glu Arg Asp Ile Gln Gly Trp Val Gln
            905                 910                 915

caa act cag tcc ggt gcg atc acc aac gaa gag ttc ttc tac cgt ctt   2899
Gln Thr Gln Ser Gly Ala Ile Thr Asn Glu Glu Phe Phe Tyr Arg Leu
        920                 925                 930

cgt cag tgc att ctt gac tat gaa atc agg aat aac cga gca cgt cag   2947
Arg Gln Cys Ile Leu Asp Tyr Glu Ile Arg Asn Asn Arg Ala Arg Gln
    935                 940                 945
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tcc atg ctc aat gcg cgc aac aac gct aac aag gag gct gtc gca cag   2995
Ser Met Leu Asn Ala Arg Asn Asn Ala Asn Lys Glu Ala Val Ala Gln
950                 955                 960                 965

gag aaa cca ctg ctc atg gtc tcc acc att cac agt gca aag ggt ctg   3043
Glu Lys Pro Leu Leu Met Val Ser Thr Ile His Ser Ala Lys Gly Leu
                970                 975                 980

gaa ttc gat aat gtc atc gtg ctt caa aaa cca agc tcc gat gca gag   3091
Glu Phe Asp Asn Val Ile Val Leu Gln Lys Pro Ser Ser Asp Ala Glu
            985                 990                 995

atg acc gaa gaa ggt aag cgc gca acc tat gtg gcg ctg acc cgt gca   3139
Met Thr Glu Glu Gly Lys Arg Ala Thr Tyr Val Ala Leu Thr Arg Ala
        1000                1005                1010

aaa aag cgt gaa ctc att att gct ggt tct act cgc gca tac cca cgc   3187
Lys Lys Arg Glu Leu Ile Ile Ala Gly Ser Thr Arg Ala Tyr Pro Arg
    1015                1020                1025

atc gtc acc gat tat gag caa atc gtt gat ctt ctt gaa aag cgc gat   3235
Ile Val Thr Asp Tyr Glu Gln Ile Val Asp Leu Leu Glu Lys Arg Asp
1030                1035                1040                1045

gag gag cgc aaa att aag gag gaa gag gct gca gca ctc gcc acc ctt   3283
Glu Glu Arg Lys Ile Lys Glu Glu Glu Ala Ala Ala Leu Ala Thr Leu
                1050                1055                1060

gaa gct gaa cag gag acg cgc gcc ctt gct gct gct gag gcg cag gct   3331
Glu Ala Glu Gln Glu Thr Arg Ala Leu Ala Ala Ala Glu Ala Gln Ala
            1065                1070                1075

cag gcg ttg ttg ctt gag cac aac ccg tgg ttg cgt gat ctc agc gat   3379
Gln Ala Leu Leu Leu Glu His Asn Pro Trp Leu Arg Asp Leu Ser Asp
        1080                1085                1090

gaa gaa gtc act gct cta act gag caa gag atc atc aac aat gtt gag   3427
Glu Glu Val Thr Ala Leu Thr Glu Gln Glu Ile Ile Asn Asn Val Glu
    1095                1100                1105

cca gcc cta cag att gaa gaa gag gag gaa gag gct cgt gca ctc gct   3475
Pro Ala Leu Gln Ile Glu Glu Glu Glu Glu Glu Ala Arg Ala Leu Ala
1110                1115                1120                1125

gca gca gag cca gca att cag cag tac ttg tct cag ttt gct ttc gat   3523
Ala Ala Glu Pro Ala Ile Gln Gln Tyr Leu Ser Gln Phe Ala Phe Asp
                1130                1135                1140

gag ttc ccg gac gac gac aat gta gcc aac act gtc gta cat gta gca   3571
Glu Phe Pro Asp Asp Asp Asn Val Ala Asn Thr Val Val His Val Ala
            1145                1150                1155

cca cag cct att ctc cac cag gca gtg cct gca gat gtg act gta caa   3619
Pro Gln Pro Ile Leu His Gln Ala Val Pro Ala Asp Val Thr Val Gln
        1160                1165                1170

tca agc acc gcc ccc gta aca cct gtt gtt gcg gat ctt gag gta acc   3667
Ser Ser Thr Ala Pro Val Thr Pro Val Val Ala Asp Leu Glu Val Thr
    1175                1180                1185

act gtt gca gct gat cca gtc gaa ccg act atc gtt gct gca cag cct   3715
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Thr Val Ala Ala Asp Pro Val Glu Pro Thr Ile Val Ala Ala Gln Pro
1190                1195                1200                1205

gag gtg gac gac aac ctt gtc tac agc acg tcc acc cct aat agt cac   3763
Glu Val Asp Asp Asn Leu Val Tyr Ser Thr Ser Thr Pro Asn Ser His
               1210                1215                1220

agt gac gtt att gca gtg aac tct gat acc tca gaa aac gct gct gtt   3811
Ser Asp Val Ile Ala Val Asn Ser Asp Thr Ser Glu Asn Ala Ala Val
           1225                1230                1235

aat cca gtt ctg tcc gat att gag gca ctc cga gca att ttc aac aac   3859
Asn Pro Val Leu Ser Asp Ile Glu Ala Leu Arg Ala Ile Phe Asn Asn
       1240                1245                1250

cag gac taaaacacct gctgctgttg agc                                3888
Gln Asp
    1255
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Application Number 10/599,347 Filed 09/29/2006

<210> 2408
<211> 1255
<212> PRT
<213> Corynebacterium glutamicum

<400> 2408

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Met Pro Ile Ile Ile Asp Asn Leu Asn Ser Asp Asp Asp Ser Thr Ile
  1               5                  10                  15

Gly Thr Ala Thr Glu Tyr Asn Pro Asp Thr Asp Ala Asp Leu Leu Asp
             20                  25                  30

Ala Ile Asn Ala Asp Ala Asp Leu Asp Gly Asp Ala Thr Ile Ser Thr
         35                  40                  45

Asn Ala Thr Glu Glu Gly Val Asp Ala Ala Ala Glu Lys Pro Lys Lys
     50                  55                  60

Lys Arg Lys Ala Pro Ala Leu Lys Pro Lys Gly Leu Thr Ala Lys Phe
 65                  70                  75                  80

Phe His Arg Asp Leu Thr Gly Val Gly Gly Arg Thr Gly Arg Leu Asn
                 85                  90                  95

Lys Asn Val His Pro Thr Asn Pro Asp Leu Ser Tyr Gln Pro Val Ser
            100                 105                 110

Asp Val Tyr Thr Pro Gln Ser Ala Asp His Lys Gly Ile Lys Thr Arg
        115                 120                 125

Tyr Ile Leu Thr His Pro Thr Pro Ala Val Val Leu Ser Glu Ser Ile
    130                 135                 140

Ser Asn Ala Phe His Val Ser Thr Leu Arg Arg Asn Asn Asn Val Asn
145                 150                 155                 160

Asn Ser Asp Ser Glu Leu Ala Ala Trp Pro Tyr Leu Tyr Gln Leu Asp
                165                 170                 175

Ile Pro Gln Leu Asp Gln Met Ile Asn Val Ala Asp Ile Cys Asp Tyr
            180                 185                 190
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His Phe His Gly Tyr Asn Leu Trp Val Asp Phe Thr Pro Gln Thr Ile
        195                 200                 205

Ala Leu Arg Ser Gly Lys Thr Val Leu Asp Asp Gly Thr Thr Ala Ser
    210                 215                 220

Asp Asn Thr Thr His Val Tyr Tyr Arg Val Thr Val His Val Ile Ala
225                 230                 235                 240

Gly Gln Asp His Gly Ser Thr Leu Leu Asp Asp Gln Gly Asn Gln Val
                245                 250                 255

Leu Asp Arg Asp Asp Asn Pro Ile Ser Thr Pro Ser Ile Lys Arg Ile
            260                 265                 270

Gly Ala Val Thr Asp Leu Phe Asp His Asn Pro Phe Gly Phe Ala Ser
        275                 280                 285

Val Asn Ser Phe Ala Phe Val Asp Phe Ser Trp Asp Pro Ala Thr Thr
    290                 295                 300

Leu Val Asp Met Leu Asn Asn Leu Asp Ser Tyr Leu Ser Asn His Ile
305                 310                 315                 320

Asn Ile Ala Ser Ser Pro Thr Pro Ile Ala Leu Asp Met Val Val Leu
                325                 330                 335

Asn Glu Trp Ser Glu Lys Ser Tyr Gln Leu Cys Glu Arg Val Val Ala
            340                 345                 350

Gln Ala Lys Leu Ile Asn Ser Asn Lys Ile Thr Ala His Val Ser Asp
        355                 360                 365

Val Ile Lys Gln Asn Ala His Asn Ile Leu Trp Phe Thr Glu Gln Met
    370                 375                 380

Asn Pro Gly Thr Thr Asn Leu Ser Glu Val Pro Ile Ser Lys Lys Ser
385                 390                 395                 400

Met Leu Pro Met Ser Arg Gln Leu Arg Ile Leu Glu His Tyr Asp Val
                405                 410                 415

Pro Leu Thr Ala Tyr Ser Ala Leu Phe Trp Thr Val Ser Ala Ile Lys
            420                 425                 430

Asn Glu Ser Met Val Gln Tyr Leu Val Arg Gln Asn Met Gln Leu Thr
        435                 440                 445

Leu Ser Ser Asn Leu Asp Ala Leu Asn Ser Ile Val Ser Gln Leu Pro
    450                 455                 460

Val Pro Asp Lys Asp Val Val Ala Ala Ser Gly Tyr Gln Ile Gln Pro
465                 470                 475                 480

His Phe Ser Thr Gln Gln Arg Glu Ala Ile Thr Thr Asp Asn Pro Leu
                485                 490                 495

Ala Ile Ile Gln Ala Gly Ala Gly Thr Gly Lys Ser Thr Val Ile Leu
            500                 505                 510
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Glu Arg Ile Glu Tyr Leu Cys Ala Ala Gly Thr Asn Pro Glu Glu Ile
515 520 525

Ala Val Leu Ser Phe Thr Asn Ala Ala Ala Asp Asn Ile Thr Ala Lys
530 535 540

Asn Asp Lys Val Thr Ser Met Thr Ile Ser Lys Met Val His Glu Ile
545 550 555 560

Tyr Ala His Asn Phe Pro Asp His Glu Ile Ser Thr Ile Asp Thr Ile
565 570 575

Ile Asn Thr Leu Asp Ile Glu Tyr Gly Asp Gln Met Val Thr Ser Asp
580 585 590

Tyr Met Ile Gln Leu Arg Asp Leu Leu Tyr Lys Val Met Thr Gln Gly
595 600 605

Gly Asn Ala Asn Leu Thr Ala Leu Ser Ile Phe Met Glu Ser His Ile
610 615 620

Glu Ala Phe Ile Ser Val Leu Asp Gln Ile Lys Gln Thr Ser Leu Glu
625 630 635 640

Leu Glu Ile Ile Ile Cys Tyr Leu Leu Leu Asp Lys Leu Ile Glu Pro
645 650 655

His Ala Ser Pro Lys Tyr Leu Ile Ile Asp Glu Val Gln Asp Asn Ser
660 665 670

Val Phe Glu Phe Val Phe Ala Leu Arg Phe Ala Ala Lys His Asn Thr
675 680 685

Ser Leu Tyr Leu Val Gly Asp Ser Ser Gln Thr Leu Tyr Glu Phe Arg
690 695 700

Ser Ala Asn Pro Lys Ala Leu Asn Ser Leu Glu Ala Ser Gly Val Phe
705 710 715 720

Gly Thr Tyr Arg Leu Thr Thr Asn Tyr Arg Ser Asn Gln Glu Ile Leu
725 730 735

Asp Phe Ala Asn Ile His Leu Ser Asp Ile Glu Ala Asn Gln Phe Ala
740 745 750

Gly Ile Gln Leu Tyr Ala Asn Ser Phe Asp Ala Pro Thr Ala Asp Ser
755 760 765

Phe Lys Glu Lys Val Glu Leu Asp Met His His Val Ser Lys Gln Ser
770 775 780

Glu Phe Thr Asp Ser Ile Pro Tyr Phe Met Glu Ser Asn Lys Ala Arg
785 790 795 800

Phe Asp Ala Ala Ile Leu Asn Asn Glu Gln Thr Ile Val Leu Ala His
805 810 815

Ser Gly Arg Glu Ile Arg Ala Ala Gln Gln Ala Leu Ala Glu Met Tyr
820 825 830

Pro Ser Ile Thr Val Arg Asn Leu Gln Ser Asp Lys Gly Phe Asn Asn

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        835                 840                 845

Thr Val Phe Ser Thr Phe Ile Lys Asp Phe Trp Phe Glu Val Thr Ala
    850                 855                 860

Val Asp Pro Ala His Ala Ala Phe Thr Phe Thr Ser Gln Val Thr Ala
865                 870                 875                 880

His Leu Asp Lys Leu Val Arg Gly Lys Arg Glu Gln Met Glu Asp Arg
                885                 890                 895

Val Ile Arg Ser Met Ala Ala Trp Trp Arg Glu Asn Glu Arg Asp Ile
            900                 905                 910

Gln Gly Trp Val Gln Gln Thr Gln Ser Gly Ala Ile Thr Asn Glu Glu
        915                 920                 925

Phe Phe Tyr Arg Leu Arg Gln Cys Ile Leu Asp Tyr Glu Ile Arg Asn
    930                 935                 940

Asn Arg Ala Arg Gln Ser Met Leu Asn Ala Arg Asn Asn Ala Asn Lys
945                 950                 955                 960

Glu Ala Val Ala Gln Glu Lys Pro Leu Leu Met Val Ser Thr Ile His
                965                 970                 975

Ser Ala Lys Gly Leu Glu Phe Asp Asn Val Ile Val Leu Gln Lys Pro
            980                 985                 990

Ser Ser Asp Ala Glu Met Thr Glu Glu Gly Lys Arg Ala Thr Tyr Val
        995                 1000                1005

Ala Leu Thr Arg Ala Lys Lys Arg Glu Leu Ile Ile Ala Gly Ser Thr
    1010                1015                1020

Arg Ala Tyr Pro Arg Ile Val Thr Asp Tyr Glu Gln Ile Val Asp Leu
1025                1030                1035                1040

Leu Glu Lys Arg Asp Glu Glu Arg Lys Ile Lys Glu Glu Glu Ala Ala
                1045                1050                1055

Ala Leu Ala Thr Leu Glu Ala Glu Gln Glu Thr Arg Ala Leu Ala Ala
            1060                1065                1070

Ala Glu Ala Gln Ala Gln Ala Leu Leu Leu Glu His Asn Pro Trp Leu
        1075                1080                1085

Arg Asp Leu Ser Asp Glu Glu Val Thr Ala Leu Thr Glu Gln Glu Ile
    1090                1095                1100

Ile Asn Asn Val Glu Pro Ala Leu Gln Ile Glu Glu Glu Glu Glu Glu
1105                1110                1115                1120

Ala Arg Ala Leu Ala Ala Ala Glu Pro Ala Ile Gln Gln Tyr Leu Ser
                1125                1130                1135

Gln Phe Ala Phe Asp Glu Phe Pro Asp Asp Asp Asn Val Ala Asn Thr
            1140                1145                1150

Val Val His Val Ala Pro Gln Pro Ile Leu His Gln Ala Val Pro Ala
        1155                1160                1165
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Asp Val Thr Val Gln Ser Ser Thr Ala Pro Val Thr Pro Val Val Ala
    1170                1175                1180

Asp Leu Glu Val Thr Thr Val Ala Ala Asp Pro Val Glu Pro Thr Ile
1185                1190                1195                1200

Val Ala Ala Gln Pro Glu Val Asp Asp Asn Leu Val Tyr Ser Thr Ser
                1205                1210                1215

Thr Pro Asn Ser His Ser Asp Val Ile Ala Val Asn Ser Asp Thr Ser
            1220                1225                1230

Glu Asn Ala Ala Val Asn Pro Val Leu Ser Asp Ile Glu Ala Leu Arg
        1235                1240                1245

Ala Ile Phe Asn Asn Gln Asp
    1250                1255


<210> 2409
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<213> Corynebacterium glutamicum

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<222> (34)..(444)
<223> RXA01773

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                                      Met Ile Thr His Ile Gln Ala
                                        1               5

ggc ctg cat ctt ggt ggc tgc cgc gca gca ggt tta ctg cct ata cca   102
Gly Leu His Leu Gly Gly Cys Arg Ala Ala Gly Leu Leu Pro Ile Pro
         10                  15                  20

gca cat att gat cat att gtg cgc ctg aca gcc gca gat ttc tat gac   150
Ala His Ile Asp His Ile Val Arg Leu Thr Ala Ala Asp Phe Tyr Asp
     25                  30                  35

acc cag tca gca ccg cag ctg ctc agc aac act gtg ctt gat gta ttg   198
Thr Gln Ser Ala Pro Gln Leu Leu Ser Asn Thr Val Leu Asp Val Leu
 40                  45                  50                  55

gac acc acc act caa gac ttg aag gca ttg tgg cct gtt gca gaa cat   246
Asp Thr Thr Thr Gln Asp Leu Lys Ala Leu Trp Pro Val Ala Glu His
                 60                  65                  70

att gct aca acc att cct gaa tct gag aac gtg ctt atc cac tgc cag   294
Ile Ala Thr Thr Ile Pro Glu Ser Glu Asn Val Leu Ile His Cys Gln
             75                  80                  85

atg ggt atc aac cgc tca gct gca ctc atg aca cgg gtg ttg atg ttg   342
Met Gly Ile Asn Arg Ser Ala Ala Leu Met Thr Arg Val Leu Met Leu
         90                  95                  100

cgc aac gat tgc acc gcc gat gaa gca att gca ctg ctg cgt gat cga   390
Arg Asn Asp Cys Thr Ala Asp Glu Ala Ile Ala Leu Leu Arg Asp Arg
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    105                 110                 115

cgc tca ccg ttt gta ctg ttc aat gag cat ttt gtg gaa caa ctt cga   438
Arg Ser Pro Phe Val Leu Phe Asn Glu His Phe Val Glu Gln Leu Arg
120                 125                 130                 135

gca ctg taagcgctca aagacccatt acc                                 467
Ala Leu
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<210> 2410
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<212> PRT
<213> Corynebacterium glutamicum

<400> 2410

```
Met Ile Thr His Ile Gln Ala Gly Leu His Leu Gly Gly Cys Arg Ala
  1               5                  10                  15

Ala Gly Leu Leu Pro Ile Pro Ala His Ile Asp His Ile Val Arg Leu
             20                  25                  30

Thr Ala Ala Asp Phe Tyr Asp Thr Gln Ser Ala Pro Gln Leu Leu Ser
         35                  40                  45

Asn Thr Val Leu Asp Val Leu Asp Thr Thr Thr Gln Asp Leu Lys Ala
     50                  55                  60

Leu Trp Pro Val Ala Glu His Ile Ala Thr Thr Ile Pro Glu Ser Glu
 65                  70                  75                  80

Asn Val Leu Ile His Cys Gln Met Gly Ile Asn Arg Ser Ala Ala Leu
                 85                  90                  95

Met Thr Arg Val Leu Met Leu Arg Asn Asp Cys Thr Ala Asp Glu Ala
            100                 105                 110

Ile Ala Leu Leu Arg Asp Arg Arg Ser Pro Phe Val Leu Phe Asn Glu
        115                 120                 125

His Phe Val Glu Gln Leu Arg Ala Leu
    130                 135
```

<210> 2411
<211> 687
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(664)
<223> RXA01775

<400> 2411

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gtggaaacca aagacgagga aagtatgtct atttgtttgt ccccaggttg tccacatttg 60

ttttattccc cgagaatgtc ctagaaagga actcgacccc atg tcc tat tca ctc   115
                                               Met Ser Tyr Ser Leu
                                                 1               5
```

```
att att tct aaa gca cca acc cac tcc atg cct ttt aat gag gct gaa   163
Ile Ile Ser Lys Ala Pro Thr His Ser Met Pro Phe Asn Glu Ala Glu
                10                  15                  20

ctc cta gag ctt gtc gat gaa ctg cac tcc gac aac acc gtg aaa aag   211
Leu Leu Glu Leu Val Asp Glu Leu His Ser Asp Asn Thr Val Lys Lys
            25                  30                  35

ccg gtt att gtg cca ctc ccc gat gat ttc tcc tac acc gta gat agc   259
Pro Val Ile Val Pro Leu Pro Asp Asp Phe Ser Tyr Thr Val Asp Ser
        40                  45                  50

gcc gtg cga cta cat gat ttg ggt gtt gac cag gaa ctg act gac tgg   307
Ala Val Arg Leu His Asp Leu Gly Val Asp Gln Glu Leu Thr Asp Trp
    55                  60                  65

att act gca caa gtt gct gca gcc tat cca aac cag atc gtc tca gag   355
Ile Thr Ala Gln Val Ala Ala Ala Tyr Pro Asn Gln Ile Val Ser Glu
70                  75                  80                  85

att gct gct gcc cct gat ccg caa gcc aag acc tta ttc tcc gcc aat   403
Ile Ala Ala Ala Pro Asp Pro Gln Ala Lys Thr Leu Phe Ser Ala Asn
                90                  95                  100

gcg tat aac acc agg tct ttt ggt act ttt tgg act gag cac cct att   451
Ala Tyr Asn Thr Arg Ser Phe Gly Thr Phe Trp Thr Glu His Pro Ile
            105                 110                 115

aca cag ctc caa tac aag cgc tgc tac caa att gtc atc gag aac gtt   499
Thr Gln Leu Gln Tyr Lys Arg Cys Tyr Gln Ile Val Ile Glu Asn Val
        120                 125                 130

acg ggt gtc tat cat ccg tta cct gtt gat aac tac cgc tac gta ccc   547
Thr Gly Val Tyr His Pro Leu Pro Val Asp Asn Tyr Arg Tyr Val Pro
    135                 140                 145

cct gtc acg ccc tca ttg cca cag ccg gtc tac cac gaa gct atc gcc   595
Pro Val Thr Pro Ser Leu Pro Gln Pro Val Tyr His Glu Ala Ile Ala
150                 155                 160                 165

tta aat gag tct gat gtc gct gat cac ggt act cgt gca gcc aag cac   643
Leu Asn Glu Ser Asp Val Ala Asp His Gly Thr Arg Ala Ala Lys His
                170                 175                 180

gca atg atc aac cgc aac gta taaccacaca cgccacagat act             687
Ala Met Ile Asn Arg Asn Val
            185
```

<210> 2412
<211> 188
<212> PRT
<213> Corynebacterium glutamicum

<400> 2412

```
Met Ser Tyr Ser Leu Ile Ile Ser Lys Ala Pro Thr His Ser Met Pro
  1               5                  10                  15

Phe Asn Glu Ala Glu Leu Leu Glu Leu Val Asp Glu Leu His Ser Asp
            20                  25                  30
```

```
Asn Thr Val Lys Lys Pro Val Ile Val Pro Leu Pro Asp Asp Phe Ser
         35                  40                  45

Tyr Thr Val Asp Ser Ala Val Arg Leu His Asp Leu Gly Val Asp Gln
     50                  55                  60

Glu Leu Thr Asp Trp Ile Thr Ala Gln Val Ala Ala Ala Tyr Pro Asn
 65                  70                  75                  80

Gln Ile Val Ser Glu Ile Ala Ala Ala Pro Asp Pro Gln Ala Lys Thr
                 85                  90                  95

Leu Phe Ser Ala Asn Ala Tyr Asn Thr Arg Ser Phe Gly Thr Phe Trp
            100                 105                 110

Thr Glu His Pro Ile Thr Gln Leu Gln Tyr Lys Arg Cys Tyr Gln Ile
        115                 120                 125

Val Ile Glu Asn Val Thr Gly Val Tyr His Pro Leu Pro Val Asp Asn
    130                 135                 140

Tyr Arg Tyr Val Pro Pro Val Thr Pro Ser Leu Pro Gln Pro Val Tyr
145                 150                 155                 160

His Glu Ala Ile Ala Leu Asn Glu Ser Asp Val Ala Asp His Gly Thr
                165                 170                 175

Arg Ala Ala Lys His Ala Met Ile Asn Arg Asn Val
            180                 185


<210> 2413
<211> 1575
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1552)
<223> RXA01776

<400> 2413
cgtataacca cacacgccac agatactcag ctatctgtgg cgtgttgttt tacatcaacc 60

tctcacccat cccccatcac tattaaagaa aatcaccatc atg acc cac act gat   115
                                            Met Thr His Thr Asp
                                              1               5

acc cca gcc cct gca cac ggc gta aca ccg agt gaa ttc gct gtt acc   163
Thr Pro Ala Pro Ala His Gly Val Thr Pro Ser Glu Phe Ala Val Thr
                10                  15                  20

tca cac gaa ctc acc acc tca cca aca cct agt ccg aca cag gtc gct   211
Ser His Glu Leu Thr Thr Ser Pro Thr Pro Ser Pro Thr Gln Val Ala
            25                  30                  35

att gca gcc cag gaa aaa att cgc cag cgc aag ctc gaa gag ctt aaa   259
Ile Ala Ala Gln Glu Lys Ile Arg Gln Arg Lys Leu Glu Glu Leu Lys
        40                  45                  50
```

```
gca aaa aag cgc aca gac acg aca gct caa cca ctt cta cct gca cct   307
Ala Lys Lys Arg Thr Asp Thr Thr Ala Gln Pro Leu Leu Pro Ala Pro
     55                  60                  65

gtg ctg cat aca cgc cca ctc ccc tca ccg aat cca ccg cga cca tct   355
Val Leu His Thr Arg Pro Leu Pro Ser Pro Asn Pro Pro Arg Pro Ser
 70                  75                  80                  85

cca ccg gca cct acc act gga cac tgg gaa ctt ctt att gtc agg tca   403
Pro Pro Ala Pro Thr Thr Gly His Trp Glu Leu Leu Ile Val Arg Ser
                90                  95                 100

cag cag aag aaa atg acc gca gcc aat ccc ttt ctc aaa ttc ctt cat   451
Gln Gln Lys Lys Met Thr Ala Ala Asn Pro Phe Leu Lys Phe Leu His
            105                 110                 115

ctc ggt aaa gcc ttc aac gtg aaa gac cta ggg ctc acc tgc gat cgc   499
Leu Gly Lys Ala Phe Asn Val Lys Asp Leu Gly Leu Thr Cys Asp Arg
        120                 125                 130

acc act gat gtt gac ctc tca cgg ctt ggc aag ctc aat ccg ccc agc   547
Thr Thr Asp Val Asp Leu Ser Arg Leu Gly Lys Leu Asn Pro Pro Ser
    135                 140                 145

tca ctt atc ctt gaa cta gca acg gca ctt gac ctg cat cca ttc ctc   595
Ser Leu Ile Leu Glu Leu Ala Thr Ala Leu Asp Leu His Pro Phe Leu
150                 155                 160                 165

tca gtc gca ctc tct tcg cac agt gcg gtc aac gcc cgt cgc aac caa   643
Ser Val Ala Leu Ser Ser His Ser Ala Val Asn Ala Arg Arg Asn Gln
                170                 175                 180

ctt gaa tta acc ctg cac aac cat gac act cag ggc aca gca tta ggt   691
Leu Glu Leu Thr Leu His Asn His Asp Thr Gln Gly Thr Ala Leu Gly
            185                 190                 195

cac agc gtt act atg gtc cag cta ccc gag gtc att aat cga gct gct   739
His Ser Val Thr Met Val Gln Leu Pro Glu Val Ile Asn Arg Ala Ala
        200                 205                 210

gta gag ccc tat atc aaa ccc aag ggc tcg ggc aat gac ccg ctt gac   787
Val Glu Pro Tyr Ile Lys Pro Lys Gly Ser Gly Asn Asp Pro Leu Asp
    215                 220                 225

caa agc ctg aac cac cgc gca ccc acc gta agt gac gtg caa aaa gcc   835
Gln Ser Leu Asn His Arg Ala Pro Thr Val Ser Asp Val Gln Lys Ala
230                 235                 240                 245

ctt gtg cag gaa aac aca ggc acg gca aca gac agc aac aac tac ctg   883
Leu Val Gln Glu Asn Thr Gly Thr Ala Thr Asp Ser Asn Asn Tyr Leu
                250                 255                 260

ctt cct ttt gat cct gat tct ggt gca cca aaa acc acc gcg ctt aat   931
Leu Pro Phe Asp Pro Asp Ser Gly Ala Pro Lys Thr Thr Ala Leu Asn
            265                 270                 275

gcg cct aat aag gat ctc cta cag gcc agg cat gag ctt gcc tat att   979
Ala Pro Asn Lys Asp Leu Leu Gln Ala Arg His Glu Leu Ala Tyr Ile
        280                 285                 290

ccc gag atc ccc gcc att gca tcg tgg ctc gat cac ctt gac ccc atc   1027
```

```
Pro Glu Ile Pro Ala Ile Ala Ser Trp Leu Asp His Leu Asp Pro Ile
    295                 300                 305

atg cgt gtg cac cgt agt ctt gcg ctt tca att ttc cca gtg cag ctt   1075
Met Arg Val His Arg Ser Leu Ala Leu Ser Ile Phe Pro Val Gln Leu
310                 315                 320                 325

cta cgt gct gcc gtt gag aat ctc cct cat aac gta acc gat ctg cat   1123
Leu Arg Ala Ala Val Glu Asn Leu Pro His Asn Val Thr Asp Leu His
                330                 335                 340

aat cac ctt gat cct gag gat ctg ctc cct gag gaa ctc acc acc tgg   1171
Asn His Leu Asp Pro Glu Asp Leu Leu Pro Glu Glu Leu Thr Thr Trp
            345                 350                 355

ctc gat cac ctc ttc gat gca gac tta acc gct ctc gct tca tgc cca   1219
Leu Asp His Leu Phe Asp Ala Asp Leu Thr Ala Leu Ala Ser Cys Pro
        360                 365                 370

cag ctt gca cca cct atc gtg cgc agc cac aat cac gcc aaa gcg atc   1267
Gln Leu Ala Pro Pro Ile Val Arg Ser His Asn His Ala Lys Ala Ile
    375                 380                 385

gca gct atc acc gtg acc tct gtc atg gac gct ctc atc gcc aaa act   1315
Ala Ala Ile Thr Val Thr Ser Val Met Asp Ala Leu Ile Ala Lys Thr
390                 395                 400                 405

ctt gat gcg cat gac gat cca ctg ccc tca cta ccg gag ttt gta gaa   1363
Leu Asp Ala His Asp Asp Pro Leu Pro Ser Leu Pro Glu Phe Val Glu
                410                 415                 420

cta ctg cgt gac gct gta gcc cag ctc gca gcg cat ttt aag cag cag   1411
Leu Leu Arg Asp Ala Val Ala Gln Leu Ala Ala His Phe Lys Gln Gln
            425                 430                 435

cgc ggc gag gta cta ccg cag ccc aat ggc ttg cga tac gcc acc gac   1459
Arg Gly Glu Val Leu Pro Gln Pro Asn Gly Leu Arg Tyr Ala Thr Asp
        440                 445                 450

ttt ggc ctg ctc tct tat att gcc gat ggc tta cat gaa tat gca ctt   1507
Phe Gly Leu Leu Ser Tyr Ile Ala Asp Gly Leu His Glu Tyr Ala Leu
    455                 460                 465

gcc atc gac ttc ggg ctg atc tac ccg aat gaa ctc atc acc gag       1552
Ala Ile Asp Phe Gly Leu Ile Tyr Pro Asn Glu Leu Ile Thr Glu
470                 475                 480

taaacccact cctagaaagg tct                                        1575


<210> 2414
<211> 484
<212> PRT
<213> Corynebacterium glutamicum

<400> 2414
Met Thr His Thr Asp Thr Pro Ala Pro Ala His Gly Val Thr Pro Ser
  1               5                  10                  15

Glu Phe Ala Val Thr Ser His Glu Leu Thr Thr Ser Pro Thr Pro Ser
             20                  25                  30
```

```
Pro Thr Gln Val Ala Ile Ala Ala Gln Glu Lys Ile Arg Gln Arg Lys
         35                  40                  45

Leu Glu Glu Leu Lys Ala Lys Lys Arg Thr Asp Thr Thr Ala Gln Pro
     50                  55                  60

Leu Leu Pro Ala Pro Val Leu His Thr Arg Pro Leu Pro Ser Pro Asn
 65                  70                  75                  80

Pro Pro Arg Pro Ser Pro Pro Ala Pro Thr Thr Gly His Trp Glu Leu
                 85                  90                  95

Leu Ile Val Arg Ser Gln Gln Lys Lys Met Thr Ala Ala Asn Pro Phe
            100                 105                 110

Leu Lys Phe Leu His Leu Gly Lys Ala Phe Asn Val Lys Asp Leu Gly
        115                 120                 125

Leu Thr Cys Asp Arg Thr Thr Asp Val Asp Leu Ser Arg Leu Gly Lys
    130                 135                 140

Leu Asn Pro Pro Ser Ser Leu Ile Leu Glu Leu Ala Thr Ala Leu Asp
145                 150                 155                 160

Leu His Pro Phe Leu Ser Val Ala Leu Ser Ser His Ser Ala Val Asn
                165                 170                 175

Ala Arg Arg Asn Gln Leu Glu Leu Thr Leu His Asn His Asp Thr Gln
            180                 185                 190

Gly Thr Ala Leu Gly His Ser Val Thr Met Val Gln Leu Pro Glu Val
        195                 200                 205

Ile Asn Arg Ala Ala Val Glu Pro Tyr Ile Lys Pro Lys Gly Ser Gly
    210                 215                 220

Asn Asp Pro Leu Asp Gln Ser Leu Asn His Arg Ala Pro Thr Val Ser
225                 230                 235                 240

Asp Val Gln Lys Ala Leu Val Gln Glu Asn Thr Gly Thr Ala Thr Asp
                245                 250                 255

Ser Asn Asn Tyr Leu Leu Pro Phe Asp Pro Asp Ser Gly Ala Pro Lys
            260                 265                 270

Thr Thr Ala Leu Asn Ala Pro Asn Lys Asp Leu Leu Gln Ala Arg His
        275                 280                 285

Glu Leu Ala Tyr Ile Pro Glu Ile Pro Ala Ile Ala Ser Trp Leu Asp
    290                 295                 300

His Leu Asp Pro Ile Met Arg Val His Arg Ser Leu Ala Leu Ser Ile
305                 310                 315                 320

Phe Pro Val Gln Leu Leu Arg Ala Ala Val Glu Asn Leu Pro His Asn
                325                 330                 335

Val Thr Asp Leu His Asn His Leu Asp Pro Glu Asp Leu Leu Pro Glu
            340                 345                 350
```

```
Glu Leu Thr Thr Trp Leu Asp His Leu Phe Asp Ala Asp Leu Thr Ala
        355                 360                 365

Leu Ala Ser Cys Pro Gln Leu Ala Pro Pro Ile Val Arg Ser His Asn
    370                 375                 380

His Ala Lys Ala Ile Ala Ala Ile Thr Val Thr Ser Val Met Asp Ala
385                 390                 395                 400

Leu Ile Ala Lys Thr Leu Asp Ala His Asp Asp Pro Leu Pro Ser Leu
                405                 410                 415

Pro Glu Phe Val Glu Leu Leu Arg Asp Ala Val Ala Gln Leu Ala Ala
            420                 425                 430

His Phe Lys Gln Gln Arg Gly Glu Val Leu Pro Gln Pro Asn Gly Leu
        435                 440                 445

Arg Tyr Ala Thr Asp Phe Gly Leu Leu Ser Tyr Ile Ala Asp Gly Leu
    450                 455                 460

His Glu Tyr Ala Leu Ala Ile Asp Phe Gly Leu Ile Tyr Pro Asn Glu
465                 470                 475                 480

Leu Ile Thr Glu
```

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<210> 2415
<211> 582
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(559)
<223> RXA01777

<400> 2415

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ccgatggctt acatgaatat gcacttgcca tcgacttcgg gctgatctac ccgaatgaac 60

tcatcaccga gtaaacccac tcctagaaag gtctttaccc atg tct cgt atc atc   115
                                              Met Ser Arg Ile Ile
                                                1               5

act gct ccc gtc cac aag cct tat att att gct cgt gaa gtc aag ggg   163
Thr Ala Pro Val His Lys Pro Tyr Ile Ile Ala Arg Glu Val Lys Gly
                10                  15                  20

gtc tcc cat gtc cac gac act gtt ggc ggc aag tgg cag gcc acc ttg   211
Val Ser His Val His Asp Thr Val Gly Gly Lys Trp Gln Ala Thr Leu
            25                  30                  35

cac aca ctt aaa ccg ggg ccc tcc tgg ccg aaa ccg tca cag ttc act   259
His Thr Leu Lys Pro Gly Pro Ser Trp Pro Lys Pro Ser Gln Phe Thr
        40                  45                  50

gcg cct aaa tcc acg tcc atc tgg ttt att gcg gta gca acc cac cca   307
Ala Pro Lys Ser Thr Ser Ile Trp Phe Ile Ala Val Ala Thr His Pro
    55                  60                  65
```

```
cgt aac cca cgg gca cgc aaa ggt acc cta ctt ggt cgc ggt ggt ctt   355
Arg Asn Pro Arg Ala Arg Lys Gly Thr Leu Leu Gly Arg Gly Gly Leu
 70                  75                  80                  85

tac gaa ctc aaa gac act gat ctg aac ttt ctc aca gag cga cag gat   403
Tyr Glu Leu Lys Asp Thr Asp Leu Asn Phe Leu Thr Glu Arg Gln Asp
                90                  95                 100

ttg ctc gcc aca tct acc tct cgt gac cca gag gat tgc cgt tta cgc   451
Leu Leu Ala Thr Ser Thr Ser Arg Asp Pro Glu Asp Cys Arg Leu Arg
            105                 110                 115

ttt aat tcg cgt cac gat gca gca gca ttt tta cat gct aac gcc cgc   499
Phe Asn Ser Arg His Asp Ala Ala Ala Phe Leu His Ala Asn Ala Arg
        120                 125                 130

cac atc aac aag ctt ttt cat cca gca cta ggt cat gct cgc tac gat   547
His Ile Asn Lys Leu Phe His Pro Ala Leu Gly His Ala Arg Tyr Asp
    135                 140                 145

ctc ata gat gtg taagcacaac gcttagctta tga                        582
Leu Ile Asp Val
150
```

Sequence Listing

<210> 2416
<211> 153
<212> PRT
<213> Corynebacterium glutamicum

<400> 2416

```
Met Ser Arg Ile Ile Thr Ala Pro Val His Lys Pro Tyr Ile Ile Ala
  1               5                  10                  15

Arg Glu Val Lys Gly Val Ser His Val His Asp Thr Val Gly Gly Lys
             20                  25                  30

Trp Gln Ala Thr Leu His Thr Leu Lys Pro Gly Pro Ser Trp Pro Lys
         35                  40                  45

Pro Ser Gln Phe Thr Ala Pro Lys Ser Thr Ser Ile Trp Phe Ile Ala
     50                  55                  60

Val Ala Thr His Pro Arg Asn Pro Arg Ala Arg Lys Gly Thr Leu Leu
 65                  70                  75                  80

Gly Arg Gly Gly Leu Tyr Glu Leu Lys Asp Thr Asp Leu Asn Phe Leu
                 85                  90                  95

Thr Glu Arg Gln Asp Leu Leu Ala Thr Ser Thr Ser Arg Asp Pro Glu
            100                 105                 110

Asp Cys Arg Leu Arg Phe Asn Ser Arg His Asp Ala Ala Ala Phe Leu
        115                 120                 125

His Ala Asn Ala Arg His Ile Asn Lys Leu Phe His Pro Ala Leu Gly
    130                 135                 140

His Ala Arg Tyr Asp Leu Ile Asp Val
145                 150
```

<210> 2417
<211> 1260
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1237)
<223> RXA01778

<400> 2417
ctactacccc ctccgggtgt ggggtagctg taacaactac cccacaatct tagccggtct 60

tccatacata actgcgaaat tggttagagt ctttttcatg atg ctc tac caa cac 115
Met Leu Tyr Gln His
1 5

acc aca cgc ggg ctg atc att agt gac gcg atc atc gcg aaa atc agc 163
Thr Thr Arg Gly Leu Ile Ile Ser Asp Ala Ile Ile Ala Lys Ile Ser
10 15 20

caa gtc aac caa ctg ctg cta cta aga ccc acg ctg ttg caa gac aaa 211
Gln Val Asn Gln Leu Leu Leu Leu Arg Pro Thr Leu Leu Gln Asp Lys
25 30 35

gat atg cac cat gcg aca ttg agt agc gac acc cca tca att cgc agt 259
Asp Met His His Ala Thr Leu Ser Ser Asp Thr Pro Ser Ile Arg Ser
40 45 50

cgc cgt cgc tcc tat cgc gag aat aaa gcc gcc tat gcg acc acg agc 307
Arg Arg Arg Ser Tyr Arg Glu Asn Lys Ala Ala Tyr Ala Thr Thr Ser
55 60 65

acc atc aga aac cgt gag acc ttt ttc agc aca tct gat att gat ttc 355
Thr Ile Arg Asn Arg Glu Thr Phe Phe Ser Thr Ser Asp Ile Asp Phe
70 75 80 85

gcc ata ctc atg att cag gac gta caa gaa tct ctc gta tct ttt gac 403
Ala Ile Leu Met Ile Gln Asp Val Gln Glu Ser Leu Val Ser Phe Asp
90 95 100

ccc acc ttg gct caa gat atg aag cca aga acc aac gca gtc att tct 451
Pro Thr Leu Ala Gln Asp Met Lys Pro Arg Thr Asn Ala Val Ile Ser
105 110 115

gca ctc aat gag cta cgc gag cca ctg gat acc ttc tac cgt gcc cat 499
Ala Leu Asn Glu Leu Arg Glu Pro Leu Asp Thr Phe Tyr Arg Ala His
120 125 130

gaa tac ggt gac atc atc agc gat ggt gct tat gag ttc gat cat gct 547
Glu Tyr Gly Asp Ile Ile Ser Asp Gly Ala Tyr Glu Phe Asp His Ala
135 140 145

gcc att gat gca caa cac agc ctt agt gaa ctc gtt gcc ggt ctg cat 595
Ala Ile Asp Ala Gln His Ser Leu Ser Glu Leu Val Ala Gly Leu His
150 155 160 165

aat tat gac aac ctc atg ttt ccc cag gaa acc gct ccg ttg atg agt 643
Asn Tyr Asp Asn Leu Met Phe Pro Gln Glu Thr Ala Pro Leu Met Ser
170 175 180

```
gaa tcc aat ggc att cag ctg gct cag tac tat aag tcc acc aaa ctc   691
Glu Ser Asn Gly Ile Gln Leu Ala Gln Tyr Tyr Lys Ser Thr Lys Leu
            185                 190                 195

gat gag tca caa ttg acg gtg gaa cct aat gag cct ggt atc agc att   739
Asp Glu Ser Gln Leu Thr Val Glu Pro Asn Glu Pro Gly Ile Ser Ile
        200                 205                 210

atg tgg cac gcc cat gat ttc acc tgg tct tgc cta gtg cgc tat gac   787
Met Trp His Ala His Asp Phe Thr Trp Ser Cys Leu Val Arg Tyr Asp
    215                 220                 225

gac atg aac cgt tac cct gag cat ttc agc att tct ttt aaa gac atg   835
Asp Met Asn Arg Tyr Pro Glu His Phe Ser Ile Ser Phe Lys Asp Met
230                 235                 240                 245

ctg atc cct gaa cag atc tat act ttc cac ttc acc cca cgt gag gca   883
Leu Ile Pro Glu Gln Ile Tyr Thr Phe His Phe Thr Pro Arg Glu Ala
                250                 255                 260

atg caa ctg cgc aag gga ctt ttt aat gcc atc gct gcc tac aag tct   931
Met Gln Leu Arg Lys Gly Leu Phe Asn Ala Ile Ala Ala Tyr Lys Ser
            265                 270                 275

cag aca tgg ggt gat gag aac act gat ctc acc aag gct gaa ctc gaa   979
Gln Thr Trp Gly Asp Glu Asn Thr Asp Leu Thr Lys Ala Glu Leu Glu
        280                 285                 290

ttt ggt ggc acc tcc atg acc ttc cgc gcc ggc ctc tca cag ctt agc   1027
Phe Gly Gly Thr Ser Met Thr Phe Arg Ala Gly Leu Ser Gln Leu Ser
    295                 300                 305

gtc acc gga cct cct gat cac cgc cag gtg ttc tgc ttg tcg tct tct   1075
Val Thr Gly Pro Pro Asp His Arg Gln Val Phe Cys Leu Ser Ser Ser
310                 315                 320                 325

ggt cgt gag gat cac aac acc ccg cca aac atg cga gac gga cat gtc   1123
Gly Arg Glu Asp His Asn Thr Pro Pro Asn Met Arg Asp Gly His Val
                330                 335                 340

att gat att gcg gtt act caa ttg tcc acc ctg cgt aac ctc att cgg   1171
Ile Asp Ile Ala Val Thr Gln Leu Ser Thr Leu Arg Asn Leu Ile Arg
            345                 350                 355

gta ctg tgc acc act cac ccg gat cat tca cca gca ctg cta cct tat   1219
Val Leu Cys Thr Thr His Pro Asp His Ser Pro Ala Leu Leu Pro Tyr
        360                 365                 370

ggt cag cag tac acc atc taacatgctc taactcgacc ccg                 1260
Gly Gln Gln Tyr Thr Ile
    375
```

<210> 2418
<211> 379
<212> PRT
<213> Corynebacterium glutamicum

<400> 2418

```
Met Leu Tyr Gln His Thr Thr Arg Gly Leu Ile Ile Ser Asp Ala Ile
```

```
  1               5                  10                  15

Ile Ala Lys Ile Ser Gln Val Asn Gln Leu Leu Leu Leu Arg Pro Thr
            20                  25                  30

Leu Leu Gln Asp Lys Asp Met His His Ala Thr Leu Ser Ser Asp Thr
        35                  40                  45

Pro Ser Ile Arg Ser Arg Arg Arg Ser Tyr Arg Glu Asn Lys Ala Ala
    50                  55                  60

Tyr Ala Thr Thr Ser Thr Ile Arg Asn Arg Glu Thr Phe Phe Ser Thr
65                  70                  75                  80

Ser Asp Ile Asp Phe Ala Ile Leu Met Ile Gln Asp Val Gln Glu Ser
                85                  90                  95

Leu Val Ser Phe Asp Pro Thr Leu Ala Gln Asp Met Lys Pro Arg Thr
            100                 105                 110

Asn Ala Val Ile Ser Ala Leu Asn Glu Leu Arg Glu Pro Leu Asp Thr
        115                 120                 125

Phe Tyr Arg Ala His Glu Tyr Gly Asp Ile Ile Ser Asp Gly Ala Tyr
    130                 135                 140

Glu Phe Asp His Ala Ala Ile Asp Ala Gln His Ser Leu Ser Glu Leu
145                 150                 155                 160

Val Ala Gly Leu His Asn Tyr Asp Asn Leu Met Phe Pro Gln Glu Thr
                165                 170                 175

Ala Pro Leu Met Ser Glu Ser Asn Gly Ile Gln Leu Ala Gln Tyr Tyr
            180                 185                 190

Lys Ser Thr Lys Leu Asp Glu Ser Gln Leu Thr Val Glu Pro Asn Glu
        195                 200                 205

Pro Gly Ile Ser Ile Met Trp His Ala His Asp Phe Thr Trp Ser Cys
    210                 215                 220

Leu Val Arg Tyr Asp Asp Met Asn Arg Tyr Pro Glu His Phe Ser Ile
225                 230                 235                 240

Ser Phe Lys Asp Met Leu Ile Pro Glu Gln Ile Tyr Thr Phe His Phe
                245                 250                 255

Thr Pro Arg Glu Ala Met Gln Leu Arg Lys Gly Leu Phe Asn Ala Ile
            260                 265                 270

Ala Ala Tyr Lys Ser Gln Thr Trp Gly Asp Glu Asn Thr Asp Leu Thr
        275                 280                 285

Lys Ala Glu Leu Glu Phe Gly Gly Thr Ser Met Thr Phe Arg Ala Gly
    290                 295                 300

Leu Ser Gln Leu Ser Val Thr Gly Pro Pro Asp His Arg Gln Val Phe
305                 310                 315                 320

Cys Leu Ser Ser Ser Gly Arg Glu Asp His Asn Thr Pro Pro Asn Met
                325                 330                 335
```

```
Arg Asp Gly His Val Ile Asp Ile Ala Val Thr Gln Leu Ser Thr Leu
            340                 345                 350

Arg Asn Leu Ile Arg Val Leu Cys Thr Thr His Pro Asp His Ser Pro
        355                 360                 365

Ala Leu Leu Pro Tyr Gly Gln Gln Tyr Thr Ile
    370                 375


<210> 2419
<211> 1542
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1519)
<223> RXA01779

<400> 2419
ttagtattta gtcaattagc caactacgat aaaactagtg aataaacata ctagttcact 60

ttgtcgcgct taaaatacta gaaagtaata taaaaaactc atg cgt tat act ccc   115
                                            Met Arg Tyr Thr Pro
                                              1               5

cgt acc cac cgc gca ctc gga ctt gct gca ctt acc gct aca gct ctc   163
Arg Thr His Arg Ala Leu Gly Leu Ala Ala Leu Thr Ala Thr Ala Leu
                10                  15                  20

cta ctg agc tca tgc tcg acc acc gct gac ctt ctc ggc gcc gat tct   211
Leu Leu Ser Ser Cys Ser Thr Thr Ala Asp Leu Leu Gly Ala Asp Ser
            25                  30                  35

gtg gcg cag gct gtc acc gat ggt ggc tct gcc ctt gat ccc act gca   259
Val Ala Gln Ala Val Thr Asp Gly Gly Ser Ala Leu Asp Pro Thr Ala
        40                  45                  50

gct cat gtg ctc acc atc acc aat gcc act gca atg act ctt gct gag   307
Ala His Val Leu Thr Ile Thr Asn Ala Thr Ala Met Thr Leu Ala Glu
    55                  60                  65

cta cca gaa aac acc gac cct gac gca gcc aat aac acg gag cca aca   355
Leu Pro Glu Asn Thr Asp Pro Asp Ala Ala Asn Asn Thr Glu Pro Thr
70                  75                  80                  85

atg gcc caa agc gcc ctc aag cgt att tac ggt ctc gaa att gcc gcc   403
Met Ala Gln Ser Ala Leu Lys Arg Ile Tyr Gly Leu Glu Ile Ala Ala
                90                  95                  100

gat ggc act ctg att gct gtc gca gcg cca tta acc tcg cga aat agt   451
Asp Gly Thr Leu Ile Ala Val Ala Ala Pro Leu Thr Ser Arg Asn Ser
            105                 110                 115

ggt tct gag cag cct act gtc gca gca atg gct gat cca gaa aac aat   499
Gly Ser Glu Gln Pro Thr Val Ala Ala Met Ala Asp Pro Glu Asn Asn
        120                 125                 130

gct gaa ctc acc aca gca cat att ctt gag atc gac cca gcc aca gga   547
```

```
Ala Glu Leu Thr Thr Ala His Ile Leu Glu Ile Asp Pro Ala Thr Gly
    135                 140                 145

act gcc aca cca cgt caa gat att gct ctg act gaa gat ttt cag acc   595
Thr Ala Thr Pro Arg Gln Asp Ile Ala Leu Thr Glu Asp Phe Gln Thr
150                 155                 160                 165

atg gct agc tct ttt agc cag atc cgt aat ggc tgg ggt act acc caa   643
Met Ala Ser Ser Phe Ser Gln Ile Arg Asn Gly Trp Gly Thr Thr Gln
                170                 175                 180

ctc atc gga caa cac cct gat gat ccc aag caa cct att cgt tca gct   691
Leu Ile Gly Gln His Pro Asp Asp Pro Lys Gln Pro Ile Arg Ser Ala
            185                 190                 195

gat acc tgg act gtc acc ggc tcc act cag atc acc ggc ttt aac acc   739
Asp Thr Trp Thr Val Thr Gly Ser Thr Gln Ile Thr Gly Phe Asn Thr
        200                 205                 210

aac acc cca acg gga acc gaa gat gct gcc tac acc atg ccg gcg act   787
Asn Thr Pro Thr Gly Thr Glu Asp Ala Ala Tyr Thr Met Pro Ala Thr
    215                 220                 225

gag cca gct gtg gga ctg tgc gct cta gaa tca ggc tcc gat gca cca   835
Glu Pro Ala Val Gly Leu Cys Ala Leu Glu Ser Gly Ser Asp Ala Pro
230                 235                 240                 245

ctg gat gaa cac cgt gag ctc agc acc agt gca ttg cgt acc gca tca   883
Leu Asp Glu His Arg Glu Leu Ser Thr Ser Ala Leu Arg Thr Ala Ser
                250                 255                 260

gta ttg tcg agc tct gga tct gcc acc ctc aag ctg cat gat cct atg   931
Val Leu Ser Ser Ser Gly Ser Ala Thr Leu Lys Leu His Asp Pro Met
            265                 270                 275

gtc atg tct gct act ggc att gtc caa gca cgc gcc tat gtc gat ggc   979
Val Met Ser Ala Thr Gly Ile Val Gln Ala Arg Ala Tyr Val Asp Gly
        280                 285                 290

gaa gtc att aac cag cac gag att ggc gat ctc cgc gag cag ctc ggt   1027
Glu Val Ile Asn Gln His Glu Ile Gly Asp Leu Arg Glu Gln Leu Gly
    295                 300                 305

atc acc atc gaa gaa tct gag gct gct caa gca gaa tcg gat gcc caa   1075
Ile Thr Ile Glu Glu Ser Glu Ala Ala Gln Ala Glu Ser Asp Ala Gln
310                 315                 320                 325

gca gcc acc gat cac cca ctt gca gcc ctg ggc tta agc aac ccc acc   1123
Ala Ala Thr Asp His Pro Leu Ala Ala Leu Gly Leu Ser Asn Pro Thr
                330                 335                 340

agc tca gcg ttg gtt cca ggt ctt gct gag ctt gat tgt ctc agt gct   1171
Ser Ser Ala Leu Val Pro Gly Leu Ala Glu Leu Asp Cys Leu Ser Ala
            345                 350                 355

gac cag gct gcc acc tgg cat aac cgc gac acc agc att ggc acc ggt   1219
Asp Gln Ala Ala Thr Trp His Asn Arg Asp Thr Ser Ile Gly Thr Gly
        360                 365                 370

aag ccc agc gtg ctt gct gtc atc aac gcg gaa atg gcc gat gac ttt   1267
Lys Pro Ser Val Leu Ala Val Ile Asn Ala Glu Met Ala Asp Asp Phe
```

```
    375                 380                 385

acc ctg cag ctg ttg agc tca ggt gcc acc act gcc gaa acg cag ctt   1315
Thr Leu Gln Leu Leu Ser Ser Gly Ala Thr Thr Ala Glu Thr Gln Leu
390                 395                 400                 405

gcc cag ctg ccg gat gaa acc gcg ttc gtg ctc att gac cca tca tct   1363
Ala Gln Leu Pro Asp Glu Thr Ala Phe Val Leu Ile Asp Pro Ser Ser
                410                 415                 420

ggt gct gtt act gac ctg ttc ttt atc caa agt ctc aac act gat ctg   1411
Gly Ala Val Thr Asp Leu Phe Phe Ile Gln Ser Leu Asn Thr Asp Leu
            425                 430                 435

ccg gca cca aca acc cag att aat tct att gct gtt gat gag cgc gac   1459
Pro Ala Pro Thr Thr Gln Ile Asn Ser Ile Ala Val Asp Glu Arg Asp
        440                 445                 450

ccc aac atc atc tac gcc act ttt agc ggc gat gac cac ctg tac caa   1507
Pro Asn Ile Ile Tyr Ala Thr Phe Ser Gly Asp Asp His Leu Tyr Gln
    455                 460                 465

atg atg ctg ggt tagttacaca actaactaac cag                        1542
Met Met Leu Gly
470
```

<210> 2420
<211> 473
<212> PRT
<213> Corynebacterium glutamicum

<400> 2420

```
Met Arg Tyr Thr Pro Arg Thr His Arg Ala Leu Gly Leu Ala Ala Leu
  1               5                  10                  15

Thr Ala Thr Ala Leu Leu Leu Ser Ser Cys Ser Thr Thr Ala Asp Leu
             20                  25                  30

Leu Gly Ala Asp Ser Val Ala Gln Ala Val Thr Asp Gly Gly Ser Ala
         35                  40                  45

Leu Asp Pro Thr Ala Ala His Val Leu Thr Ile Thr Asn Ala Thr Ala
     50                  55                  60

Met Thr Leu Ala Glu Leu Pro Glu Asn Thr Asp Pro Asp Ala Ala Asn
 65                  70                  75                  80

Asn Thr Glu Pro Thr Met Ala Gln Ser Ala Leu Lys Arg Ile Tyr Gly
                 85                  90                  95

Leu Glu Ile Ala Ala Asp Gly Thr Leu Ile Ala Val Ala Ala Pro Leu
            100                 105                 110

Thr Ser Arg Asn Ser Gly Ser Glu Gln Pro Thr Val Ala Ala Met Ala
        115                 120                 125

Asp Pro Glu Asn Asn Ala Glu Leu Thr Thr Ala His Ile Leu Glu Ile
    130                 135                 140

Asp Pro Ala Thr Gly Thr Ala Thr Pro Arg Gln Asp Ile Ala Leu Thr
```

```
145                 150                 155                 160

Glu Asp Phe Gln Thr Met Ala Ser Ser Phe Ser Gln Ile Arg Asn Gly
                165                 170                 175

Trp Gly Thr Thr Gln Leu Ile Gly Gln His Pro Asp Asp Pro Lys Gln
            180                 185                 190

Pro Ile Arg Ser Ala Asp Thr Trp Thr Val Thr Gly Ser Thr Gln Ile
        195                 200                 205

Thr Gly Phe Asn Thr Asn Thr Pro Thr Gly Thr Glu Asp Ala Ala Tyr
    210                 215                 220

Thr Met Pro Ala Thr Glu Pro Ala Val Gly Leu Cys Ala Leu Glu Ser
225                 230                 235                 240

Gly Ser Asp Ala Pro Leu Asp Glu His Arg Glu Leu Ser Thr Ser Ala
                245                 250                 255

Leu Arg Thr Ala Ser Val Leu Ser Ser Ser Gly Ser Ala Thr Leu Lys
            260                 265                 270

Leu His Asp Pro Met Val Met Ser Ala Thr Gly Ile Val Gln Ala Arg
        275                 280                 285

Ala Tyr Val Asp Gly Glu Val Ile Asn Gln His Glu Ile Gly Asp Leu
    290                 295                 300

Arg Glu Gln Leu Gly Ile Thr Ile Glu Glu Ser Glu Ala Ala Gln Ala
305                 310                 315                 320

Glu Ser Asp Ala Gln Ala Ala Thr Asp His Pro Leu Ala Ala Leu Gly
                325                 330                 335

Leu Ser Asn Pro Thr Ser Ser Ala Leu Val Pro Gly Leu Ala Glu Leu
            340                 345                 350

Asp Cys Leu Ser Ala Asp Gln Ala Ala Thr Trp His Asn Arg Asp Thr
        355                 360                 365

Ser Ile Gly Thr Gly Lys Pro Ser Val Leu Ala Val Ile Asn Ala Glu
    370                 375                 380

Met Ala Asp Asp Phe Thr Leu Gln Leu Leu Ser Ser Gly Ala Thr Thr
385                 390                 395                 400

Ala Glu Thr Gln Leu Ala Gln Leu Pro Asp Glu Thr Ala Phe Val Leu
                405                 410                 415

Ile Asp Pro Ser Ser Gly Ala Val Thr Asp Leu Phe Phe Ile Gln Ser
            420                 425                 430

Leu Asn Thr Asp Leu Pro Ala Pro Thr Thr Gln Ile Asn Ser Ile Ala
        435                 440                 445

Val Asp Glu Arg Asp Pro Asn Ile Ile Tyr Ala Thr Phe Ser Gly Asp
    450                 455                 460

Asp His Leu Tyr Gln Met Met Leu Gly
465                 470
```

<210> 2421
<211> 498
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(475)
<223> RXA01780

<400> 2421
ccacttttag cggcgatgac cacctgtacc aaatgatgct gggttagtta cacaactaac 60

taaccaggca ccaacatttt cttaaagaaa cacccttatc atg act ttt ctc cac 115
Met Thr Phe Leu His
1 5

ccc aag gct gcg ttc tac cct ctc acc atg gat cat ctt acc gat ctc 163
Pro Lys Ala Ala Phe Tyr Pro Leu Thr Met Asp His Leu Thr Asp Leu
10 15 20

ggt ctt gat cct gag caa ctc att aat gag ttg ccg acg att acc tac 211
Gly Leu Asp Pro Glu Gln Leu Ile Asn Glu Leu Pro Thr Ile Thr Tyr
25 30 35

gac gtt caa cca cac aat gtc ttt gtt cta cag ttc agc acc gcc gat 259
Asp Val Gln Pro His Asn Val Phe Val Leu Gln Phe Ser Thr Ala Asp
40 45 50

gtg cgc gtc tac cag gaa ggt aat acc ctt ttt atc cgc agt gct gaa 307
Val Arg Val Tyr Gln Glu Gly Asn Thr Leu Phe Ile Arg Ser Ala Glu
55 60 65

tta atc aac cct gaa cta cga caa cga cag cgc aca cag ctc aac gac 355
Leu Ile Asn Pro Glu Leu Arg Gln Arg Gln Arg Thr Gln Leu Asn Asp
70 75 80 85

gat ctc aac aac cct gct tca ctt cgc gtc tgt gat gag atc agt ggc 403
Asp Leu Asn Asn Pro Ala Ser Leu Arg Val Cys Asp Glu Ile Ser Gly
90 95 100

cgc agc acc gtg ttc ctc aaa gac aaa agt gtt gtc act cac gat cac 451
Arg Ser Thr Val Phe Leu Lys Asp Lys Ser Val Val Thr His Asp His
105 110 115

ggg acc aat tgc tgt gat tcc gca taatcctgat gaagccagcg cca 498
Gly Thr Asn Cys Cys Asp Ser Ala
120 125

<210> 2422
<211> 125
<212> PRT
<213> Corynebacterium glutamicum

<400> 2422
Met Thr Phe Leu His Pro Lys Ala Ala Phe Tyr Pro Leu Thr Met Asp
1 5 10 15

```
His Leu Thr Asp Leu Gly Leu Asp Pro Glu Gln Leu Ile Asn Glu Leu
            20                  25                  30

Pro Thr Ile Thr Tyr Asp Val Gln Pro His Asn Val Phe Val Leu Gln
        35                  40                  45

Phe Ser Thr Ala Asp Val Arg Val Tyr Gln Glu Gly Asn Thr Leu Phe
    50                  55                  60

Ile Arg Ser Ala Glu Leu Ile Asn Pro Glu Leu Arg Gln Arg Gln Arg
65                  70                  75                  80

Thr Gln Leu Asn Asp Asp Leu Asn Asn Pro Ala Ser Leu Arg Val Cys
                85                  90                  95

Asp Glu Ile Ser Gly Arg Ser Thr Val Phe Leu Lys Asp Lys Ser Val
            100                 105                 110

Val Thr His Asp His Gly Thr Asn Cys Cys Asp Ser Ala
        115                 120                 125
```

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<210> 2423
<211> 384
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(361)
<223> RXA01781

<400> 2423

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cgacagcgca cacagctcaa cgacgatctc aacaaccctg cttcacttcg cgtctgtgat 60

gagatcagtg gccgcagcac cgtgttcctc aaagacaaaa gtg ttg tca ctc acg   115
                                              Val Leu Ser Leu Thr
                                                1               5

atc acg gga cca att gct gtg att ccg cat aat cct gat gaa gcc agc   163
Ile Thr Gly Pro Ile Ala Val Ile Pro His Asn Pro Asp Glu Ala Ser
            10                  15                  20

gcc aag gct gtc gct acc aaa cat aag cac acc ttg tcc ggc gct acc   211
Ala Lys Ala Val Ala Thr Lys His Lys His Thr Leu Ser Gly Ala Thr
        25                  30                  35

tct gat cac cct tat gcc ggc atg acg ctt aaa gac atg att gaa cag   259
Ser Asp His Pro Tyr Ala Gly Met Thr Leu Lys Asp Met Ile Glu Gln
    40                  45                  50

ggc ttt acg ctc aca ccg ctg gaa ttc ccg ctc tgt gct gtc gat gat   307
Gly Phe Thr Leu Thr Pro Leu Glu Phe Pro Leu Cys Ala Val Asp Asp
55                  60                  65

cca aca gat tct gat cgc acc atg cac gtg atc aat gtt cgc gag cac   355
Pro Thr Asp Ser Asp Arg Thr Met His Val Ile Asn Val Arg Glu His
70                  75                  80                  85

agt atg tagattctaa agtgcggtac aac                                384
Ser Met
```

<210> 2424
<211> 87
<212> PRT
<213> Corynebacterium glutamicum

<400> 2424

```
Val Leu Ser Leu Thr Ile Thr Gly Pro Ile Ala Val Ile Pro His Asn
  1               5                  10                  15

Pro Asp Glu Ala Ser Ala Lys Ala Val Ala Thr Lys His Lys His Thr
             20                  25                  30

Leu Ser Gly Ala Thr Ser Asp His Pro Tyr Ala Gly Met Thr Leu Lys
         35                  40                  45

Asp Met Ile Glu Gln Gly Phe Thr Leu Thr Pro Leu Glu Phe Pro Leu
     50                  55                  60

Cys Ala Val Asp Asp Pro Thr Asp Ser Asp Arg Thr Met His Val Ile
 65                  70                  75                  80

Asn Val Arg Glu His Ser Met
                 85
```

<210> 2425
<211> 519
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(496)
<223> RXA01782

<400> 2425

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acgtgatcaa tgttcgcgag cacagtatgt agattctaaa gtgcggtaca acctgtaccg 60

cccacacaat tccacccttt aagaaaagga cttagccatc atg acc acc ttc gcc   115
                                            Met Thr Thr Phe Ala
                                              1               5

ctt att gct agc ccc aac aat gtt gat ccc act gct gag tcc cca ctc   163
Leu Ile Ala Ser Pro Asn Asn Val Asp Pro Thr Ala Glu Ser Pro Leu
                 10                  15                  20

gcc att gaa atc cat acc gat gag gac agc agc tat cca cta ggg ctt   211
Ala Ile Glu Ile His Thr Asp Glu Asp Ser Ser Tyr Pro Leu Gly Leu
             25                  30                  35

att gac tca gac cac ctg gtt cct gct gtg att tac ggc gat atg gtg   259
Ile Asp Ser Asp His Leu Val Pro Ala Val Ile Tyr Gly Asp Met Val
         40                  45                  50

atc tac acc aaa aca ctg ctc gca cag acc cca cca gat gat gtg tcc   307
Ile Tyr Thr Lys Thr Leu Leu Ala Gln Thr Pro Pro Asp Asp Val Ser
     55                  60                  65
```

```
act gct agc gcc ttc ttc gac aaa ctc acc gca ctt gac gct cag ggt   355
Thr Ala Ser Ala Phe Phe Asp Lys Leu Thr Ala Leu Asp Ala Gln Gly
 70                  75                  80                  85

cgc acc cgt gat ctg gtc tac agc gcc acc tac agc caa ctt gtt att   403
Arg Thr Arg Asp Leu Val Tyr Ser Ala Thr Tyr Ser Gln Leu Val Ile
                90                  95                 100

gcc ggc cac aac cgc act gta tta act gac gac tca gag ttc tac gat   451
Ala Gly His Asn Arg Thr Val Leu Thr Asp Asp Ser Glu Phe Tyr Asp
            105                 110                 115

gag ttt tac cag gtt att gag gct gct cct ggg gtg atc ttg aaa       496
Glu Phe Tyr Gln Val Ile Glu Ala Ala Pro Gly Val Ile Leu Lys
        120                 125                 130

tgatgtttat cgggcaacac ctc                                        519
```

<210> 2426
<211> 132
<212> PRT
<213> Corynebacterium glutamicum

<400> 2426

```
Met Thr Thr Phe Ala Leu Ile Ala Ser Pro Asn Asn Val Asp Pro Thr
  1               5                  10                  15

Ala Glu Ser Pro Leu Ala Ile Glu Ile His Thr Asp Glu Asp Ser Ser
             20                  25                  30

Tyr Pro Leu Gly Leu Ile Asp Ser Asp His Leu Val Pro Ala Val Ile
         35                  40                  45

Tyr Gly Asp Met Val Ile Tyr Thr Lys Thr Leu Leu Ala Gln Thr Pro
     50                  55                  60

Pro Asp Asp Val Ser Thr Ala Ser Ala Phe Phe Asp Lys Leu Thr Ala
 65                  70                  75                  80

Leu Asp Ala Gln Gly Arg Thr Arg Asp Leu Val Tyr Ser Ala Thr Tyr
                85                  90                  95

Ser Gln Leu Val Ile Ala Gly His Asn Arg Thr Val Leu Thr Asp Asp
            100                 105                 110

Ser Glu Phe Tyr Asp Glu Phe Tyr Gln Val Ile Glu Ala Ala Pro Gly
        115                 120                 125

Val Ile Leu Lys
    130
```

<210> 2427
<211> 360
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(337)

<223> RXA01783

<400> 2427
accaggttat tgaggctgct cctggggtga tcttgaaatg atgtttatcg ggcaacacct 60

cacacttagg ctaggtctct aacatgaagc agatagcgcc atg atc aat ctt ttt 115
Met Ile Asn Leu Phe
1 5

gct gca gcc ctg ccc gca ttc gag cct ttg agt att acc tcc ata ctc 163
Ala Ala Ala Leu Pro Ala Phe Glu Pro Leu Ser Ile Thr Ser Ile Leu
10 15 20

gtg ctc ggt gct gtg gca ttg atc tgt ggc ctc cct gtt ttt ctc gca 211
Val Leu Gly Ala Val Ala Leu Ile Cys Gly Leu Pro Val Phe Leu Ala
25 30 35

ctg gaa aaa agc gct gag ctc gat gat ctc ttc gca gca ctc atc atc 259
Leu Glu Lys Ser Ala Glu Leu Asp Asp Leu Phe Ala Ala Leu Ile Ile
40 45 50

gct gta ctt tta ggt ttt gct gct tat acg ttt gtg ctc ccc aag ctc 307
Ala Val Leu Leu Gly Phe Ala Ala Tyr Thr Phe Val Leu Pro Lys Leu
55 60 65

gtt gaa ttg ggc tgt act att tgc cag ctc tgactagcga cacttacact 357
Val Glu Leu Gly Cys Thr Ile Cys Gln Leu
70 75

ttc 360

<210> 2428
<211> 79
<212> PRT
<213> Corynebacterium glutamicum

<400> 2428
Met Ile Asn Leu Phe Ala Ala Ala Leu Pro Ala Phe Glu Pro Leu Ser
1 5 10 15

Ile Thr Ser Ile Leu Val Leu Gly Ala Val Ala Leu Ile Cys Gly Leu
20 25 30

Pro Val Phe Leu Ala Leu Glu Lys Ser Ala Glu Leu Asp Asp Leu Phe
35 40 45

Ala Ala Leu Ile Ile Ala Val Leu Leu Gly Phe Ala Ala Tyr Thr Phe
50 55 60

Val Leu Pro Lys Leu Val Glu Leu Gly Cys Thr Ile Cys Gln Leu
65 70 75

<210> 2429
<211> 699
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(676)
<223> RXA01785

<400> 2429
gaccctggcc caactttgca acagcaccat ccacagtgat ggcactacca atactgagcc 60

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tgactacgca tctaaggcgg cgcacattag tgatgcaact gtg gat cag ttc gtt   115
                                              Val Asp Gln Phe Val
                                                1               5

gag ttc ggc ggt gga caa gca aac att aac cct gat gga tca gcg acc   163
Glu Phe Gly Gly Gly Gln Ala Asn Ile Asn Pro Asp Gly Ser Ala Thr
                10                  15                  20

gtt gat tgg gag ggt tct ttc agc atc aac ttc tac gat ggt ttg gtg   211
Val Asp Trp Glu Gly Ser Phe Ser Ile Asn Phe Tyr Asp Gly Leu Val
            25                  30                  35

ccg ttt acc atc acg aat ccg cac ctc gag gtt tct gta gct ggt act   259
Pro Phe Thr Ile Thr Asn Pro His Leu Glu Val Ser Val Ala Gly Thr
        40                  45                  50

ggt gtt ttg act ggt gac ctc act agc tat gca gtg gag atg tcg aac   307
Gly Val Leu Thr Gly Asp Leu Thr Ser Tyr Ala Val Glu Met Ser Asn
    55                  60                  65

ccg aat gag aaa acc ccg ttg act gac ttg tat gag gat gtc acg atc   355
Pro Asn Glu Lys Thr Pro Leu Thr Asp Leu Tyr Glu Asp Val Thr Ile
70                  75                  80                  85

aca acg ttt ggg gga gtg aac ctt gat cct gaa ggt gtt gtg aca agc   403
Thr Thr Phe Gly Gly Val Asn Leu Asp Pro Glu Gly Val Val Thr Ser
                90                  95                 100

aat cct gat tat gac gga gtg att gtt gat gtc cca ctg gat gcc acc   451
Asn Pro Asp Tyr Asp Gly Val Ile Val Asp Val Pro Leu Asp Ala Thr
            105                 110                 115

tct cag gtt act tcc ggt gca ggt tgg gga gcg tgg ccg cag ggc ttc   499
Ser Gln Val Thr Ser Gly Ala Gly Trp Gly Ala Trp Pro Gln Gly Phe
        120                 125                 130

ctt gat ttc cac ttt gat acc aac ttg cct tcc tac tgg tat tcc tca   547
Leu Asp Phe His Phe Asp Thr Asn Leu Pro Ser Tyr Trp Tyr Ser Ser
    135                 140                 145

gat ggc gca ggt gat cct aag aag gcg cct atg agc ttt aat gtt gat   595
Asp Gly Ala Gly Asp Pro Lys Lys Ala Pro Met Ser Phe Asn Val Asp
150                 155                 160                 165

ttc act aat ggt cca ggt ctg gtg aac agc caa ttg ctc cac agg caa   643
Phe Thr Asn Gly Pro Gly Leu Val Asn Ser Gln Leu Leu His Arg Gln
                170                 175                 180

gtg atc tca atg ccg gaa acc aag gca gtc tcg tagttccatc ggaggcagaa 696
Val Ile Ser Met Pro Glu Thr Lys Ala Val Ser
            185                 190

gct                                                               699
```

<210> 2430
<211> 192
<212> PRT
<213> Corynebacterium glutamicum

<400> 2430
Val Asp Gln Phe Val Glu Phe Gly Gly Gly Gln Ala Asn Ile Asn Pro
1 5 10 15

Asp Gly Ser Ala Thr Val Asp Trp Glu Gly Ser Phe Ser Ile Asn Phe
20 25 30

Tyr Asp Gly Leu Val Pro Phe Thr Ile Thr Asn Pro His Leu Glu Val
35 40 45

Ser Val Ala Gly Thr Gly Val Leu Thr Gly Asp Leu Thr Ser Tyr Ala
50 55 60

Val Glu Met Ser Asn Pro Asn Glu Lys Thr Pro Leu Thr Asp Leu Tyr
65 70 75 80

Glu Asp Val Thr Ile Thr Thr Phe Gly Gly Val Asn Leu Asp Pro Glu
85 90 95

Gly Val Val Thr Ser Asn Pro Asp Tyr Asp Gly Val Ile Val Asp Val
100 105 110

Pro Leu Asp Ala Thr Ser Gln Val Thr Ser Gly Ala Gly Trp Gly Ala
115 120 125

Trp Pro Gln Gly Phe Leu Asp Phe His Phe Asp Thr Asn Leu Pro Ser
130 135 140

Tyr Trp Tyr Ser Ser Asp Gly Ala Gly Asp Pro Lys Lys Ala Pro Met
145 150 155 160

Ser Phe Asn Val Asp Phe Thr Asn Gly Pro Gly Leu Val Asn Ser Gln
165 170 175

Leu Leu His Arg Gln Val Ile Ser Met Pro Glu Thr Lys Ala Val Ser
180 185 190

<210> 2431
<211> 564
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(541)
<223> RXA01788

<400> 2431
cctttaaccc aaattcctat atcactacag ataccgtgcg catcgttgtc gatcctgtac 60

cggaaactaa tcccgacgat gagaaagcag gacgctagcc atg tct cgc agc tac 115
Met Ser Arg Ser Tyr

```
                                                    1               5

ccc atc tac atc att tct ttt gcc cca gcg gat gat ctc cac ggc gtt   163
Pro Ile Tyr Ile Ile Ser Phe Ala Pro Ala Asp Asp Leu His Gly Val
                10                  15                  20

gga gga ttc gag tgg gtt cca gca tca aca cca gaa aac aaa gct gcc   211
Gly Gly Phe Glu Trp Val Pro Ala Ser Thr Pro Glu Asn Lys Ala Ala
            25                  30                  35

gcc ttc acg acc ttt gat cgt caa ttc gat gat tct cgt aac aat ggt   259
Ala Phe Thr Thr Phe Asp Arg Gln Phe Asp Asp Ser Arg Asn Asn Gly
        40                  45                  50

ggc tcg cat att gtg cgt cta ctc aat atc tct gat ccc aat atc aca   307
Gly Ser His Ile Val Arg Leu Leu Asn Ile Ser Asp Pro Asn Ile Thr
    55                  60                  65

gcg gat atg acc caa gac gat att acc gcg tac ctc gac tca aac atc   355
Ala Asp Met Thr Gln Asp Asp Ile Thr Ala Tyr Leu Asp Ser Asn Ile
70                  75                  80                  85

gac cgc tgg gaa tcc acg gaa cat gcg ctc aag cag ttt gtc cca ctt   403
Asp Arg Trp Glu Ser Thr Glu His Ala Leu Lys Gln Phe Val Pro Leu
                90                  95                  100

aac gcg ggt gct gat cgc gta cct acc ggt ggt gcc gac gag cac att   451
Asn Ala Gly Ala Asp Arg Val Pro Thr Gly Gly Ala Asp Glu His Ile
            105                 110                 115

acc cac gcc tgc cgc ata ata act gtg cag cgt agc tgc aca cgg att   499
Thr His Ala Cys Arg Ile Ile Thr Val Gln Arg Ser Cys Thr Arg Ile
        120                 125                 130

cac ctg cgc tgt gga tgc atc cca aca cca caa cac cgc ccc           541
His Leu Arg Cys Gly Cys Ile Pro Thr Pro Gln His Arg Pro
    135                 140                 145

tagtgccata aatgctaggg gtg                                        564
```

Translated by Tool - Serial No. 10/590,944

<210> 2432
<211> 147
<212> PRT
<213> Corynebacterium glutamicum

<400> 2432

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Met Ser Arg Ser Tyr Pro Ile Tyr Ile Ile Ser Phe Ala Pro Ala Asp
  1               5                  10                  15

Asp Leu His Gly Val Gly Gly Phe Glu Trp Val Pro Ala Ser Thr Pro
            20                  25                  30

Glu Asn Lys Ala Ala Ala Phe Thr Thr Phe Asp Arg Gln Phe Asp Asp
        35                  40                  45

Ser Arg Asn Asn Gly Gly Ser His Ile Val Arg Leu Leu Asn Ile Ser
    50                  55                  60

Asp Pro Asn Ile Thr Ala Asp Met Thr Gln Asp Asp Ile Thr Ala Tyr
65                  70                  75                  80
```

```
Leu Asp Ser Asn Ile Asp Arg Trp Glu Ser Thr Glu His Ala Leu Lys
                85                  90                  95

Gln Phe Val Pro Leu Asn Ala Gly Ala Asp Arg Val Pro Thr Gly Gly
            100                 105                 110

Ala Asp Glu His Ile Thr His Ala Cys Arg Ile Ile Thr Val Gln Arg
        115                 120                 125

Ser Cys Thr Arg Ile His Leu Arg Cys Gly Cys Ile Pro Thr Pro Gln
    130                 135                 140

His Arg Pro
145
```

<210> 2433
<211> 765
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(742)
<223> RXA01789

<400> 2433

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tgcatcccaa caccacaaca ccgcccctag tgccataaat gctaggggtg ttttttttcat 60

acccacaaca ccgttcttct ctagaaagag actcgatact atg cct cat aac ccc   115
                                             Met Pro His Asn Pro
                                               1               5

atc gaa ctt cac act aat gat gta ctc gat gct ctc gac att gac gcc   163
Ile Glu Leu His Thr Asn Asp Val Leu Asp Ala Leu Asp Ile Asp Ala
                10                  15                  20

atc tgc gac gat gtg ttt ctc tac acc gac ttc gag cac acc cca ggt   211
Ile Cys Asp Asp Val Phe Leu Tyr Thr Asp Phe Glu His Thr Pro Gly
            25                  30                  35

cag ctt gat cgc ttc gag caa ctc gcc ttc aca aaa atc tac gac atg   259
Gln Leu Asp Arg Phe Glu Gln Leu Ala Phe Thr Lys Ile Tyr Asp Met
        40                  45                  50

ctg gaa aca gct gct gaa aaa ttc cca gat gta gca att aat gac act   307
Leu Glu Thr Ala Ala Glu Lys Phe Pro Asp Val Ala Ile Asn Asp Thr
    55                  60                  65

tta agc act ggc aac cac gct gct gaa cag tac ttt ctt gcc aat ccc   355
Leu Ser Thr Gly Asn His Ala Ala Glu Gln Tyr Phe Leu Ala Asn Pro
70                  75                  80                  85

ggc aac atc atc gtg ctg acc agc ttc gcg ctc aat cag acc gat ctc   403
Gly Asn Ile Ile Val Leu Thr Ser Phe Ala Leu Asn Gln Thr Asp Leu
                90                  95                  100

cgc gac ctc ata atc tca ccg tgc att aag tac aca gca cat gca cga   451
Arg Asp Leu Ile Ile Ser Pro Cys Ile Lys Tyr Thr Ala His Ala Arg
            105                 110                 115
```

```
gca ctc atg cgt gcg gtg aca cga aca ttg tgc act gca aac aac cct   499
Ala Leu Met Arg Ala Val Thr Arg Thr Leu Cys Thr Ala Asn Asn Pro
        120                 125                 130

gta gaa cgc gcg act atc ttc cct gtg tct gtc gct aat gcc tta agc   547
Val Glu Arg Ala Thr Ile Phe Pro Val Ser Val Ala Asn Ala Leu Ser
    135                 140                 145

atc gaa gcg ctg tgt tcc gaa tat cat gcg ttc cgc acc aag cag gtg   595
Ile Glu Ala Leu Cys Ser Glu Tyr His Ala Phe Arg Thr Lys Gln Val
150                 155                 160                 165

ctc aac act gct gca ctc atc aat cct gat aac act ctt ata ccc atg   643
Leu Asn Thr Ala Ala Leu Ile Asn Pro Asp Asn Thr Leu Ile Pro Met
                170                 175                 180

ttg ttg agc aaa gcg tat gag gca tac gcc tgg cac aag ggt gtc gaa   691
Leu Leu Ser Lys Ala Tyr Glu Ala Tyr Ala Trp His Lys Gly Val Glu
            185                 190                 195

tcc gcg caa cga ggt agc aac cta gct cgt gag tac tac gca gga ctt   739
Ser Ala Gln Arg Gly Ser Asn Leu Ala Arg Glu Tyr Tyr Ala Gly Leu
        200                 205                 210

atc tgaaaattca ctactcaact ctg                                    765
Ile
```

Application Filed 2004-12-22 09:22:22 EST

<210> 2434
<211> 214
<212> PRT
<213> Corynebacterium glutamicum

<400> 2434

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Met Pro His Asn Pro Ile Glu Leu His Thr Asn Asp Val Leu Asp Ala
  1               5                  10                  15

Leu Asp Ile Asp Ala Ile Cys Asp Asp Val Phe Leu Tyr Thr Asp Phe
             20                  25                  30

Glu His Thr Pro Gly Gln Leu Asp Arg Phe Glu Gln Leu Ala Phe Thr
         35                  40                  45

Lys Ile Tyr Asp Met Leu Glu Thr Ala Ala Glu Lys Phe Pro Asp Val
     50                  55                  60

Ala Ile Asn Asp Thr Leu Ser Thr Gly Asn His Ala Ala Glu Gln Tyr
 65                  70                  75                  80

Phe Leu Ala Asn Pro Gly Asn Ile Ile Val Leu Thr Ser Phe Ala Leu
                 85                  90                  95

Asn Gln Thr Asp Leu Arg Asp Leu Ile Ile Ser Pro Cys Ile Lys Tyr
            100                 105                 110

Thr Ala His Ala Arg Ala Leu Met Arg Ala Val Thr Arg Thr Leu Cys
        115                 120                 125

Thr Ala Asn Asn Pro Val Glu Arg Ala Thr Ile Phe Pro Val Ser Val
```

```
    130                 135                 140

Ala Asn Ala Leu Ser Ile Glu Ala Leu Cys Ser Glu Tyr His Ala Phe
145                 150                 155                 160

Arg Thr Lys Gln Val Leu Asn Thr Ala Ala Leu Ile Asn Pro Asp Asn
                165                 170                 175

Thr Leu Ile Pro Met Leu Leu Ser Lys Ala Tyr Glu Ala Tyr Ala Trp
            180                 185                 190

His Lys Gly Val Glu Ser Ala Gln Arg Gly Ser Asn Leu Ala Arg Glu
        195                 200                 205

Tyr Tyr Ala Gly Leu Ile
    210
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<210> 2435
<211> 183
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(160)
<223> RXA01790

<400> 2435
gaaaggctcg aacacccatg atcgttgagg tagctccgag accgaagaga tcagcctcat 60

tgatgatgat tcccctgatc tcgatgagga cgataacacc gtg ctc atc gcc gaa 115
                                            Val Leu Ile Ala Glu
                                              1   5

gac atc cgt gat atg gat gac tat ggc gaa gat cat cct gat ctt 160
Asp Ile Arg Asp Met Asp Asp Tyr Gly Glu Asp His Pro Asp Leu
                10   15   20

taaagctcac tgttaagccc gca 183

<210> 2436
<211> 20
<212> PRT
<213> Corynebacterium glutamicum

<400> 2436
Val Leu Ile Ala Glu Asp Ile Arg Asp Met Asp Asp Tyr Gly Glu Asp
  1   5   10   15

His Pro Asp Leu
            20

<210> 2437
<211> 486
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(463)
<223> RXA01791

<400> 2437
ccgcctgtgc aactaaccct gttgtgcagg cggttttctc tatctacacc aacaactcca 60

caacactatc cggtccaaat ctagaaaaga gacaaccccc atg acc tcc ccc acc 115
Met Thr Ser Pro Thr
1 5

acg tta aag ccc tgg tct att cgc gga ccc atc gac ggt gaa tac acc 163
Thr Leu Lys Pro Trp Ser Ile Arg Gly Pro Ile Asp Gly Glu Tyr Thr
10 15 20

atg ctt gag gca tat ccg ttt cag tat gta gca aat act cgc ccg gcc 211
Met Leu Glu Ala Tyr Pro Phe Gln Tyr Val Ala Asn Thr Arg Pro Ala
25 30 35

atc atg ctc tac gca ctc gat gaa aac ggt gta ccg gaa caa tat gcc 259
Ile Met Leu Tyr Ala Leu Asp Glu Asn Gly Val Pro Glu Gln Tyr Ala
40 45 50

gac ctc acc atc aac ctt gcc gat gtg gag ctc aag caa ctt aac cac 307
Asp Leu Thr Ile Asn Leu Ala Asp Val Glu Leu Lys Gln Leu Asn His
55 60 65

gtc atc att aac cca gat ctg cac gct gat gtt acc gaa ctg tgc att 355
Val Ile Ile Asn Pro Asp Leu His Ala Asp Val Thr Glu Leu Cys Ile
70 75 80 85

agc gcc ggc ctg ctg cga cct ggt gtt ctg ggc cag cac caa gtc ggt 403
Ser Ala Gly Leu Leu Arg Pro Gly Val Leu Gly Gln His Gln Val Gly
90 95 100

agc acc acc gcc aag gtc tac cga ctc act gag cgt gct gat ggc tgg 451
Ser Thr Thr Ala Lys Val Tyr Arg Leu Thr Glu Arg Ala Asp Gly Trp
105 110 115

cta cag ctg ttt tagcagctac ctgcgcctaa tcc 486
Leu Gln Leu Phe
120

<210> 2438
<211> 121
<212> PRT
<213> Corynebacterium glutamicum

<400> 2438
Met Thr Ser Pro Thr Thr Leu Lys Pro Trp Ser Ile Arg Gly Pro Ile
1 5 10 15

Asp Gly Glu Tyr Thr Met Leu Glu Ala Tyr Pro Phe Gln Tyr Val Ala
20 25 30

Asn Thr Arg Pro Ala Ile Met Leu Tyr Ala Leu Asp Glu Asn Gly Val
35 40 45

Pro Glu Gln Tyr Ala Asp Leu Thr Ile Asn Leu Ala Asp Val Glu Leu
50 55 60

```
Lys Gln Leu Asn His Val Ile Ile Asn Pro Asp Leu His Ala Asp Val
 65                  70                  75                  80

Thr Glu Leu Cys Ile Ser Ala Gly Leu Leu Arg Pro Gly Val Leu Gly
                 85                  90                  95

Gln His Gln Val Gly Ser Thr Thr Ala Lys Val Tyr Arg Leu Thr Glu
            100                 105                 110

Arg Ala Asp Gly Trp Leu Gln Leu Phe
        115                 120


<210> 2439
<211> 396
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(373)
<223> RXA01792

<400> 2439
gactcactga gcgtgctgat ggctggctac agctgtttta gcagctacct gcgcctaatc 60

cccccaccca tactcactcc aaaacaagaa agtagtcatc atg cct cag tac acc   115
                                            Met Pro Gln Tyr Thr
                                              1               5

atc aca atc acc gac gag cag aaa gct gtt cta cac agc ctc acc aac   163
Ile Thr Ile Thr Asp Glu Gln Lys Ala Val Leu His Ser Leu Thr Asn
                 10                  15                  20

ccc cat atc gcc act gct gaa cac ggc gct atc acc gca atc gag att   211
Pro His Ile Ala Thr Ala Glu His Gly Ala Ile Thr Ala Ile Glu Ile
             25                  30                  35

cat gac gac cac gat gtt gtt gtc tat cac gtt caa cca gac ggc aca   259
His Asp Asp His Asp Val Val Val Tyr His Val Gln Pro Asp Gly Thr
         40                  45                  50

cta act tac gag cgc ctt gtt gaa ggc ttc cat tac ggc tgg aca cgt   307
Leu Thr Tyr Glu Arg Leu Val Glu Gly Phe His Tyr Gly Trp Thr Arg
     55                  60                  65

ttt gac agc gaa ggt ttt gag atc gac tcc gac aat aac cgc gtt gta   355
Phe Asp Ser Glu Gly Phe Glu Ile Asp Ser Asp Asn Asn Arg Val Val
 70                  75                  80                  85

gac gga ctc cgc gac gaa tagttaacaa caacgaccgc aca                 396
Asp Gly Leu Arg Asp Glu
                 90


<210> 2440
<211> 91
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 2440
Met Pro Gln Tyr Thr Ile Thr Ile Thr Asp Glu Gln Lys Ala Val Leu
1 5 10 15

His Ser Leu Thr Asn Pro His Ile Ala Thr Ala Glu His Gly Ala Ile
20 25 30

Thr Ala Ile Glu Ile His Asp Asp His Asp Val Val Val Tyr His Val
35 40 45

Gln Pro Asp Gly Thr Leu Thr Tyr Glu Arg Leu Val Glu Gly Phe His
50 55 60

Tyr Gly Trp Thr Arg Phe Asp Ser Glu Gly Phe Glu Ile Asp Ser Asp
65 70 75 80

Asn Asn Arg Val Val Asp Gly Leu Arg Asp Glu
85 90

<210> 2441
<211> 357
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(334)
<223> RXA01793

<400> 2441
ccttctctgc aggctacgca gtgctgcgcc tagttcgcag cctgcgccga cttttgcagc 60

gccactaaac acccaaacac aacaagaaag aaacaccact atg gca caa tac cgc 115
Met Ala Gln Tyr Arg
1 5

gtc agt ttt atc gcg ctc gcc gag tca acc atc gag gtc gaa gca gac 163
Val Ser Phe Ile Ala Leu Ala Glu Ser Thr Ile Glu Val Glu Ala Asp
10 15 20

agt cct gaa gaa gca ctc gac cta gcc aat gca gaa ttt gac tac ccg 211
Ser Pro Glu Glu Ala Leu Asp Leu Ala Asn Ala Glu Phe Asp Tyr Pro
25 30 35

gtc acc ttg gcc ggc gat ccc tat gag ctg cac gac tgg gaa gca cgc 259
Val Thr Leu Ala Gly Asp Pro Tyr Glu Leu His Asp Trp Glu Ala Arg
40 45 50

gct gaa att gaa tgg ctc gat acc agc tcg acc ccg cag caa cgc ctt 307
Ala Glu Ile Glu Trp Leu Asp Thr Ser Ser Thr Pro Gln Gln Arg Leu
55 60 65

gga gaa cat gtc gtc aag atc gaa gat taaactcgat cattaaacac 354
Gly Glu His Val Val Lys Ile Glu Asp
70 75

act 357

<210> 2442

<211> 78
<212> PRT
<213> Corynebacterium glutamicum

<400> 2442
Met Ala Gln Tyr Arg Val Ser Phe Ile Ala Leu Ala Glu Ser Thr Ile
1 5 10 15

Glu Val Glu Ala Asp Ser Pro Glu Glu Ala Leu Asp Leu Ala Asn Ala
20 25 30

Glu Phe Asp Tyr Pro Val Thr Leu Ala Gly Asp Pro Tyr Glu Leu His
35 40 45

Asp Trp Glu Ala Arg Ala Glu Ile Glu Trp Leu Asp Thr Ser Ser Thr
50 55 60

Pro Gln Gln Arg Leu Gly Glu His Val Val Lys Ile Glu Asp
65 70 75

<210> 2443
<211> 357
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(334)
<223> RXA01794

<400> 2443
ataccagctc gaccccgcag caacgccttg gagaacatgt cgtcaagatc gaagattaaa 60

ctcgatcatt aaacacactc ttaagataag gacactaatt atg gca acc cac cgc 115
Met Ala Thr His Arg
1 5

gtt cat ttt gtc gca acc gca tcc gcc tac atc gac gtt gag gca gat 163
Val His Phe Val Ala Thr Ala Ser Ala Tyr Ile Asp Val Glu Ala Asp
10 15 20

tcc ccc gaa gat gct ata gaa aaa gcg tat gat ctc gcc ggt gat ctg 211
Ser Pro Glu Asp Ala Ile Glu Lys Ala Tyr Asp Leu Ala Gly Asp Leu
25 30 35

ccc ggc ctc atc gcc gac aac gaa ttt gat ctc ggt gaa tgg gag gta 259
Pro Gly Leu Ile Ala Asp Asn Glu Phe Asp Leu Gly Glu Trp Glu Val
40 45 50

cag gcc gat gtc cag tgg cct gat aac tct gta cct cgc gag caa cgc 307
Gln Ala Asp Val Gln Trp Pro Asp Asn Ser Val Pro Arg Glu Gln Arg
55 60 65

ctt gaa gag ggc gtt gac ctg ctc gat taaacagaat taactcaaac 354
Leu Glu Glu Gly Val Asp Leu Leu Asp
70 75

ccc 357

<210> 2444
<211> 78
<212> PRT
<213> Corynebacterium glutamicum

<400> 2444
Met Ala Thr His Arg Val His Phe Val Ala Thr Ala Ser Ala Tyr Ile
1 5 10 15

Asp Val Glu Ala Asp Ser Pro Glu Asp Ala Ile Glu Lys Ala Tyr Asp
20 25 30

Leu Ala Gly Asp Leu Pro Gly Leu Ile Ala Asp Asn Glu Phe Asp Leu
35 40 45

Gly Glu Trp Glu Val Gln Ala Asp Val Gln Trp Pro Asp Asn Ser Val
50 55 60

Pro Arg Glu Gln Arg Leu Glu Glu Gly Val Asp Leu Leu Asp
65 70 75

<210> 2445
<211> 1317
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1294)
<223> RXA01799

<400> 2445
tattttgggc atgcactcgt catatcttca cagacgtatg gttttgtaac aacctccccc 60

aaaatcccca tagtttcccc cggtgcatat ccttaaaggt atg gaa att ccg ctg 115
Met Glu Ile Pro Leu
1 5

ccc aca tcc ctt atc gat gtc atc act gat ggt gcc ctc ggc caa acc 163
Pro Thr Ser Leu Ile Asp Val Ile Thr Asp Gly Ala Leu Gly Gln Thr
10 15 20

tgc att gat cag gca ttt gct gcc caa ttg ggg cga gtt act gga gtc 211
Cys Ile Asp Gln Ala Phe Ala Ala Gln Leu Gly Arg Val Thr Gly Val
25 30 35

gaa ttc aac ctt tct gac gat aaa acc gcg gct gaa gtg agg atc aat 259
Glu Phe Asn Leu Ser Asp Asp Lys Thr Ala Ala Glu Val Arg Ile Asn
40 45 50

aag gcg tcg ggg agt cct ttt gat acc acc ggt gaa gtc att gcg tgg 307
Lys Ala Ser Gly Ser Pro Phe Asp Thr Thr Gly Glu Val Ile Ala Trp
55 60 65

att aat aat cag gaa ttt gag tgg gtc agc acg cgc ggt gag gat ttg 355
Ile Asn Asn Gln Glu Phe Glu Trp Val Ser Thr Arg Gly Glu Asp Leu
70 75 80 85

gga ctg cct gaa ttg cag ggc att cag ccg ctc gac gat gat ctg atc 403
Gly Leu Pro Glu Leu Gln Gly Ile Gln Pro Leu Asp Asp Asp Leu Ile

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                    90                  95                 100

acc gcc gca cgc acg ctg tat agc aat gcg ccg gcg ttc atc gcc ccg   451
Thr Ala Ala Arg Thr Leu Tyr Ser Asn Ala Pro Ala Phe Ile Ala Pro
            105                 110                 115

ttg cgc gat ggt cgc agg gcg ttg gtt gcg atc aat cac acg cca aaa   499
Leu Arg Asp Gly Arg Arg Ala Leu Val Ala Ile Asn His Thr Pro Lys
        120                 125                 130

ctg gtt ggt atc cgt cgc acg ctc atc gaa ggc ctg cag gcg ctg aag   547
Leu Val Gly Ile Arg Arg Thr Leu Ile Glu Gly Leu Gln Ala Leu Lys
    135                 140                 145

cct gga act gac ctc aaa cgg gca ttg act tca ttt gct gca ttc tgc   595
Pro Gly Thr Asp Leu Lys Arg Ala Leu Thr Ser Phe Ala Ala Phe Cys
150                 155                 160                 165

gaa ctg ggc atc cga ttc gat gac aac cgc atc tcc ttc agc gat ggc   643
Glu Leu Gly Ile Arg Phe Asp Asp Asn Arg Ile Ser Phe Ser Asp Gly
                170                 175                 180

acc tcg ctg ttg ctt cgt ggc ggc aaa gtc atc gaa atc gca ggc ggg   691
Thr Ser Leu Leu Leu Arg Gly Gly Lys Val Ile Glu Ile Ala Gly Gly
            185                 190                 195

ctg agc ttg cgc gac gta cgc gcg gat gcg gcg ttc atg tcc gct gag   739
Leu Ser Leu Arg Asp Val Arg Ala Asp Ala Ala Phe Met Ser Ala Glu
        200                 205                 210

cat caa ttg ctt ttc gac gcc atc tcc tcg tct cac aac gtc acc ttt   787
His Gln Leu Leu Phe Asp Ala Ile Ser Ser Ser His Asn Val Thr Phe
    215                 220                 225

gac cca cac acc aac gtg gcg acc gtg gca aac gaa cac caa gtt cac   835
Asp Pro His Thr Asn Val Ala Thr Val Ala Asn Glu His Gln Val His
230                 235                 240                 245

gcc atc ccc ctt gct gtt atc gac ggc acg cgt tgg gta tgg aca tgg   883
Ala Ile Pro Leu Ala Val Ile Asp Gly Thr Arg Trp Val Trp Thr Trp
                250                 255                 260

tct tta aaa gaa ctc aat ggt caa gca act gaa ggc ctt gcc cgc ttt   931
Ser Leu Lys Glu Leu Asn Gly Gln Ala Thr Glu Gly Leu Ala Arg Phe
            265                 270                 275

ggt ttc gat aac ggc cta cta ctg ctc acc aat gca gag atc ctt gct   979
Gly Phe Asp Asn Gly Leu Leu Leu Leu Thr Asn Ala Glu Ile Leu Ala
        280                 285                 290

gag gaa gcc acc gca ttc aac ctg att gat gtg gct aaa cag gtg ctc   1027
Glu Glu Ala Thr Ala Phe Asn Leu Ile Asp Val Ala Lys Gln Val Leu
    295                 300                 305

aac act tgg acg cac acc atc gtg cag caa cct gat ggc acc gga att   1075
Asn Thr Trp Thr His Thr Ile Val Gln Gln Pro Asp Gly Thr Gly Ile
310                 315                 320                 325

gtc ctg ctg ctg gat cat cct cgg ctg cag ctt ccg cca gca tca cat   1123
Val Leu Leu Leu Asp His Pro Arg Leu Gln Leu Pro Pro Ala Ser His
                330                 335                 340
```

```
gca gct gtt gag gcc acg ctg tat cac cag cta cca ggc gat att gat   1171
Ala Ala Val Glu Ala Thr Leu Tyr His Gln Leu Pro Gly Asp Ile Asp
            345                 350                 355

gcc cgc cgc gcg gtg gcg tcc tat gca gct cac cga cag ctt cct ttt   1219
Ala Arg Arg Ala Val Ala Ser Tyr Ala Ala His Arg Gln Leu Pro Phe
        360                 365                 370

gat ggc tac gca ctc acc gtt gag ggc caa caa gtc ggc gtg act ttt   1267
Asp Gly Tyr Ala Leu Thr Val Glu Gly Gln Gln Val Gly Val Thr Phe
    375                 380                 385

gac ggc gag cat tta aca aag gtg ggc tagttttcta gcaaaaccca         1314
Asp Gly Glu His Leu Thr Lys Val Gly
390                 395

acc                                                               1317
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<210> 2446
<211> 398
<212> PRT
<213> Corynebacterium glutamicum

<400> 2446

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Met Glu Ile Pro Leu Pro Thr Ser Leu Ile Asp Val Ile Thr Asp Gly
  1               5                  10                  15

Ala Leu Gly Gln Thr Cys Ile Asp Gln Ala Phe Ala Ala Gln Leu Gly
             20                  25                  30

Arg Val Thr Gly Val Glu Phe Asn Leu Ser Asp Asp Lys Thr Ala Ala
         35                  40                  45

Glu Val Arg Ile Asn Lys Ala Ser Gly Ser Pro Phe Asp Thr Thr Gly
     50                  55                  60

Glu Val Ile Ala Trp Ile Asn Asn Gln Glu Phe Glu Trp Val Ser Thr
 65                  70                  75                  80

Arg Gly Glu Asp Leu Gly Leu Pro Glu Leu Gln Gly Ile Gln Pro Leu
                 85                  90                  95

Asp Asp Asp Leu Ile Thr Ala Ala Arg Thr Leu Tyr Ser Asn Ala Pro
            100                 105                 110

Ala Phe Ile Ala Pro Leu Arg Asp Gly Arg Arg Ala Leu Val Ala Ile
        115                 120                 125

Asn His Thr Pro Lys Leu Val Gly Ile Arg Arg Thr Leu Ile Glu Gly
    130                 135                 140

Leu Gln Ala Leu Lys Pro Gly Thr Asp Leu Lys Arg Ala Leu Thr Ser
145                 150                 155                 160

Phe Ala Ala Phe Cys Glu Leu Gly Ile Arg Phe Asp Asp Asn Arg Ile
                165                 170                 175

Ser Phe Ser Asp Gly Thr Ser Leu Leu Leu Arg Gly Gly Lys Val Ile
            180                 185                 190
```

```
Glu Ile Ala Gly Gly Leu Ser Leu Arg Asp Val Arg Ala Asp Ala Ala
        195                 200                 205

Phe Met Ser Ala Glu His Gln Leu Leu Phe Asp Ala Ile Ser Ser Ser
    210                 215                 220

His Asn Val Thr Phe Asp Pro His Thr Asn Val Ala Thr Val Ala Asn
225                 230                 235                 240

Glu His Gln Val His Ala Ile Pro Leu Ala Val Ile Asp Gly Thr Arg
                245                 250                 255

Trp Val Trp Thr Trp Ser Leu Lys Glu Leu Asn Gly Gln Ala Thr Glu
            260                 265                 270

Gly Leu Ala Arg Phe Gly Phe Asp Asn Gly Leu Leu Leu Leu Thr Asn
        275                 280                 285

Ala Glu Ile Leu Ala Glu Glu Ala Thr Ala Phe Asn Leu Ile Asp Val
    290                 295                 300

Ala Lys Gln Val Leu Asn Thr Trp Thr His Thr Ile Val Gln Gln Pro
305                 310                 315                 320

Asp Gly Thr Gly Ile Val Leu Leu Leu Asp His Pro Arg Leu Gln Leu
                325                 330                 335

Pro Pro Ala Ser His Ala Ala Val Glu Ala Thr Leu Tyr His Gln Leu
            340                 345                 350

Pro Gly Asp Ile Asp Ala Arg Arg Ala Val Ala Ser Tyr Ala Ala His
        355                 360                 365

Arg Gln Leu Pro Phe Asp Gly Tyr Ala Leu Thr Val Glu Gly Gln Gln
    370                 375                 380

Val Gly Val Thr Phe Asp Gly Glu His Leu Thr Lys Val Gly
385                 390                 395


<210> 2447
<211> 843
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(820)
<223> RXA01800

<400> 2447
ccagcgcagt tcataaaacc gccaaacttt tgatagcgta gcaatggccc tttcggtgga 60

tggggccatg tttgcacaat gcttgaagaa gggtagggca gtg aag ccg ctg ggc   115
                                              Val Lys Pro Leu Gly
                                                1               5

aag atc gcc gtt cct tgg act tgg tac ctg gga att gtt ggg gtc atc   163
Lys Ile Ala Val Pro Trp Thr Trp Tyr Leu Gly Ile Val Gly Val Ile
                10                  15                  20
```

```
ata ttt gat gtg gtg gca gca ata acg atg ctc acc ctc gtg ccc aac   211
Ile Phe Asp Val Val Ala Ala Ile Thr Met Leu Thr Leu Val Pro Asn
            25                  30                  35

aaa atg ccc gaa aga gtc aac agt ggg ctt gtc gcg ctg ggt gga tcg   259
Lys Met Pro Glu Arg Val Asn Ser Gly Leu Val Ala Leu Gly Gly Ser
        40                  45                  50

tat gca ccc ccg atg agc cgg gaa aca ctc att gcc aga gtc att gcc   307
Tyr Ala Pro Pro Met Ser Arg Glu Thr Leu Ile Ala Arg Val Ile Ala
    55                  60                  65

ggt gca gtg ctg gtt ctg gtg att tct tta ggt att tcg ctg ctg att   355
Gly Ala Val Leu Val Leu Val Ile Ser Leu Gly Ile Ser Leu Leu Ile
70                  75                  80                  85

tcc gcg cag tcc aag aac ctc gcg tcc gat cac ccg gat gca tct gcc   403
Ser Ala Gln Ser Lys Asn Leu Ala Ser Asp His Pro Asp Ala Ser Ala
                90                  95                  100

att cag att gct cgg cgt tgg gcg ttt ttg aac aat att caa agc tgt   451
Ile Gln Ile Ala Arg Arg Trp Ala Phe Leu Asn Asn Ile Gln Ser Cys
            105                 110                 115

atc ggc tgg ttt agt ttc ttc ctc gca gcg att ttg agc atc tca tcg   499
Ile Gly Trp Phe Ser Phe Phe Leu Ala Ala Ile Leu Ser Ile Ser Ser
        120                 125                 130

cta aga ctc aac ggc cca ggt gcc acc acg cat ctt gag atg gcc gtt   547
Leu Arg Leu Asn Gly Pro Gly Ala Thr Thr His Leu Glu Met Ala Val
    135                 140                 145

tac atc atc gct gtg tcg gtg ttg gct tgg gcg ttg atg att tcc ttg   595
Tyr Ile Ile Ala Val Ser Val Leu Ala Trp Ala Leu Met Ile Ser Leu
150                 155                 160                 165

cga cgc ggc cag gtg gcg att gat cgt gcc att cca att cgg gaa gat   643
Arg Arg Gly Gln Val Ala Ile Asp Arg Ala Ile Pro Ile Arg Glu Asp
                170                 175                 180

gat tcc gaa ctg aaa tgg ggc atg atc tac cac gat gct tca gac aaa   691
Asp Ser Glu Leu Lys Trp Gly Met Ile Tyr His Asp Ala Ser Asp Lys
            185                 190                 195

cga gtt ttc gtg gaa ctc gat gat ggc cac acg acc gtc atc aac atg   739
Arg Val Phe Val Glu Leu Asp Asp Gly His Thr Thr Val Ile Asn Met
        200                 205                 210

gcg cgc ggg gga gcg tgg ctg ctc atc gca gtg atg gtg ctg cct gcg   787
Ala Arg Gly Gly Ala Trp Leu Leu Ile Ala Val Met Val Leu Pro Ala
    215                 220                 225

ctg gcc atc gtc ggt tgg gtt ttg cta gaa aac tagcccacct ttgttaaatg 840
Leu Ala Ile Val Gly Trp Val Leu Leu Glu Asn
230                 235                 240

ctc                                                               843
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<210> 2448

<211> 240
<212> PRT
<213> Corynebacterium glutamicum

<400> 2448

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Val Lys Pro Leu Gly Lys Ile Ala Val Pro Trp Thr Trp Tyr Leu Gly
  1               5                  10                  15

Ile Val Gly Val Ile Ile Phe Asp Val Val Ala Ala Ile Thr Met Leu
             20                  25                  30

Thr Leu Val Pro Asn Lys Met Pro Glu Arg Val Asn Ser Gly Leu Val
         35                  40                  45

Ala Leu Gly Gly Ser Tyr Ala Pro Pro Met Ser Arg Glu Thr Leu Ile
     50                  55                  60

Ala Arg Val Ile Ala Gly Ala Val Leu Val Leu Val Ile Ser Leu Gly
 65                  70                  75                  80

Ile Ser Leu Leu Ile Ser Ala Gln Ser Lys Asn Leu Ala Ser Asp His
                 85                  90                  95

Pro Asp Ala Ser Ala Ile Gln Ile Ala Arg Arg Trp Ala Phe Leu Asn
            100                 105                 110

Asn Ile Gln Ser Cys Ile Gly Trp Phe Ser Phe Phe Leu Ala Ala Ile
        115                 120                 125

Leu Ser Ile Ser Ser Leu Arg Leu Asn Gly Pro Gly Ala Thr Thr His
    130                 135                 140

Leu Glu Met Ala Val Tyr Ile Ile Ala Val Ser Val Leu Ala Trp Ala
145                 150                 155                 160

Leu Met Ile Ser Leu Arg Arg Gly Gln Val Ala Ile Asp Arg Ala Ile
                165                 170                 175

Pro Ile Arg Glu Asp Asp Ser Glu Leu Lys Trp Gly Met Ile Tyr His
            180                 185                 190

Asp Ala Ser Asp Lys Arg Val Phe Val Glu Leu Asp Asp Gly His Thr
        195                 200                 205

Thr Val Ile Asn Met Ala Arg Gly Gly Ala Trp Leu Leu Ile Ala Val
    210                 215                 220

Met Val Leu Pro Ala Leu Ala Ile Val Gly Trp Val Leu Leu Glu Asn
225                 230                 235                 240
```

<210> 2449
<211> 444
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(421)
<223> RXA01804

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ttttgggtca aagttttgtg aaacgaagta agcttaagtt atg cat atc gtc aac 115
Met His Ile Val Asn
1 5

att cgc ttc aag ccc aag gct aag tac gtg gat aca ttc cgc tac aca 163
Ile Arg Phe Lys Pro Lys Ala Lys Tyr Val Asp Thr Phe Arg Tyr Thr
10 15 20

gtc gac aaa ttc act gag tca acc agg aca gag gaa ggc tgt ctc tac 211
Val Asp Lys Phe Thr Glu Ser Thr Arg Thr Glu Glu Gly Cys Leu Tyr
25 30 35

ttt gat tgg ttc cgc aac acc gat tac cca ggc gag tac ctt gta att 259
Phe Asp Trp Phe Arg Asn Thr Asp Tyr Pro Gly Glu Tyr Leu Val Ile
40 45 50

ggt gtg tgg acg gat gaa ggt gcg acg gaa cat aag aag agc gag cac 307
Gly Val Trp Thr Asp Glu Gly Ala Thr Glu His Lys Lys Ser Glu His
55 60 65

ttc ttg cga gct caa gaa aca ctt cca ccg ttg ctg caa caa act cca 355
Phe Leu Arg Ala Gln Glu Thr Leu Pro Pro Leu Leu Gln Gln Thr Pro
70 75 80 85

atg att att cag agt gag ttt tcc aag aag aag ggt tgg gaa cgt ttc 403
Met Ile Ile Gln Ser Glu Phe Ser Lys Lys Lys Gly Trp Glu Arg Phe
90 95 100

agc gat ttc acc gtc tac taaggagccc gcaaaagctt tgt 444
Ser Asp Phe Thr Val Tyr
105

<210> 2450
<211> 107
<212> PRT
<213> Corynebacterium glutamicum

<400> 2450
Met His Ile Val Asn Ile Arg Phe Lys Pro Lys Ala Lys Tyr Val Asp
1 5 10 15

Thr Phe Arg Tyr Thr Val Asp Lys Phe Thr Glu Ser Thr Arg Thr Glu
20 25 30

Glu Gly Cys Leu Tyr Phe Asp Trp Phe Arg Asn Thr Asp Tyr Pro Gly
35 40 45

Glu Tyr Leu Val Ile Gly Val Trp Thr Asp Glu Gly Ala Thr Glu His
50 55 60

Lys Lys Ser Glu His Phe Leu Arg Ala Gln Glu Thr Leu Pro Pro Leu
65 70 75 80

Leu Gln Gln Thr Pro Met Ile Ile Gln Ser Glu Phe Ser Lys Lys Lys

```
                85                  90                  95

Gly Trp Glu Arg Phe Ser Asp Phe Thr Val Tyr
            100                 105


<210> 2451
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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(430)
<223> RXA01805

<400> 2451
ggcattgtcg agcgaactca tggtttaact cccttcatga aatgtgtgcg gggtcactgg 60

ttcccagcct agtctgaact ggctaaacaa gatcggtaca gtg gtg gtc gtg att   115
                                            Val Val Val Val Ile
                                              1               5


ttg att aat gtg aaa ttc aag cca ttg cca gaa tat gta gac acc ttc   163
Leu Ile Asn Val Lys Phe Lys Pro Leu Pro Glu Tyr Val Asp Thr Phe
                10                  15                  20

cgc gag cag gta gcg gag ttt aca gaa aag acc cgt gcg gaa gaa gga   211
Arg Glu Gln Val Ala Glu Phe Thr Glu Lys Thr Arg Ala Glu Glu Gly
            25                  30                  35

aac atc ttc ttc gat tgg tca att aac acc gac aac cca aac gag ttc   259
Asn Ile Phe Phe Asp Trp Ser Ile Asn Thr Asp Asn Pro Asn Glu Phe
        40                  45                  50

atc ctc atc gaa gca ttc cag gac gac gct gcc gaa gct cac gtc aac   307
Ile Leu Ile Glu Ala Phe Gln Asp Asp Ala Ala Glu Ala His Val Asn
    55                  60                  65

agc gac cac ttc aag gcg gcc tgt gag ctg ttc cca acc atc ctg tct   355
Ser Asp His Phe Lys Ala Ala Cys Glu Leu Phe Pro Thr Ile Leu Ser
70                  75                  80                  85

gag acc cca gag atc atc aac acc ctt atc gag ggc aag act gag tgg   403
Glu Thr Pro Glu Ile Ile Asn Thr Leu Ile Glu Gly Lys Thr Glu Trp
                90                  95                  100

gac cgc atg gca gag ttc gca gtc aac taaaatatga cctttgctgg         450
Asp Arg Met Ala Glu Phe Ala Val Asn
            105                 110

ttg                                                               453


<210> 2452
<211> 110
<212> PRT
<213> Corynebacterium glutamicum

<400> 2452
Val Val Val Val Ile Leu Ile Asn Val Lys Phe Lys Pro Leu Pro Glu
```

```
  1               5                  10                  15

Tyr Val Asp Thr Phe Arg Glu Gln Val Ala Glu Phe Thr Glu Lys Thr
            20                  25                  30

Arg Ala Glu Glu Gly Asn Ile Phe Phe Asp Trp Ser Ile Asn Thr Asp
        35                  40                  45

Asn Pro Asn Glu Phe Ile Leu Ile Glu Ala Phe Gln Asp Asp Ala Ala
    50                  55                  60

Glu Ala His Val Asn Ser Asp His Phe Lys Ala Ala Cys Glu Leu Phe
65                  70                  75                  80

Pro Thr Ile Leu Ser Glu Thr Pro Glu Ile Ile Asn Thr Leu Ile Glu
                85                  90                  95

Gly Lys Thr Glu Trp Asp Arg Met Ala Glu Phe Ala Val Asn
            100                 105                 110
```

Sequence Listing - Page 2793 of 3000

<210> 2453
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(580)
<223> RXA01806

<400> 2453

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aatcaaaatc acgaccacca ctgtaccgat cttgtttagc cagttcagac taggctggga 60

accagtgacc ccgcacacat ttcatgaagg gagttaaacc atg agt tcg ctc gac   115
                                            Met Ser Ser Leu Asp
                                              1               5

aat gcc ccg ctg ctg gaa ttg gat gtt cag gaa tgg gta aac cac gaa   163
Asn Ala Pro Leu Leu Glu Leu Asp Val Gln Glu Trp Val Asn His Glu
                  10                  15                  20

ggc ttg agc aat gag gac ctg cgc ggc aag gtt gtg gtg gtg gag gtg   211
Gly Leu Ser Asn Glu Asp Leu Arg Gly Lys Val Val Val Val Glu Val
              25                  30                  35

ttt cag atg cta tgc cct gga tgc gtg aat cac ggt gtc cct cag gct   259
Phe Gln Met Leu Cys Pro Gly Cys Val Asn His Gly Val Pro Gln Ala
          40                  45                  50

caa aaa atc cac cgc atg att gat gaa tcc caa gtg caa gtc atc ggg   307
Gln Lys Ile His Arg Met Ile Asp Glu Ser Gln Val Gln Val Ile Gly
      55                  60                  65

ctg cac agc gtg ttt gag cac cat gat gtg atg aca cct gag gct ttg   355
Leu His Ser Val Phe Glu His His Asp Val Met Thr Pro Glu Ala Leu
  70                  75                  80                  85

aaa gtg ttc atc gat gag ttt ggg atc aag ttc ccc gtg gca gtg gat   403
Lys Val Phe Ile Asp Glu Phe Gly Ile Lys Phe Pro Val Ala Val Asp
                  90                  95                 100
```

```
atg ccg agg gaa ggc cag cgg att cct tcg acg atg aaa aag tat cgt   451
Met Pro Arg Glu Gly Gln Arg Ile Pro Ser Thr Met Lys Lys Tyr Arg
            105                 110                 115

ttg gaa gga acg ccc agc atc att ttg gct gat cga aaa gga cgg att   499
Leu Glu Gly Thr Pro Ser Ile Ile Leu Ala Asp Arg Lys Gly Arg Ile
        120                 125                 130

cgt cag gtg cag ttc ggg cag gtt gat gat ttc gtg ctg gga ttg ctg   547
Arg Gln Val Gln Phe Gly Gln Val Asp Asp Phe Val Leu Gly Leu Leu
    135                 140                 145

ctc ggc agt ttg ctg tca gag acg gac gaa acc taaagcgctt tggtctgcag 600
Leu Gly Ser Leu Leu Ser Glu Thr Asp Glu Thr
150                 155                 160

gcc                                                               603
```

<210> 2454
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 2454

```
Met Ser Ser Leu Asp Asn Ala Pro Leu Leu Glu Leu Asp Val Gln Glu
  1               5                  10                  15

Trp Val Asn His Glu Gly Leu Ser Asn Glu Asp Leu Arg Gly Lys Val
             20                  25                  30

Val Val Val Glu Val Phe Gln Met Leu Cys Pro Gly Cys Val Asn His
         35                  40                  45

Gly Val Pro Gln Ala Gln Lys Ile His Arg Met Ile Asp Glu Ser Gln
     50                  55                  60

Val Gln Val Ile Gly Leu His Ser Val Phe Glu His His Asp Val Met
 65                  70                  75                  80

Thr Pro Glu Ala Leu Lys Val Phe Ile Asp Glu Phe Gly Ile Lys Phe
                 85                  90                  95

Pro Val Ala Val Asp Met Pro Arg Glu Gly Gln Arg Ile Pro Ser Thr
            100                 105                 110

Met Lys Lys Tyr Arg Leu Glu Gly Thr Pro Ser Ile Ile Leu Ala Asp
        115                 120                 125

Arg Lys Gly Arg Ile Arg Gln Val Gln Phe Gly Gln Val Asp Asp Phe
    130                 135                 140

Val Leu Gly Leu Leu Leu Gly Ser Leu Leu Ser Glu Thr Asp Glu Thr
145                 150                 155                 160
```

<210> 2455

<211> 855
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(832)
<223> RXA01816

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gttagagtcc ttcttcccct gccagaaagg cacctcacag gtg caa tta tta cac 115
Val Gln Leu Leu His
1 5

acc ccc gca gcc ata tcc att tcc ttc gac gac ccc aac ctc atc tct 163
Thr Pro Ala Ala Ile Ser Ile Ser Phe Asp Asp Pro Asn Leu Ile Ser
10 15 20

acc gca ggg ctg gtc ccg acc atg gcc ctg gcc gag gac cgg tta aca 211
Thr Ala Gly Leu Val Pro Thr Met Ala Leu Ala Glu Asp Arg Leu Thr
25 30 35

gta cca acc gac aaa ggt gct aac cca ggt gcc aaa atc acg acc ctc 259
Val Pro Thr Asp Lys Gly Ala Asn Pro Gly Ala Lys Ile Thr Thr Leu
40 45 50

att gcg ggg atg gtc gcc ggt gcc gac tcc atc gac gat atc gat gca 307
Ile Ala Gly Met Val Ala Gly Ala Asp Ser Ile Asp Asp Ile Asp Ala
55 60 65

ctc cgc cac ggc ggt atg cac cga ctc ttt gac tgg atc tac gcc ccc 355
Leu Arg His Gly Gly Met His Arg Leu Phe Asp Trp Ile Tyr Ala Pro
70 75 80 85

tcc acg ttg ggg tcg ttc ctc cgg gcc ttt acc ttc ggg cat gtc cgc 403
Ser Thr Leu Gly Ser Phe Leu Arg Ala Phe Thr Phe Gly His Val Arg
90 95 100

caa ctc gac gct gtg gcc tcc cgg ttc ctg gtg ggt ctg gca aca cag 451
Gln Leu Asp Ala Val Ala Ser Arg Phe Leu Val Gly Leu Ala Thr Gln
105 110 115

gcc ccg gcc ctg gtc ccg gtt gat gct tct acc agt gat tac gtc ttc 499
Ala Pro Ala Leu Val Pro Val Asp Ala Ser Thr Ser Asp Tyr Val Phe
120 125 130

atc gat gtt gat gac acc atc att aag gtc cac gga cat cag aaa caa 547
Ile Asp Val Asp Asp Thr Ile Ile Lys Val His Gly His Gln Lys Gln
135 140 145

ggc gct ggt ttt ggt tac tcc ggt atc cgt gga ctc aac gcc ctg ctg 595
Gly Ala Gly Phe Gly Tyr Ser Gly Ile Arg Gly Leu Asn Ala Leu Leu
150 155 160 165

gcc aca gtg acc aca cca gag tca gca cca gtg gtc gtg gcc caa cga 643
Ala Thr Val Thr Thr Pro Glu Ser Ala Pro Val Val Val Ala Gln Arg
170 175 180

tta cgg aaa gga tcg tgc ggt tcc ccg cgg ggt gca ggc cgg ttg att 691

```
Leu Arg Lys Gly Ser Cys Gly Ser Pro Arg Gly Ala Gly Arg Leu Ile
            185                 190                 195

gct gat gcg gtg gct acc acc cgg cgt ttg ccg ggg atg gag gat gag   739
Ala Asp Ala Val Ala Thr Thr Arg Arg Leu Pro Gly Met Glu Asp Glu
        200                 205                 210

aag atc ctt tta cgc gcg gat tct gcc ttt tat ggc cat ccc agt atc   787
Lys Ile Leu Leu Arg Ala Asp Ser Ala Phe Tyr Gly His Pro Ser Ile
    215                 220                 225

agt gct gcg atc aag gca ggg gcg gat gtg tct tca cgg tgc gga       832
Ser Ala Ala Ile Lys Ala Gly Ala Asp Val Ser Ser Arg Cys Gly
230                 235                 240

tgacccccaa tgtcaagaaa gcg                                        855


<210> 2456
<211> 244
<212> PRT
<213> Corynebacterium glutamicum

<400> 2456
Val Gln Leu Leu His Thr Pro Ala Ala Ile Ser Ile Ser Phe Asp Asp
  1               5                  10                  15

Pro Asn Leu Ile Ser Thr Ala Gly Leu Val Pro Thr Met Ala Leu Ala
             20                  25                  30

Glu Asp Arg Leu Thr Val Pro Thr Asp Lys Gly Ala Asn Pro Gly Ala
         35                  40                  45

Lys Ile Thr Thr Leu Ile Ala Gly Met Val Ala Gly Ala Asp Ser Ile
     50                  55                  60

Asp Asp Ile Asp Ala Leu Arg His Gly Gly Met His Arg Leu Phe Asp
 65                  70                  75                  80

Trp Ile Tyr Ala Pro Ser Thr Leu Gly Ser Phe Leu Arg Ala Phe Thr
                 85                  90                  95

Phe Gly His Val Arg Gln Leu Asp Ala Val Ala Ser Arg Phe Leu Val
            100                 105                 110

Gly Leu Ala Thr Gln Ala Pro Ala Leu Val Pro Val Asp Ala Ser Thr
        115                 120                 125

Ser Asp Tyr Val Phe Ile Asp Val Asp Asp Thr Ile Ile Lys Val His
    130                 135                 140

Gly His Gln Lys Gln Gly Ala Gly Phe Gly Tyr Ser Gly Ile Arg Gly
145                 150                 155                 160

Leu Asn Ala Leu Leu Ala Thr Val Thr Thr Pro Glu Ser Ala Pro Val
                165                 170                 175

Val Val Ala Gln Arg Leu Arg Lys Gly Ser Cys Gly Ser Pro Arg Gly
            180                 185                 190

Ala Gly Arg Leu Ile Ala Asp Ala Val Ala Thr Thr Arg Arg Leu Pro
```

```
        195                 200                 205

Gly Met Glu Asp Glu Lys Ile Leu Leu Arg Ala Asp Ser Ala Phe Tyr
    210                 215                 220

Gly His Pro Ser Ile Ser Ala Ala Ile Lys Ala Gly Ala Asp Val Ser
225                 230                 235                 240

Ser Arg Cys Gly
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<210> 2457
<211> 756
<212> DNA
<213> Corynebacterium glutamicum

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<221> CDS
<222> (101)..(733)
<223> RXA01817

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ctgcgatcaa ggcaggggcg gatgtgtctt cacggtgcgg atg acc ccc aat gtc   115
                                              Met Thr Pro Asn Val
                                                1               5

aag aaa gcg atc gcc cag gtt cct gat gat gcg tgg cag aca att aag   163
Lys Lys Ala Ile Ala Gln Val Pro Asp Asp Ala Trp Gln Thr Ile Lys
                10                  15                  20

tac acc aac gcg atc ttc gac gag gac acc ggg cgc tgg atc tcg gtg   211
Tyr Thr Asn Ala Ile Phe Asp Glu Asp Thr Gly Arg Trp Ile Ser Val
            25                  30                  35

gcc gag gtc gcc gag ata ccg ttc acc gca ttt acc tcc cgg aag aaa   259
Ala Glu Val Ala Glu Ile Pro Phe Thr Ala Phe Thr Ser Arg Lys Lys
        40                  45                  50

acc gac cac atc ccc gga ctg ctg gtg gta cgc cgg ata ccg gag ctg   307
Thr Asp His Ile Pro Gly Leu Leu Val Val Arg Arg Ile Pro Glu Leu
    55                  60                  65

aat aac aag gat gtg gat cag ccg ggg ttg ttt gat cta cac cgc ttc   355
Asn Asn Lys Asp Val Asp Gln Pro Gly Leu Phe Asp Leu His Arg Phe
70                  75                  80                  85

cat gcg gtg ttc acc acc gcc gac cca ggc atc ctc gat act gtt gct   403
His Ala Val Phe Thr Thr Ala Asp Pro Gly Ile Leu Asp Thr Val Ala
                90                  95                  100

gcg gat aaa acc cac cgt caa cac gca atc atc gaa caa gtc aac gcg   451
Ala Asp Lys Thr His Arg Gln His Ala Ile Ile Glu Gln Val Asn Ala
            105                 110                 115

gac gta aag gcc agt gcg ttg gcg cat atg cca tca ggt gta ttc acc   499
Asp Val Lys Ala Ser Ala Leu Ala His Met Pro Ser Gly Val Phe Thr
        120                 125                 130
```

```
gcc aac agc gcc tgg ttg gtg tgt gcg gtc atg gcg ttc aac ctc acc   547
Ala Asn Ser Ala Trp Leu Val Cys Ala Val Met Ala Phe Asn Leu Thr
    135                 140                 145

cgc aca gcc ggt gtg atc gct gca ggc gcg atg gcc agg gcc acc acc   595
Arg Thr Ala Gly Val Ile Ala Ala Gly Ala Met Ala Arg Ala Thr Thr
150                 155                 160                 165

gca acg atc cgg cgg aaa ctt gtg gcc gtt ccg gcc agg att gca cgc   643
Ala Thr Ile Arg Arg Lys Leu Val Ala Val Pro Ala Arg Ile Ala Arg
                170                 175                 180

agc gcc cgg aga ttg att ctt cac ttg cca cgg aac tgg cgg tgg gaa   691
Ser Ala Arg Arg Leu Ile Leu His Leu Pro Arg Asn Trp Arg Trp Glu
            185                 190                 195

acc cag tgg tca aga ttg tgt gat cac ggc cgt tta cca ccg           733
Thr Gln Trp Ser Arg Leu Cys Asp His Gly Arg Leu Pro Pro
        200                 205                 210

taaccggtag ctccctgact acc                                        756
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<210> 2458
<211> 211
<212> PRT
<213> Corynebacterium glutamicum

<400> 2458

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Met Thr Pro Asn Val Lys Lys Ala Ile Ala Gln Val Pro Asp Asp Ala
  1               5                  10                  15

Trp Gln Thr Ile Lys Tyr Thr Asn Ala Ile Phe Asp Glu Asp Thr Gly
             20                  25                  30

Arg Trp Ile Ser Val Ala Glu Val Ala Glu Ile Pro Phe Thr Ala Phe
         35                  40                  45

Thr Ser Arg Lys Lys Thr Asp His Ile Pro Gly Leu Leu Val Val Arg
     50                  55                  60

Arg Ile Pro Glu Leu Asn Asn Lys Asp Val Asp Gln Pro Gly Leu Phe
 65                  70                  75                  80

Asp Leu His Arg Phe His Ala Val Phe Thr Thr Ala Asp Pro Gly Ile
                 85                  90                  95

Leu Asp Thr Val Ala Ala Asp Lys Thr His Arg Gln His Ala Ile Ile
            100                 105                 110

Glu Gln Val Asn Ala Asp Val Lys Ala Ser Ala Leu Ala His Met Pro
        115                 120                 125

Ser Gly Val Phe Thr Ala Asn Ser Ala Trp Leu Val Cys Ala Val Met
    130                 135                 140

Ala Phe Asn Leu Thr Arg Thr Ala Gly Val Ile Ala Ala Gly Ala Met
145                 150                 155                 160

Ala Arg Ala Thr Thr Ala Thr Ile Arg Arg Lys Leu Val Ala Val Pro
                165                 170                 175
```

```
Ala Arg Ile Ala Arg Ser Ala Arg Arg Leu Ile Leu His Leu Pro Arg
            180                 185                 190

Asn Trp Arg Trp Glu Thr Gln Trp Ser Arg Leu Cys Asp His Gly Arg
        195                 200                 205

Leu Pro Pro
    210


<210> 2459
<211> 1497
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1474)
<223> RXA01820

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aggcacctca caggtgcaat tattacacaa ccccacagcg atg tcc gca tcc ttt   115
                                              Met Ser Ala Ser Phe
                                                1               5

gat gac ccc aac ctc atc tcg ctt gct gga ctg gtt cca acc atg cac   163
Asp Asp Pro Asn Leu Ile Ser Leu Ala Gly Leu Val Pro Thr Met His
                10                  15                  20

tta gcc gat gct gcc agc ctg tcc acc ttg gcc cag gac cgg ttg agc   211
Leu Ala Asp Ala Ala Ser Leu Ser Thr Leu Ala Gln Asp Arg Leu Ser
            25                  30                  35

atc acc ggt gat aaa ggt gcc aat gct ggt gcg aag atc gcc tcc cta   259
Ile Thr Gly Asp Lys Gly Ala Asn Ala Gly Ala Lys Ile Ala Ser Leu
        40                  45                  50

gtc gcg ggc atg gtc gcc ggt gct gat tcc atc gat gac atg gat gta   307
Val Ala Gly Met Val Ala Gly Ala Asp Ser Ile Asp Asp Met Asp Val
    55                  60                  65

ctc cgc cac gga ggt atg cgc cga ctt ttc gac cgg atc tac gcc cca   355
Leu Arg His Gly Gly Met Arg Arg Leu Phe Asp Arg Ile Tyr Ala Pro
70                  75                  80                  85

tcc aca ttg ggg tct ttt ctg cgg gcc ttc act ttc ggc cac gta cgc   403
Ser Thr Leu Gly Ser Phe Leu Arg Ala Phe Thr Phe Gly His Val Arg
                90                  95                  100

caa ctc gat gct gtg gcc tcc cga ttc ctg gtc aac ctg gcc agg cag   451
Gln Leu Asp Ala Val Ala Ser Arg Phe Leu Val Asn Leu Ala Arg Gln
            105                 110                 115

gca cca cac ctg gtg cca cca cca ccg gca ggc agt ggc ggt aac ggg   499
Ala Pro His Leu Val Pro Pro Pro Pro Ala Gly Ser Gly Gly Asn Gly
        120                 125                 130

tat gtg ttc gtt gat gtt gat gac acc atc att gaa gtc cac ggc cac   547
```

```
Tyr Val Phe Val Asp Val Asp Asp Thr Ile Ile Glu Val His Gly His
    135                 140                 145

acc aaa caa ggt gcc ggc ttt ggt tac tcc ggt atc cgt gga ctc aac   595
Thr Lys Gln Gly Ala Gly Phe Gly Tyr Ser Gly Ile Arg Gly Leu Asn
150                 155                 160                 165

gcc ttg ctg gcc acg gtc acc acc gca cag tcc gcc ccc atc att gtg   643
Ala Leu Leu Ala Thr Val Thr Thr Ala Gln Ser Ala Pro Ile Ile Val
                170                 175                 180

ggc caa cga ttg cgg aaa gga tcg tgt ggt tcc cca cga ggg gcc cac   691
Gly Gln Arg Leu Arg Lys Gly Ser Cys Gly Ser Pro Arg Gly Ala His
            185                 190                 195

cgc ctg atc gcc gat gcg atg acc acc acc agg cgc ctg ccc ggg atg   739
Arg Leu Ile Ala Asp Ala Met Thr Thr Thr Arg Arg Leu Pro Gly Met
        200                 205                 210

gag gat aag aaa atc ctc gtc cgg gca gat tcg gcg tat tat ggt cat   787
Glu Asp Lys Lys Ile Leu Val Arg Ala Asp Ser Ala Tyr Tyr Gly His
    215                 220                 225

ccc agt gtc agt gtg gcc cta agg tcc ggt gcg gat gtg tcc gtc acg   835
Pro Ser Val Ser Val Ala Leu Arg Ser Gly Ala Asp Val Ser Val Thr
230                 235                 240                 245

gtg cgg atg acc ccg aac gtc aag aaa gcg atc gtc gcg atc ccg gaa   883
Val Arg Met Thr Pro Asn Val Lys Lys Ala Ile Val Ala Ile Pro Glu
                250                 255                 260

gat gcg tgg cag acg att cag tac acc gat gcg atc ttc gat gag gca   931
Asp Ala Trp Gln Thr Ile Gln Tyr Thr Asp Ala Ile Phe Asp Glu Ala
            265                 270                 275

tca caa tcg tgg atc tcc tta gcc cag gtc gcc gaa gtg cct ttc acc   979
Ser Gln Ser Trp Ile Ser Leu Ala Gln Val Ala Glu Val Pro Phe Thr
        280                 285                 290

gcg ttt acc tcc cgg aag aag gcc gac cat gtt ccc gga cgc ttg gtg   1027
Ala Phe Thr Ser Arg Lys Lys Ala Asp His Val Pro Gly Arg Leu Val
    295                 300                 305

gta cgc cgg att cct gag ctg aat aag aag gat gtg tat cag ccg ggc   1075
Val Arg Arg Ile Pro Glu Leu Asn Lys Lys Asp Val Tyr Gln Pro Gly
310                 315                 320                 325

ttg ttt gat ctt cac cgc ttc cat gcg gtc ttc acc acc gcc gac cca   1123
Leu Phe Asp Leu His Arg Phe His Ala Val Phe Thr Thr Ala Asp Pro
                330                 335                 340

ggc gtg ctg gat act gtt gct gcg gat aaa acc cac cgt cag cac gcg   1171
Gly Val Leu Asp Thr Val Ala Ala Asp Lys Thr His Arg Gln His Ala
            345                 350                 355

atc att gaa cag gtc aac gca gac ttg aag gca agc gcg ttg gcg cat   1219
Ile Ile Glu Gln Val Asn Ala Asp Leu Lys Ala Ser Ala Leu Ala His
        360                 365                 370

ctg ccg tcg ggg acg ttc acc gcc aac agt gcc tgg ctc gta tgc gcg   1267
Leu Pro Ser Gly Thr Phe Thr Ala Asn Ser Ala Trp Leu Val Cys Ala
```

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    375                 380                 385

gtc atg gcg ttt aat ctc acc cgt gcc acc ggg gtt atc gct gca ggc   1315
Val Met Ala Phe Asn Leu Thr Arg Ala Thr Gly Val Ile Ala Ala Gly
390                 395                 400                 405

ggg atg gcc aag gcc acc acc gcg acg atc cgg cgg aca ctg atg gcc   1363
Gly Met Ala Lys Ala Thr Thr Ala Thr Ile Arg Arg Thr Leu Met Ala
                410                 415                 420

gtt cca gcc cgg gtc gcc cgc agg tcc cgc cga ctg gtg ctc cac ctt   1411
Val Pro Ala Arg Val Ala Arg Arg Ser Arg Arg Leu Val Leu His Leu
            425                 430                 435

ccc gag ggg tgg acg tgg caa cca cag tgg cag aaa ctg ttt gat cac   1459
Pro Glu Gly Trp Thr Trp Gln Pro Gln Trp Gln Lys Leu Phe Asp His
        440                 445                 450

ggc cat tca cca ccg taaccggtag ctccctgacc acc                     1497
Gly His Ser Pro Pro
    455


<210> 2460
<211> 458
<212> PRT
<213> Corynebacterium glutamicum

<400> 2460
Met Ser Ala Ser Phe Asp Asp Pro Asn Leu Ile Ser Leu Ala Gly Leu
  1               5                  10                  15

Val Pro Thr Met His Leu Ala Asp Ala Ala Ser Leu Ser Thr Leu Ala
             20                  25                  30

Gln Asp Arg Leu Ser Ile Thr Gly Asp Lys Gly Ala Asn Ala Gly Ala
         35                  40                  45

Lys Ile Ala Ser Leu Val Ala Gly Met Val Ala Gly Ala Asp Ser Ile
     50                  55                  60

Asp Asp Met Asp Val Leu Arg His Gly Gly Met Arg Arg Leu Phe Asp
 65                  70                  75                  80

Arg Ile Tyr Ala Pro Ser Thr Leu Gly Ser Phe Leu Arg Ala Phe Thr
                 85                  90                  95

Phe Gly His Val Arg Gln Leu Asp Ala Val Ala Ser Arg Phe Leu Val
            100                 105                 110

Asn Leu Ala Arg Gln Ala Pro His Leu Val Pro Pro Pro Pro Ala Gly
        115                 120                 125

Ser Gly Gly Asn Gly Tyr Val Phe Val Asp Val Asp Asp Thr Ile Ile
    130                 135                 140

Glu Val His Gly His Thr Lys Gln Gly Ala Gly Phe Gly Tyr Ser Gly
145                 150                 155                 160

Ile Arg Gly Leu Asn Ala Leu Leu Ala Thr Val Thr Thr Ala Gln Ser
                165                 170                 175
```

Ala Pro Ile Ile Val Gly Gln Arg Leu Arg Lys Gly Ser Cys Gly Ser
180 185 190

Pro Arg Gly Ala His Arg Leu Ile Ala Asp Ala Met Thr Thr Thr Arg
195 200 205

Arg Leu Pro Gly Met Glu Asp Lys Lys Ile Leu Val Arg Ala Asp Ser
210 215 220

Ala Tyr Tyr Gly His Pro Ser Val Ser Val Ala Leu Arg Ser Gly Ala
225 230 235 240

Asp Val Ser Val Thr Val Arg Met Thr Pro Asn Val Lys Lys Ala Ile
245 250 255

Val Ala Ile Pro Glu Asp Ala Trp Gln Thr Ile Gln Tyr Thr Asp Ala
260 265 270

Ile Phe Asp Glu Ala Ser Gln Ser Trp Ile Ser Leu Ala Gln Val Ala
275 280 285

Glu Val Pro Phe Thr Ala Phe Thr Ser Arg Lys Lys Ala Asp His Val
290 295 300

Pro Gly Arg Leu Val Val Arg Arg Ile Pro Glu Leu Asn Lys Lys Asp
305 310 315 320

Val Tyr Gln Pro Gly Leu Phe Asp Leu His Arg Phe His Ala Val Phe
325 330 335

Thr Thr Ala Asp Pro Gly Val Leu Asp Thr Val Ala Ala Asp Lys Thr
340 345 350

His Arg Gln His Ala Ile Ile Glu Gln Val Asn Ala Asp Leu Lys Ala
355 360 365

Ser Ala Leu Ala His Leu Pro Ser Gly Thr Phe Thr Ala Asn Ser Ala
370 375 380

Trp Leu Val Cys Ala Val Met Ala Phe Asn Leu Thr Arg Ala Thr Gly
385 390 395 400

Val Ile Ala Ala Gly Gly Met Ala Lys Ala Thr Thr Ala Thr Ile Arg
405 410 415

Arg Thr Leu Met Ala Val Pro Ala Arg Val Ala Arg Arg Ser Arg Arg
420 425 430

Leu Val Leu His Leu Pro Glu Gly Trp Thr Trp Gln Pro Gln Trp Gln
435 440 445

Lys Leu Phe Asp His Gly His Ser Pro Pro
450 455

<210> 2461
<211> 1041
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1018)
<223> RXA01842

<400> 2461
cacgtcatgg tctcgcggtg atcatcttcc taccgtgaca ggcaaggccg caaacggccg 60

tgaccacagg aaagaaattc acgaggagag gaagcacacg atg tcg aag gta tac 115
Met Ser Lys Val Tyr
1 5

gtg tcc aac gag tac ggc ggc ccg gaa aac cag gaa ctg atc acc cgc 163
Val Ser Asn Glu Tyr Gly Gly Pro Glu Asn Gln Glu Leu Ile Thr Arg
10 15 20

aac acc ccc cag cca ggc ccg gga gaa ctc ggg gtc aag gtc cac gcg 211
Asn Thr Pro Gln Pro Gly Pro Gly Glu Leu Gly Val Lys Val His Ala
25 30 35

gcc ggg gtc aac ccg ctt gat tgg aag gtc cgt tcc ggg gtt gcc gga 259
Ala Gly Val Asn Pro Leu Asp Trp Lys Val Arg Ser Gly Val Ala Gly
40 45 50

acc ccg cga gag ctt ccg gca ccc ctg ggc gag gag gcc tcc ggg atc 307
Thr Pro Arg Glu Leu Pro Ala Pro Leu Gly Glu Glu Ala Ser Gly Ile
55 60 65

gtc acc gcc gtt gga gac ggt gtg gag ggc ttc gcg gtc ggc gat ccg 355
Val Thr Ala Val Gly Asp Gly Val Glu Gly Phe Ala Val Gly Asp Pro
70 75 80 85

gtg ctc ggc ctg gtg gcc ccc ggc gtc ggc gga tat gcc gag gac acc 403
Val Leu Gly Leu Val Ala Pro Gly Val Gly Gly Tyr Ala Glu Asp Thr
90 95 100

ctg ctg gtg gca gag agt acc gtg cta aag ccg gag gag atc tcg ttc 451
Leu Leu Val Ala Glu Ser Thr Val Leu Lys Pro Glu Glu Ile Ser Phe
105 110 115

acc gac gcc gcc gcg atc ccg gtc gct ggg gcg agc gcc tac gcc ggc 499
Thr Asp Ala Ala Ala Ile Pro Val Ala Gly Ala Ser Ala Tyr Ala Gly
120 125 130

act cac cag gtc gag ctt gaa cca ggc cag tcg ttg ctg atc aat ggg 547
Thr His Gln Val Glu Leu Glu Pro Gly Gln Ser Leu Leu Ile Asn Gly
135 140 145

gcc ggt ggt ggg gtc ggg ctg atg gcc gcg cag atc gga cgg gtc cac 595
Ala Gly Gly Gly Val Gly Leu Met Ala Ala Gln Ile Gly Arg Val His
150 155 160 165

aag ttc cag gtc gtc ggc gtt gac cac gag gac aag cgc gag ctc atc 643
Lys Phe Gln Val Val Gly Val Asp His Glu Asp Lys Arg Glu Leu Ile
170 175 180

gaa tcc acc ggt gct atc ttc gtc gcc acc ggc gac gcc gtc gcg gag 691
Glu Ser Thr Gly Ala Ile Phe Val Ala Thr Gly Asp Ala Val Ala Glu
185 190 195

cag gtg cgt gcg ctg ctc cct gac ggt gtg gac gta gtc ttc gac cta 739

```
Gln Val Arg Ala Leu Leu Pro Asp Gly Val Asp Val Val Phe Asp Leu
        200                 205                 210

gtc ggc ggg gag gcg ttg cgg gtg gtt gct ccc tta gcg aag aat ccg   787
Val Gly Gly Glu Ala Leu Arg Val Val Ala Pro Leu Ala Lys Asn Pro
    215                 220                 225

gcg cac gtg atc tcg gcg gct gat gct gcc acc gtg gga gaa ctc ggt   835
Ala His Val Ile Ser Ala Ala Asp Ala Ala Thr Val Gly Glu Leu Gly
230                 235                 240                 245

gga cag gtg ctg cgc cgc acc ccg gaa atg gtc gga cag atc acc ggg   883
Gly Gln Val Leu Arg Arg Thr Pro Glu Met Val Gly Gln Ile Thr Gly
                250                 255                 260

gtg gtc cag tac ggg ctg gtc gac ccg aag gtc gat acg acc tac ccg   931
Val Val Gln Tyr Gly Leu Val Asp Pro Lys Val Asp Thr Thr Tyr Pro
            265                 270                 275

ctg gaa cag gcc ggt aag gcc ctg gcc cac gtt gag cag ggc cac gcc   979
Leu Glu Gln Ala Gly Lys Ala Leu Ala His Val Glu Gln Gly His Ala
        280                 285                 290

cgc ggc aag atc gtc ctc gag ctc atc acc tcc cag gac taaccagaca   1028
Arg Gly Lys Ile Val Leu Glu Leu Ile Thr Ser Gln Asp
    295                 300                 305

acgcggtgac ctc                                                  1041


<210> 2462
<211> 306
<212> PRT
<213> Corynebacterium glutamicum

<400> 2462
Met Ser Lys Val Tyr Val Ser Asn Glu Tyr Gly Gly Pro Glu Asn Gln
  1               5                  10                  15

Glu Leu Ile Thr Arg Asn Thr Pro Gln Pro Gly Pro Gly Glu Leu Gly
             20                  25                  30

Val Lys Val His Ala Ala Gly Val Asn Pro Leu Asp Trp Lys Val Arg
         35                  40                  45

Ser Gly Val Ala Gly Thr Pro Arg Glu Leu Pro Ala Pro Leu Gly Glu
     50                  55                  60

Glu Ala Ser Gly Ile Val Thr Ala Val Gly Asp Gly Val Glu Gly Phe
 65                  70                  75                  80

Ala Val Gly Asp Pro Val Leu Gly Leu Val Ala Pro Gly Val Gly Gly
                 85                  90                  95

Tyr Ala Glu Asp Thr Leu Leu Val Ala Glu Ser Thr Val Leu Lys Pro
            100                 105                 110

Glu Glu Ile Ser Phe Thr Asp Ala Ala Ala Ile Pro Val Ala Gly Ala
        115                 120                 125

Ser Ala Tyr Ala Gly Thr His Gln Val Glu Leu Glu Pro Gly Gln Ser
```

```
    130                 135                 140

Leu Leu Ile Asn Gly Ala Gly Gly Gly Val Gly Leu Met Ala Ala Gln
145                 150                 155                 160

Ile Gly Arg Val His Lys Phe Gln Val Val Gly Val Asp His Glu Asp
                165                 170                 175

Lys Arg Glu Leu Ile Glu Ser Thr Gly Ala Ile Phe Val Ala Thr Gly
            180                 185                 190

Asp Ala Val Ala Glu Gln Val Arg Ala Leu Leu Pro Asp Gly Val Asp
        195                 200                 205

Val Val Phe Asp Leu Val Gly Gly Glu Ala Leu Arg Val Val Ala Pro
    210                 215                 220

Leu Ala Lys Asn Pro Ala His Val Ile Ser Ala Ala Asp Ala Ala Thr
225                 230                 235                 240

Val Gly Glu Leu Gly Gly Gln Val Leu Arg Arg Thr Pro Glu Met Val
                245                 250                 255

Gly Gln Ile Thr Gly Val Val Gln Tyr Gly Leu Val Asp Pro Lys Val
            260                 265                 270

Asp Thr Thr Tyr Pro Leu Glu Gln Ala Gly Lys Ala Leu Ala His Val
        275                 280                 285

Glu Gln Gly His Ala Arg Gly Lys Ile Val Leu Glu Leu Ile Thr Ser
    290                 295                 300

Gln Asp
305
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Sequence Listing

<210> 2463
<211> 303
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(280)
<223> RXA01844

<400> 2463
gaccaattgg tcctgctgca tccgcatgat cgccaacgcc agttgcgggt aggcgtccac 60

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gacctcggcc agggcctcga cgggcaggta gagcgcgcag gtg gtc tca atc gcc   115
                                            Val Val Ser Ile Ala
                                              1               5

cag gag ttg gag atc att gag gac ggc acg ggt gcg gtg ctc gtc tcg   163
Gln Glu Leu Glu Ile Ile Glu Asp Gly Thr Gly Ala Val Leu Val Ser
                 10                  15                  20

gag cag gca acc acc ttc gac aac ggg ttc atc ggc tac tcc tac ttc   211
Glu Gln Ala Thr Thr Phe Asp Asn Gly Phe Ile Gly Tyr Ser Tyr Phe
             25                  30                  35
```

```
acc acc ggt acg gac gga gcc acc tgc atc acc gac ctt cgc ctc agg   259
Thr Thr Gly Thr Asp Gly Ala Thr Cys Ile Thr Asp Leu Arg Leu Arg
         40                  45                  50

gcc tcc cca ctg ccg cag gtt taaccggtac tagccggttt ttc             303
Ala Ser Pro Leu Pro Gln Val
     55                  60


<210> 2464
<211> 60
<212> PRT
<213> Corynebacterium glutamicum

<400> 2464
Val Val Ser Ile Ala Gln Glu Leu Glu Ile Ile Glu Asp Gly Thr Gly
  1               5                  10                  15

Ala Val Leu Val Ser Glu Gln Ala Thr Thr Phe Asp Asn Gly Phe Ile
             20                  25                  30

Gly Tyr Ser Tyr Phe Thr Thr Gly Thr Asp Gly Ala Thr Cys Ile Thr
         35                  40                  45

Asp Leu Arg Leu Arg Ala Ser Pro Leu Pro Gln Val
     50                  55                  60


<210> 2465
<211> 531
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(508)
<223> RXA01845

<400> 2465
ggctccgtcc gtaccggtgg tgaagtagga gtagccgatg aacccgttgt cgaaggtggt 60

tgcctgctcc gagacgagca ccgcacccgt gccgtcctca atg atc tcc aac tcc   115
                                            Met Ile Ser Asn Ser
                                              1               5

tgg gcg att gag acc acc tgc gcg ctc tac ctg ccc gtc gag gcc ctg   163
Trp Ala Ile Glu Thr Thr Cys Ala Leu Tyr Leu Pro Val Glu Ala Leu
                 10                  15                  20

gcc gag gtc gtg gac gcc tac ccg caa ctg gcg ttg gcg atc atg cgg   211
Ala Glu Val Val Asp Ala Tyr Pro Gln Leu Ala Leu Ala Ile Met Arg
             25                  30                  35

atg cag cag gac caa ttg gtc cgg tcc cgg gaa cgc gag acc gca cag   259
Met Gln Gln Asp Gln Leu Val Arg Ser Arg Glu Arg Glu Thr Ala Gln
         40                  45                  50

acc acc tcg act gtc gag cag cgc gtg gcc gcc gcc ctc caa cac ctg   307
Thr Thr Ser Thr Val Glu Gln Arg Val Ala Ala Ala Leu Gln His Leu
     55                  60                  65
```

```
gac gcc aag ctc ggg caa atc cga caa gac gga tcc agc ctg ctg cag   355
Asp Ala Lys Leu Gly Gln Ile Arg Gln Asp Gly Ser Ser Leu Leu Gln
 70                  75                  80                  85

gtc cgc ctg cgc cgc gac gac gtg gcc ggc acc acc gtc gag tcc gcc   403
Val Arg Leu Arg Arg Asp Asp Val Ala Gly Thr Thr Val Glu Ser Ala
                90                  95                 100

tcc cgg gca atg gcg cgg atg aag aaa acc ggt gtc atc gac tcc ggc   451
Ser Arg Ala Met Ala Arg Met Lys Lys Thr Gly Val Ile Asp Ser Gly
            105                 110                 115

cgc gaa tgg atc gcc att acc aac cac cag gcc ctg gcc gac ctg gtc   499
Arg Glu Trp Ile Ala Ile Thr Asn His Gln Ala Leu Ala Asp Leu Val
        120                 125                 130

gcc ggc ctc taaacgccca catccctctc tct                            531
Ala Gly Leu
    135
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<210> 2466
<211> 136
<212> PRT
<213> Corynebacterium glutamicum

<400> 2466

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Met Ile Ser Asn Ser Trp Ala Ile Glu Thr Thr Cys Ala Leu Tyr Leu
  1               5                  10                  15

Pro Val Glu Ala Leu Ala Glu Val Val Asp Ala Tyr Pro Gln Leu Ala
             20                  25                  30

Leu Ala Ile Met Arg Met Gln Gln Asp Gln Leu Val Arg Ser Arg Glu
         35                  40                  45

Arg Glu Thr Ala Gln Thr Thr Ser Thr Val Glu Gln Arg Val Ala Ala
     50                  55                  60

Ala Leu Gln His Leu Asp Ala Lys Leu Gly Gln Ile Arg Gln Asp Gly
 65                  70                  75                  80

Ser Ser Leu Leu Gln Val Arg Leu Arg Arg Asp Asp Val Ala Gly Thr
                 85                  90                  95

Thr Val Glu Ser Ala Ser Arg Ala Met Ala Arg Met Lys Lys Thr Gly
            100                 105                 110

Val Ile Asp Ser Gly Arg Glu Trp Ile Ala Ile Thr Asn His Gln Ala
        115                 120                 125

Leu Ala Asp Leu Val Ala Gly Leu
    130                 135
```

<210> 2467
<211> 669
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(646)
<223> RXA01856

<400> 2467
cactctccag cgttcgcgcc agatatgcag ccaactcttg atcgtggtgt ggaagcgctg 60

gttgtagctg cttctgcgtg gctagtaaaa taattggcta atg aat cct ttt ctt 115
Met Asn Pro Phe Leu
1 5

tcg gac acg ttg att gtc cag cag acc tct tcc ttc ctg tct aac aac 163
Ser Asp Thr Leu Ile Val Gln Gln Thr Ser Ser Phe Leu Ser Asn Asn
10 15 20

ttt gag atc tac aat cca gac ggc gaa gtt gtt atc aga atc aaa act 211
Phe Glu Ile Tyr Asn Pro Asp Gly Glu Val Val Ile Arg Ile Lys Thr
25 30 35

gaa ggg tcg ttg ggc tct cgg ctg gtc aag ggc gac cgc aga ttc aca 259
Glu Gly Ser Leu Gly Ser Arg Leu Val Lys Gly Asp Arg Arg Phe Thr
40 45 50

ctg gaa gac gcc ttc ggc acc cca ttg atg cag gtg cgc gat ccc atg 307
Leu Glu Asp Ala Phe Gly Thr Pro Leu Met Gln Val Arg Asp Pro Met
55 60 65

aac ttt gtt cgc gac acc tat gaa att gat gat cca aat ggc aat ccc 355
Asn Phe Val Arg Asp Thr Tyr Glu Ile Asp Asp Pro Asn Gly Asn Pro
70 75 80 85

att gct cat gtg cgg aag cgt ttc acc ttc ttc aac aag cgg atg gac 403
Ile Ala His Val Arg Lys Arg Phe Thr Phe Phe Asn Lys Arg Met Asp
90 95 100

atc gaa cta cca ggt gac cgc gtt att gaa atg cac ggt aac ttc ctt 451
Ile Glu Leu Pro Gly Asp Arg Val Ile Glu Met His Gly Asn Phe Leu
105 110 115

gga ttt gaa ttt gag ttc cgc atg ggc gat cgg att cct gcg aaa gta 499
Gly Phe Glu Phe Glu Phe Arg Met Gly Asp Arg Ile Pro Ala Lys Val
120 125 130

acc cga aaa tgg tcc ggc gct ggc aac gga tac cta ggc cga agc acc 547
Thr Arg Lys Trp Ser Gly Ala Gly Asn Gly Tyr Leu Gly Arg Ser Thr
135 140 145

tac gcc ctt att ttc gat gaa gaa gcc cct gat gaa atc aga aaa gtc 595
Tyr Ala Leu Ile Phe Asp Glu Glu Ala Pro Asp Glu Ile Arg Lys Val
150 155 160 165

atc att gga ggc atg gtc gcg cta gat ctg atc cgg gag aag gaa cgt 643
Ile Ile Gly Gly Met Val Ala Leu Asp Leu Ile Arg Glu Lys Glu Arg
170 175 180

aat taagccaccc ccgtttcatg tct 669
Asn

<210> 2468

<211> 182
<212> PRT
<213> Corynebacterium glutamicum

<400> 2468
Met Asn Pro Phe Leu Ser Asp Thr Leu Ile Val Gln Gln Thr Ser Ser
1 5 10 15

Phe Leu Ser Asn Asn Phe Glu Ile Tyr Asn Pro Asp Gly Glu Val Val
20 25 30

Ile Arg Ile Lys Thr Glu Gly Ser Leu Gly Ser Arg Leu Val Lys Gly
35 40 45

Asp Arg Arg Phe Thr Leu Glu Asp Ala Phe Gly Thr Pro Leu Met Gln
50 55 60

Val Arg Asp Pro Met Asn Phe Val Arg Asp Thr Tyr Glu Ile Asp Asp
65 70 75 80

Pro Asn Gly Asn Pro Ile Ala His Val Arg Lys Arg Phe Thr Phe Phe
85 90 95

Asn Lys Arg Met Asp Ile Glu Leu Pro Gly Asp Arg Val Ile Glu Met
100 105 110

His Gly Asn Phe Leu Gly Phe Glu Phe Glu Phe Arg Met Gly Asp Arg
115 120 125

Ile Pro Ala Lys Val Thr Arg Lys Trp Ser Gly Ala Gly Asn Gly Tyr
130 135 140

Leu Gly Arg Ser Thr Tyr Ala Leu Ile Phe Asp Glu Glu Ala Pro Asp
145 150 155 160

Glu Ile Arg Lys Val Ile Ile Gly Gly Met Val Ala Leu Asp Leu Ile
165 170 175

Arg Glu Lys Glu Arg Asn
180

<210> 2469
<211> 774
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(751)
<223> RXA01857

<400> 2469
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tcgtactaat ctaacttaat ctctccctag gagttctccc atg gct tca cgc cgt 115
Met Ala Ser Arg Arg
1 5

ttc cgt atg atg ctc acc gca agc atc acc gca gct tcc ctt ggt ttt 163
Phe Arg Met Met Leu Thr Ala Ser Ile Thr Ala Ala Ser Leu Gly Phe

```
                10                  15                  20

tcc ctc acc cca gca atc gcc gat gaa gct gta acc gtt gct acg gca   211
Ser Leu Thr Pro Ala Ile Ala Asp Glu Ala Val Thr Val Ala Thr Ala
            25                  30                  35

ccc tcc gtc gga ttc gat tcc ggc gtc gaa cgc gat gca cca ttc acc   259
Pro Ser Val Gly Phe Asp Ser Gly Val Glu Arg Asp Ala Pro Phe Thr
        40                  45                  50

gca gtt cca cac gac gta gtt ctc ggc gtt gga gcg acc cag tcc gag   307
Ala Val Pro His Asp Val Val Leu Gly Val Gly Ala Thr Gln Ser Glu
    55                  60                  65

ctc att ttc aac tgg atc acc gcg cag ggc cta acc ggc cag gtt gca   355
Leu Ile Phe Asn Trp Ile Thr Ala Gln Gly Leu Thr Gly Gln Val Ala
70                  75                  80                  85

cag atc tcc ctg gac gat acc ttc gca tcc cca atc acc gtt gat gca   403
Gln Ile Ser Leu Asp Asp Thr Phe Ala Ser Pro Ile Thr Val Asp Ala
                90                  95                  100

gtt tct gaa aac gtc agc atc gtg aac acc gaa ggc gat tcc cgc gac   451
Val Ser Glu Asn Val Ser Ile Val Asn Thr Glu Gly Asp Ser Arg Asp
            105                 110                 115

cga gct gaa ggt gaa tac gtt gaa tac cgc gat ggc gca gtc aac cgc   499
Arg Ala Glu Gly Glu Tyr Val Glu Tyr Arg Asp Gly Ala Val Asn Arg
        120                 125                 130

gca acc gta gat agc ctc gca gaa aac acc acc tac tcc tac cgc gtc   547
Ala Thr Val Asp Ser Leu Ala Glu Asn Thr Thr Tyr Ser Tyr Arg Val
    135                 140                 145

ggc tcc gaa gct gac ggc tgg tcc gaa gtg caa acc ttc aac acc ggc   595
Gly Ser Glu Ala Asp Gly Trp Ser Glu Val Gln Thr Phe Asn Thr Gly
150                 155                 160                 165

acc tac ggt gac aac tgg aac ttc ctc ttc ttc ggc gac acc cag ctg   643
Thr Tyr Gly Asp Asn Trp Asn Phe Leu Phe Phe Gly Asp Thr Gln Leu
                170                 175                 180

tac aac acc cac tcc aac cgt gca gaa gaa gtc cag aac tgg gca aac   691
Tyr Asn Thr His Ser Asn Arg Ala Glu Glu Val Gln Asn Trp Ala Asn
            185                 190                 195

aac ctg gaa cgg cgg ccc acc aat cga aaa ccc agg aac ctc ctt cat   739
Asn Leu Glu Arg Arg Pro Thr Asn Arg Lys Pro Arg Asn Leu Leu His
        200                 205                 210

cct ctc cgc ggg tgatcaggca aaccactcca gct                        774
Pro Leu Arg Gly
    215
```

<210> 2470
<211> 217
<212> PRT
<213> Corynebacterium glutamicum

<400> 2470

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Met Ala Ser Arg Arg Phe Arg Met Met Leu Thr Ala Ser Ile Thr Ala
  1               5                  10                  15

Ala Ser Leu Gly Phe Ser Leu Thr Pro Ala Ile Ala Asp Glu Ala Val
             20                  25                  30

Thr Val Ala Thr Ala Pro Ser Val Gly Phe Asp Ser Gly Val Glu Arg
         35                  40                  45

Asp Ala Pro Phe Thr Ala Val Pro His Asp Val Val Leu Gly Val Gly
     50                  55                  60

Ala Thr Gln Ser Glu Leu Ile Phe Asn Trp Ile Thr Ala Gln Gly Leu
 65                  70                  75                  80

Thr Gly Gln Val Ala Gln Ile Ser Leu Asp Asp Thr Phe Ala Ser Pro
                 85                  90                  95

Ile Thr Val Asp Ala Val Ser Glu Asn Val Ser Ile Val Asn Thr Glu
            100                 105                 110

Gly Asp Ser Arg Asp Arg Ala Glu Gly Glu Tyr Val Glu Tyr Arg Asp
        115                 120                 125

Gly Ala Val Asn Arg Ala Thr Val Asp Ser Leu Ala Glu Asn Thr Thr
    130                 135                 140

Tyr Ser Tyr Arg Val Gly Ser Glu Ala Asp Gly Trp Ser Glu Val Gln
145                 150                 155                 160

Thr Phe Asn Thr Gly Thr Tyr Gly Asp Asn Trp Asn Phe Leu Phe Phe
                165                 170                 175

Gly Asp Thr Gln Leu Tyr Asn Thr His Ser Asn Arg Ala Glu Glu Val
            180                 185                 190

Gln Asn Trp Ala Asn Asn Leu Glu Arg Arg Pro Thr Asn Arg Lys Pro
        195                 200                 205

Arg Asn Leu Leu His Pro Leu Arg Gly
    210                 215
```

<210> 2471
<211> 673
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(673)
<223> RXA01858

<400> 2471
cgtgtgtttg ttttgactgg aacagcgtcg gcttttcggc cacgcggcct gcggacagta 60

gcggaatcac gcgggacatt gatccccgga cgtaaagccg atg ttt atg aca ccg 115
                                                Met Phe Met Thr Pro
                                                  1   5

cgg gcg ttg acc gaa gat aat gag ttg acc ctg gct ttg aaa tca ctc 163

```
Arg Ala Leu Thr Glu Asp Asn Glu Leu Thr Leu Ala Leu Lys Ser Leu
                10                  15                  20

gga ggg ctt atg gtg tca ccc aat gag tgc tca gta gtg aca gaa gtg   211
Gly Gly Leu Met Val Ser Pro Asn Glu Cys Ser Val Val Thr Glu Val
            25                  30                  35

atg ccg act tgg aga gaa tta tgg cat caa agg ctt cga tgg caa cgc   259
Met Pro Thr Trp Arg Glu Leu Trp His Gln Arg Leu Arg Trp Gln Arg
        40                  45                  50

ggt gcg ctg gaa aac ctc ggt gct tat ggc atc aca cca caa acg aca   307
Gly Ala Leu Glu Asn Leu Gly Ala Tyr Gly Ile Thr Pro Gln Thr Thr
    55                  60                  65

cgg tat tgg ttc cag cag ctg gga atc ggt tac ggc gca tta gcc ttg   355
Arg Tyr Trp Phe Gln Gln Leu Gly Ile Gly Tyr Gly Ala Leu Ala Leu
70                  75                  80                  85

gtc gcc tat ttc gca gtc att atc att acg ttt ctc gcc cgc gat caa   403
Val Ala Tyr Phe Ala Val Ile Ile Ile Thr Phe Leu Ala Arg Asp Gln
                90                  95                  100

tgg atc tgg tat cca ttc tgg atg ctg ctg gga ctg ttg ttc atg att   451
Trp Ile Trp Tyr Pro Phe Trp Met Leu Leu Gly Leu Leu Phe Met Ile
            105                 110                 115

gaa cgc gtg cta acg gtg tgg aga tcc aca tgg ttt gcc agg ttt gtt   499
Glu Arg Val Leu Thr Val Trp Arg Ser Thr Trp Phe Ala Arg Phe Val
        120                 125                 130

gct gcg tta tta atc cca gag ctc atc tac gcc agc tat ctc aac ctg   547
Ala Ala Leu Leu Ile Pro Glu Leu Ile Tyr Ala Ser Tyr Leu Asn Leu
    135                 140                 145

gta ttt ctc aaa ggc gtt gtg gat att cta ttg gcc aag caa gct cac   595
Val Phe Leu Lys Gly Val Val Asp Ile Leu Leu Ala Lys Gln Ala His
150                 155                 160                 165

tgg ggt gag cat ggt gac aag aca atg cag gta gcc gat gca gct gcc   643
Trp Gly Glu His Gly Asp Lys Thr Met Gln Val Ala Asp Ala Ala Ala
                170                 175                 180

gaa att aac gat gaa ggg gag gaa cgc cga                          673
Glu Ile Asn Asp Glu Gly Glu Glu Arg Arg
            185                 190
```

<210> 2472
<211> 191
<212> PRT
<213> Corynebacterium glutamicum

<400> 2472

```
Met Phe Met Thr Pro Arg Ala Leu Thr Glu Asp Asn Glu Leu Thr Leu
  1               5                  10                  15

Ala Leu Lys Ser Leu Gly Gly Leu Met Val Ser Pro Asn Glu Cys Ser
            20                  25                  30

Val Val Thr Glu Val Met Pro Thr Trp Arg Glu Leu Trp His Gln Arg
```

```
         35                  40                  45

Leu Arg Trp Gln Arg Gly Ala Leu Glu Asn Leu Gly Ala Tyr Gly Ile
     50                  55                  60

Thr Pro Gln Thr Thr Arg Tyr Trp Phe Gln Gln Leu Gly Ile Gly Tyr
 65                  70                  75                  80

Gly Ala Leu Ala Leu Val Ala Tyr Phe Ala Val Ile Ile Ile Thr Phe
                 85                  90                  95

Leu Ala Arg Asp Gln Trp Ile Trp Tyr Pro Phe Trp Met Leu Leu Gly
            100                 105                 110

Leu Leu Phe Met Ile Glu Arg Val Leu Thr Val Trp Arg Ser Thr Trp
        115                 120                 125

Phe Ala Arg Phe Val Ala Ala Leu Leu Ile Pro Glu Leu Ile Tyr Ala
    130                 135                 140

Ser Tyr Leu Asn Leu Val Phe Leu Lys Gly Val Val Asp Ile Leu Leu
145                 150                 155                 160

Ala Lys Gln Ala His Trp Gly Glu His Gly Asp Lys Thr Met Gln Val
                165                 170                 175

Ala Asp Ala Ala Ala Glu Ile Asn Asp Glu Gly Glu Glu Arg Arg
            180                 185                 190


<210> 2473
<211> 798
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(775)
<223> RXA01870

<400> 2473
ggatcatgtc caccccagaa ggtagcctgt cagtgtgagc gtaatcgagg gcaagtacca 60

gctgaaacct caaggccgag gtggcctgtg gtggtcaatc gtg ggt gtg gca gtt   115
                                            Val Gly Val Ala Val
                                              1               5

gtt ttg ttg ctg ctt cca acg ttg atc aac ctg gtg gtt ccg gat aaa   163
Val Leu Leu Leu Leu Pro Thr Leu Ile Asn Leu Val Val Pro Asp Lys
                10                  15                  20

gcc aat gac tac aag cag cta gaa atc gat ctt ctg ggt gtg gat tgg   211
Ala Asn Asp Tyr Lys Gln Leu Glu Ile Asp Leu Leu Gly Val Asp Trp
            25                  30                  35

tca gtg cca atc acc acg gag gaa tcc gct gcg gtg ctg tgt gag gaa   259
Ser Val Pro Ile Thr Thr Glu Glu Ser Ala Ala Val Leu Cys Glu Glu
        40                  45                  50

aca tct gat gaa atc aca cag aag tat tgg gac tgc aac ggg gac acc   307
Thr Ser Asp Glu Ile Thr Gln Lys Tyr Trp Asp Cys Asn Gly Asp Thr
```

```
     55                  60                  65

acg gtg gtg acc atg atc gtc gag ggc gtg aaa gat ccg tcc aat acg   355
Thr Val Val Thr Met Ile Val Glu Gly Val Lys Asp Pro Ser Asn Thr
 70                  75                  80                  85

ttg cgt cgc atg gtg ggt tca tcg ctg ata acc agt gtg gat gac agc   403
Leu Arg Arg Met Val Gly Ser Ser Leu Ile Thr Ser Val Asp Asp Ser
                 90                  95                 100

cta gag gca gta tct agc gaa gat ggc cgt gcg cat gcg ttg tat gtg   451
Leu Glu Ala Val Ser Ser Glu Asp Gly Arg Ala His Ala Leu Tyr Val
            105                 110                 115

cca ggt cag caa gaa gga tct ttg tgg acg ctg cct atc gtg gca ctg   499
Pro Gly Gln Gln Glu Gly Ser Leu Trp Thr Leu Pro Ile Val Ala Leu
        120                 125                 130

agc gtg cag ggt tcg ggt gat tat gaa gac ctc aca gcg atc gca att   547
Ser Val Gln Gly Ser Gly Asp Tyr Glu Asp Leu Thr Ala Ile Ala Ile
    135                 140                 145

atc aac ggc acc tcg ttg gat tat tac agc acc cac att tgg tcc agc   595
Ile Asn Gly Thr Ser Leu Asp Tyr Tyr Ser Thr His Ile Trp Ser Ser
150                 155                 160                 165

atg gcc gct gac cgc ggg ttg ccg tac cag cag gac ttc ccc ctg atg   643
Met Ala Ala Asp Arg Gly Leu Pro Tyr Gln Gln Asp Phe Pro Leu Met
                170                 175                 180

ctg gaa gag gag cca tgg caa gac acc ccc ggc ggg gat cgt ccc ttc   691
Leu Glu Glu Glu Pro Trp Gln Asp Thr Pro Gly Gly Asp Arg Pro Phe
            185                 190                 195

gag ctg ccc aat gat ttc ttt gat cag tac ccc gat ctt ttt ggc cca   739
Glu Leu Pro Asn Asp Phe Phe Asp Gln Tyr Pro Asp Leu Phe Gly Pro
        200                 205                 210

ggc tcc gtc att ccc aac ctt gaa gga gaa tcc cta tgagtcgcat        785
Gly Ser Val Ile Pro Asn Leu Glu Gly Glu Ser Leu
    215                 220                 225

gtttagcatc acc                                                   798


<210> 2474
<211> 225
<212> PRT
<213> Corynebacterium glutamicum

<400> 2474
Val Gly Val Ala Val Val Leu Leu Leu Leu Pro Thr Leu Ile Asn Leu
  1               5                  10                  15

Val Val Pro Asp Lys Ala Asn Asp Tyr Lys Gln Leu Glu Ile Asp Leu
             20                  25                  30

Leu Gly Val Asp Trp Ser Val Pro Ile Thr Thr Glu Glu Ser Ala Ala
         35                  40                  45

Val Leu Cys Glu Glu Thr Ser Asp Glu Ile Thr Gln Lys Tyr Trp Asp
```

```
     50                  55                  60

Cys Asn Gly Asp Thr Thr Val Val Thr Met Ile Val Glu Gly Val Lys
 65                  70                  75                  80

Asp Pro Ser Asn Thr Leu Arg Arg Met Val Gly Ser Ser Leu Ile Thr
                 85                  90                  95

Ser Val Asp Asp Ser Leu Glu Ala Val Ser Ser Glu Asp Gly Arg Ala
            100                 105                 110

His Ala Leu Tyr Val Pro Gly Gln Gln Glu Gly Ser Leu Trp Thr Leu
        115                 120                 125

Pro Ile Val Ala Leu Ser Val Gln Gly Ser Gly Asp Tyr Glu Asp Leu
    130                 135                 140

Thr Ala Ile Ala Ile Ile Asn Gly Thr Ser Leu Asp Tyr Tyr Ser Thr
145                 150                 155                 160

His Ile Trp Ser Ser Met Ala Ala Asp Arg Gly Leu Pro Tyr Gln Gln
                165                 170                 175

Asp Phe Pro Leu Met Leu Glu Glu Glu Pro Trp Gln Asp Thr Pro Gly
            180                 185                 190

Gly Asp Arg Pro Phe Glu Leu Pro Asn Asp Phe Phe Asp Gln Tyr Pro
        195                 200                 205

Asp Leu Phe Gly Pro Gly Ser Val Ile Pro Asn Leu Glu Gly Glu Ser
    210                 215                 220

Leu
225


<210> 2475
<211> 1086
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1063)
<223> RXA01871

<400> 2475
gcggggatcg tcccttcgag ctgcccaatg atttctttga tcagtacccc gatctttttg 60

gcccaggctc cgtcattccc aaccttgaag gagaatccct atg agt cgc atg ttt   115
                                               Met Ser Arg Met Phe
                                                 1               5

agc atc acc ttg tgg gtt gcc atc ctc ctc tca acc ccg gcg ctg ttt   163
Ser Ile Thr Leu Trp Val Ala Ile Leu Leu Ser Thr Pro Ala Leu Phe
                10                  15                  20

ttg agc ttg gcc acg ttc atc ttc gtg gat ggc atc tct gtc ctc gtg   211
Leu Ser Leu Ala Thr Phe Ile Phe Val Asp Gly Ile Ser Val Leu Val
            25                  30                  35
```

```
aat ata gtg ttc gcg gtg ctc tac ttg gta gtc att gtt ttc ctg tta   259
Asn Ile Val Phe Ala Val Leu Tyr Leu Val Val Ile Val Phe Leu Leu
         40                  45                  50

agt cgc acc ccg ctg tgg cca cgt ttt aaa ggc tcc ggc agc aag aag   307
Ser Arg Thr Pro Leu Trp Pro Arg Phe Lys Gly Ser Gly Ser Lys Lys
     55                  60                  65

gga ggc gga ttc gcg tgg gcg gcg tca tca ttg ttg tgg ggc gcg ttc   355
Gly Gly Gly Phe Ala Trp Ala Ala Ser Ser Leu Leu Trp Gly Ala Phe
 70                  75                  80                  85

gtt ggt ttc ggc atc gtc atg ttg ttt gcc ggt ccg gtc atg gat ctc   403
Val Gly Phe Gly Ile Val Met Leu Phe Ala Gly Pro Val Met Asp Leu
                 90                  95                 100

acg gac aaa ctc ggc tgg gat ttc gtt gcc atg agt ttc acc gga gcg   451
Thr Asp Lys Leu Gly Trp Asp Phe Val Ala Met Ser Phe Thr Gly Ala
            105                 110                 115

tat cca gaa gaa atc gcc aaa gcg tta ggc gtt gcc atc atc ttg ttg   499
Tyr Pro Glu Glu Ile Ala Lys Ala Leu Gly Val Ala Ile Ile Leu Leu
        120                 125                 130

agc ttc cgc caa ctc aac cgt ccg tgg cat gga ttt atc acc ggc gcg   547
Ser Phe Arg Gln Leu Asn Arg Pro Trp His Gly Phe Ile Thr Gly Ala
    135                 140                 145

cta gtg ggc tta ggt ttt gag gtc aac gaa aac ctc ctc tat ggc gcc   595
Leu Val Gly Leu Gly Phe Glu Val Asn Glu Asn Leu Leu Tyr Gly Ala
150                 155                 160                 165

acc ggt gca atc atg gac ccc aac gct gac ctc gac ggc gtc ctt atg   643
Thr Gly Ala Ile Met Asp Pro Asn Ala Asp Leu Asp Gly Val Leu Met
                170                 175                 180

atg tgg caa tac cgc acc atg ttg ggc cca ctc atc cat acg ttg ctc   691
Met Trp Gln Tyr Arg Thr Met Leu Gly Pro Leu Ile His Thr Leu Leu
            185                 190                 195

acc gga ttc gca ggt tac ggc atc gcg ttg gca ttc ttc cgc gca cga   739
Thr Gly Phe Ala Gly Tyr Gly Ile Ala Leu Ala Phe Phe Arg Ala Arg
        200                 205                 210

aaa aca gtc gcc tgg cgc tgg ggc gtg gcg atc ggt tgg act ctc atc   787
Lys Thr Val Ala Trp Arg Trp Gly Val Ala Ile Gly Trp Thr Leu Ile
    215                 220                 225

gcc ttc gca ctg cat ttt tca tgg aac ctg atg tgg gaa aac gta atc   835
Ala Phe Ala Leu His Phe Ser Trp Asn Leu Met Trp Glu Asn Val Ile
230                 235                 240                 245

ggt tcc tat gtc acc atc atc gtg gtc agc gtt gtc atg tac ggt ctg   883
Gly Ser Tyr Val Thr Ile Ile Val Val Ser Val Val Met Tyr Gly Leu
                250                 255                 260

gct atc tac atc ctc tgg agt aat tgg gcc gaa gcc cgc aac gac tcc   931
Ala Ile Tyr Ile Leu Trp Ser Asn Trp Ala Glu Ala Arg Asn Asp Ser
            265                 270                 275

agc tac gct ttc gtc ccg gga atc atc aca aac acc aaa gat tta tcg   979
```

```
Ser Tyr Ala Phe Val Pro Gly Ile Ile Thr Asn Thr Lys Asp Leu Ser
        280                 285                 290

ctt ctt gac gcc ccc att cca gta ggc gct gag gtt ccc gag tcg cgc   1027
Leu Leu Asp Ala Pro Ile Pro Val Gly Ala Glu Val Pro Glu Ser Arg
    295                 300                 305

att ccc caa cag ata gag gaa ccc aag gcg gag aac tagctttcac        1073
Ile Pro Gln Gln Ile Glu Glu Pro Lys Ala Glu Asn
310                 315                 320

tcgctctcca tcc                                                   1086


<210> 2476
<211> 321
<212> PRT
<213> Corynebacterium glutamicum

<400> 2476
Met Ser Arg Met Phe Ser Ile Thr Leu Trp Val Ala Ile Leu Leu Ser
  1               5                  10                  15

Thr Pro Ala Leu Phe Leu Ser Leu Ala Thr Phe Ile Phe Val Asp Gly
             20                  25                  30

Ile Ser Val Leu Val Asn Ile Val Phe Ala Val Leu Tyr Leu Val Val
         35                  40                  45

Ile Val Phe Leu Leu Ser Arg Thr Pro Leu Trp Pro Arg Phe Lys Gly
     50                  55                  60

Ser Gly Ser Lys Lys Gly Gly Gly Phe Ala Trp Ala Ala Ser Ser Leu
 65                  70                  75                  80

Leu Trp Gly Ala Phe Val Gly Phe Gly Ile Val Met Leu Phe Ala Gly
                 85                  90                  95

Pro Val Met Asp Leu Thr Asp Lys Leu Gly Trp Asp Phe Val Ala Met
            100                 105                 110

Ser Phe Thr Gly Ala Tyr Pro Glu Glu Ile Ala Lys Ala Leu Gly Val
        115                 120                 125

Ala Ile Ile Leu Leu Ser Phe Arg Gln Leu Asn Arg Pro Trp His Gly
    130                 135                 140

Phe Ile Thr Gly Ala Leu Val Gly Leu Gly Phe Glu Val Asn Glu Asn
145                 150                 155                 160

Leu Leu Tyr Gly Ala Thr Gly Ala Ile Met Asp Pro Asn Ala Asp Leu
                165                 170                 175

Asp Gly Val Leu Met Met Trp Gln Tyr Arg Thr Met Leu Gly Pro Leu
            180                 185                 190

Ile His Thr Leu Leu Thr Gly Phe Ala Gly Tyr Gly Ile Ala Leu Ala
        195                 200                 205

Phe Phe Arg Ala Arg Lys Thr Val Ala Trp Arg Trp Gly Val Ala Ile
    210                 215                 220
```

```
Gly Trp Thr Leu Ile Ala Phe Ala Leu His Phe Ser Trp Asn Leu Met
225                 230                 235                 240

Trp Glu Asn Val Ile Gly Ser Tyr Val Thr Ile Ile Val Val Ser Val
                245                 250                 255

Val Met Tyr Gly Leu Ala Ile Tyr Ile Leu Trp Ser Asn Trp Ala Glu
            260                 265                 270

Ala Arg Asn Asp Ser Ser Tyr Ala Phe Val Pro Gly Ile Ile Thr Asn
        275                 280                 285

Thr Lys Asp Leu Ser Leu Leu Asp Ala Pro Ile Pro Val Gly Ala Glu
    290                 295                 300

Val Pro Glu Ser Arg Ile Pro Gln Gln Ile Glu Glu Pro Lys Ala Glu
305                 310                 315                 320

Asn
```

<210> 2477
<211> 302
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(279)
<223> RXA01903

<400> 2477

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gct cac ctt gat gac cgt ggc atc tat atc atc cca gct caa tat cct   48
Ala His Leu Asp Asp Arg Gly Ile Tyr Ile Ile Pro Ala Gln Tyr Pro
  1               5                  10                  15

tgg gga tac gag gaa atc att aac cta ccg gca cgc gct acc tct aca   96
Trp Gly Tyr Glu Glu Ile Ile Asn Leu Pro Ala Arg Ala Thr Ser Thr
             20                  25                  30

cct gct gtt gct cct cgc act gag gct gct cca gct aca gta tct gat   144
Pro Ala Val Ala Pro Arg Thr Glu Ala Ala Pro Ala Thr Val Ser Asp
         35                  40                  45

gct gag gtc cag agc ctg ctt gag tac ttg cgt act aat gct ttc gta   192
Ala Glu Val Gln Ser Leu Leu Glu Tyr Leu Arg Thr Asn Ala Phe Val
     50                  55                  60

agt cgt cac gac ggc gac acc acg aag gcc gac atc ttc aac aag cac   240
Ser Arg His Asp Gly Asp Thr Thr Lys Ala Asp Ile Phe Asn Lys His
 65                  70                  75                  80

gcg gat act gtc aac aag ctt gca gca cta cgt gca ccc taaacccaca    289
Ala Asp Thr Val Asn Lys Leu Ala Ala Leu Arg Ala Pro
                 85                  90

ccgcataacc ccc                                                   302
```

<210> 2478
<211> 93
<212> PRT
<213> Corynebacterium glutamicum

<400> 2478
Ala His Leu Asp Asp Arg Gly Ile Tyr Ile Ile Pro Ala Gln Tyr Pro
1 5 10 15

Trp Gly Tyr Glu Glu Ile Ile Asn Leu Pro Ala Arg Ala Thr Ser Thr
20 25 30

Pro Ala Val Ala Pro Arg Thr Glu Ala Ala Pro Ala Thr Val Ser Asp
35 40 45

Ala Glu Val Gln Ser Leu Leu Glu Tyr Leu Arg Thr Asn Ala Phe Val
50 55 60

Ser Arg His Asp Gly Asp Thr Thr Lys Ala Asp Ile Phe Asn Lys His
65 70 75 80

Ala Asp Thr Val Asn Lys Leu Ala Ala Leu Arg Ala Pro
85 90

<210> 2479
<211> 546
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(523)
<223> RXA01904

<400> 2479
attagttttt attcgcaagg gtggtctaaa ttttttacta ctgcgtcgtg tccaccggat 60

acacttgagg taatacagtt acgaggctaa ggagtatgta atg agc att tcg ccg 115
Met Ser Ile Ser Pro
1 5

aag aat tcc ggt aca cca aac gag aac gcc gca gca gcg cag gtg gca 163
Lys Asn Ser Gly Thr Pro Asn Glu Asn Ala Ala Ala Ala Gln Val Ala
10 15 20

gca aat ctg gct aat tta acg tcg cag gct aca ggg tcc atg gac gaa 211
Ala Asn Leu Ala Asn Leu Thr Ser Gln Ala Thr Gly Ser Met Asp Glu
25 30 35

act aat gag caa gtc att aaa agt aac gag cat ggc tct gat gct tat 259
Thr Asn Glu Gln Val Ile Lys Ser Asn Glu His Gly Ser Asp Ala Tyr
40 45 50

ttg gcg gat att aaa gcc agt cga gag atg tgg gca aaa att gcg ctc 307
Leu Ala Asp Ile Lys Ala Ser Arg Glu Met Trp Ala Lys Ile Ala Leu
55 60 65

gat ccg aat caa tct gaa gaa act agg aaa gaa gct cgg gag aat atg 355
Asp Pro Asn Gln Ser Glu Glu Thr Arg Lys Glu Ala Arg Glu Asn Met
70 75 80 85

```
gcg cgg ata gat gag tac gct cgt gag cac gat aaa gac aac aag ggt   403
Ala Arg Ile Asp Glu Tyr Ala Arg Glu His Asp Lys Asp Asn Lys Gly
                 90                  95                 100

ttg ttg cag aag tta gcg aaa aac aaa gca gag ctc atc ggg act gtt   451
Leu Leu Gln Lys Leu Ala Lys Asn Lys Ala Glu Leu Ile Gly Thr Val
            105                 110                 115

gcg gtt gca acc tta ggt gta gtg gca gcc att gct aac aat ggc aag   499
Ala Val Ala Thr Leu Gly Val Val Ala Ala Ile Ala Asn Asn Gly Lys
        120                 125                 130

ata ccg atg att cag ttg aaa aaa taacccccgc acaggctgga cat         546
Ile Pro Met Ile Gln Leu Lys Lys
    135                 140
```

<210> 2480
<211> 141
<212> PRT
<213> Corynebacterium glutamicum

<400> 2480

```
Met Ser Ile Ser Pro Lys Asn Ser Gly Thr Pro Asn Glu Asn Ala Ala
  1               5                  10                  15

Ala Ala Gln Val Ala Ala Asn Leu Ala Asn Leu Thr Ser Gln Ala Thr
             20                  25                  30

Gly Ser Met Asp Glu Thr Asn Glu Gln Val Ile Lys Ser Asn Glu His
         35                  40                  45

Gly Ser Asp Ala Tyr Leu Ala Asp Ile Lys Ala Ser Arg Glu Met Trp
     50                  55                  60

Ala Lys Ile Ala Leu Asp Pro Asn Gln Ser Glu Glu Thr Arg Lys Glu
 65                  70                  75                  80

Ala Arg Glu Asn Met Ala Arg Ile Asp Glu Tyr Ala Arg Glu His Asp
                 85                  90                  95

Lys Asp Asn Lys Gly Leu Leu Gln Lys Leu Ala Lys Asn Lys Ala Glu
            100                 105                 110

Leu Ile Gly Thr Val Ala Val Ala Thr Leu Gly Val Val Ala Ala Ile
        115                 120                 125

Ala Asn Asn Gly Lys Ile Pro Met Ile Gln Leu Lys Lys
    130                 135                 140
```

<210> 2481
<211> 654
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(631)
<223> RXA01905

<400> 2481
aaatgaaagt cacaaacttt gttggggttt ctttaaagta aaatacagaa gtttctctgg 60

caaaaaacct cactactttc tacagaaagg cgtcttcctc atg aag gct tct cag 115
Met Lys Ala Ser Gln
1 5

acc ctc acc cgc aac act cgt gca cgc aag ctc ggc atg ggt att ctc 163
Thr Leu Thr Arg Asn Thr Arg Ala Arg Lys Leu Gly Met Gly Ile Leu
10 15 20

gca gca act att atg gct acc ggt gca ctt gct ggc act gct cca cag 211
Ala Ala Thr Ile Met Ala Thr Gly Ala Leu Ala Gly Thr Ala Pro Gln
25 30 35

gcg aca gca gca gta gat acc act gcg cca tac gtg tcc tat gtc gtt 259
Ala Thr Ala Ala Val Asp Thr Thr Ala Pro Tyr Val Ser Tyr Val Val
40 45 50

gac att cct ggc aag gtt ggt gaa cca atc aag cct cag tac ctc acc 307
Asp Ile Pro Gly Lys Val Gly Glu Pro Ile Lys Pro Gln Tyr Leu Thr
55 60 65

atc tcc gat cag tcc gcc tac acc gtg acc ttc aag tac atg cca tcc 355
Ile Ser Asp Gln Ser Ala Tyr Thr Val Thr Phe Lys Tyr Met Pro Ser
70 75 80 85

tgg ttg aag tac gac gca aac aag aag atg ctg tac ggt acc cca acc 403
Trp Leu Lys Tyr Asp Ala Asn Lys Lys Met Leu Tyr Gly Thr Pro Thr
90 95 100

gag gtt gat gtc tgg act cct gag gta cat gtt gtt gat gct cat ggc 451
Glu Val Asp Val Trp Thr Pro Glu Val His Val Val Asp Ala His Gly
105 110 115

aac aag act gtc cgt tac ttc acc gtt gta gca gtc cca gca aac act 499
Asn Lys Thr Val Arg Tyr Phe Thr Val Val Ala Val Pro Ala Asn Thr
120 125 130

gga cca acc acc acc acg cca tct act tca aag cca tct acc ccg cag 547
Gly Pro Thr Thr Thr Thr Pro Ser Thr Ser Lys Pro Ser Thr Pro Gln
135 140 145

gtg acc acc cca act act ccg aag gcg cct acc ttg cca aag tcc acc 595
Val Thr Thr Pro Thr Thr Pro Lys Ala Pro Thr Leu Pro Lys Ser Thr
150 155 160 165

ttc gac tgg acc ttg tgg ggc tcc atc ttt ggt ttc tagttctcac 641
Phe Asp Trp Thr Leu Trp Gly Ser Ile Phe Gly Phe
170 175

tagcacctca aaa 654

<210> 2482
<211> 177
<212> PRT
<213> Corynebacterium glutamicum

<400> 2482

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Met Lys Ala Ser Gln Thr Leu Thr Arg Asn Thr Arg Ala Arg Lys Leu
  1               5                  10                  15

Gly Met Gly Ile Leu Ala Ala Thr Ile Met Ala Thr Gly Ala Leu Ala
            20                  25                  30

Gly Thr Ala Pro Gln Ala Thr Ala Ala Val Asp Thr Thr Ala Pro Tyr
         35                  40                  45

Val Ser Tyr Val Val Asp Ile Pro Gly Lys Val Gly Glu Pro Ile Lys
     50                  55                  60

Pro Gln Tyr Leu Thr Ile Ser Asp Gln Ser Ala Tyr Thr Val Thr Phe
 65                  70                  75                  80

Lys Tyr Met Pro Ser Trp Leu Lys Tyr Asp Ala Asn Lys Lys Met Leu
                85                  90                  95

Tyr Gly Thr Pro Thr Glu Val Asp Val Trp Thr Pro Glu Val His Val
            100                 105                 110

Val Asp Ala His Gly Asn Lys Thr Val Arg Tyr Phe Thr Val Val Ala
        115                 120                 125

Val Pro Ala Asn Thr Gly Pro Thr Thr Thr Thr Pro Ser Thr Ser Lys
    130                 135                 140

Pro Ser Thr Pro Gln Val Thr Thr Pro Thr Thr Pro Lys Ala Pro Thr
145                 150                 155                 160

Leu Pro Lys Ser Thr Phe Asp Trp Thr Leu Trp Gly Ser Ile Phe Gly
                165                 170                 175

Phe
```

<210> 2483
<211> 588
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(565)
<223> RXA01906

<400> 2483
gcgttcgggt aaacccgtga caatcgcacg gggcttgttt acctgacact caagccccgt 60

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gcaccacaac aacccacctt aaagaaaggt ttttccaccc atg tcc gaa ttc cct   115
                                              Met Ser Glu Phe Pro
                                                1               5

aca cct acg act ttt cac gtc gaa cca gaa acg ctt agc tcc gcc acc   163
Thr Pro Thr Thr Phe His Val Glu Pro Glu Thr Leu Ser Ser Ala Thr
                10                  15                  20

gat ctc act gtt gat gca cat aaa atc gca gaa ctg ctg ctc agc acc   211
Asp Leu Thr Val Asp Ala His Lys Ile Ala Glu Leu Leu Leu Ser Thr
            25                  30                  35
```

```
act gat tac cgt gtg ttc tac atg ccg cgt ctc gcc ggt gtg act cct   259
Thr Asp Tyr Arg Val Phe Tyr Met Pro Arg Leu Ala Gly Val Thr Pro
         40                  45                  50

atc gtg tcc tac ctc tat gtc tac gat ggt gaa aac ttc ctc att gtt   307
Ile Val Ser Tyr Leu Tyr Val Tyr Asp Gly Glu Asn Phe Leu Ile Val
     55                  60                  65

ggt cgc tcc act cat gtg ccg tgg gag tac tac gtt cac tac ccc atc   355
Gly Arg Ser Thr His Val Pro Trp Glu Tyr Tyr Val His Tyr Pro Ile
 70                  75                  80                  85

aag cca tca cgt gaa ttt ggc tct gct att gct gtg cct ctc gat gat   403
Lys Pro Ser Arg Glu Phe Gly Ser Ala Ile Ala Val Pro Leu Asp Asp
                 90                  95                 100

tct gat gac cct tat gat gca gca gaa gtt gtt gct cta gta aag cag   451
Ser Asp Asp Pro Tyr Asp Ala Ala Glu Val Val Ala Leu Val Lys Gln
            105                 110                 115

tac atg acg ccc acg ctc act cct ggt gag ggt tat atg cag ggc ttt   499
Tyr Met Thr Pro Thr Leu Thr Pro Gly Glu Gly Tyr Met Gln Gly Phe
        120                 125                 130

tac aag ggt ctc acc ttc acc aac cac ctc gat ata cat cga cca ctg   547
Tyr Lys Gly Leu Thr Phe Thr Asn His Leu Asp Ile His Arg Pro Leu
    135                 140                 145

acc cag att atc tca gac taacagctat attcacccac cta                 588
Thr Gln Ile Ile Ser Asp
150                 155
```

Sequence Listing.ST25.txt

<210> 2484
<211> 155
<212> PRT
<213> Corynebacterium glutamicum

<400> 2484

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Met Ser Glu Phe Pro Thr Pro Thr Thr Phe His Val Glu Pro Glu Thr
  1               5                  10                  15

Leu Ser Ser Ala Thr Asp Leu Thr Val Asp Ala His Lys Ile Ala Glu
             20                  25                  30

Leu Leu Leu Ser Thr Thr Asp Tyr Arg Val Phe Tyr Met Pro Arg Leu
         35                  40                  45

Ala Gly Val Thr Pro Ile Val Ser Tyr Leu Tyr Val Tyr Asp Gly Glu
     50                  55                  60

Asn Phe Leu Ile Val Gly Arg Ser Thr His Val Pro Trp Glu Tyr Tyr
 65                  70                  75                  80

Val His Tyr Pro Ile Lys Pro Ser Arg Glu Phe Gly Ser Ala Ile Ala
                 85                  90                  95

Val Pro Leu Asp Asp Ser Asp Asp Pro Tyr Asp Ala Ala Glu Val Val
            100                 105                 110
```

```
Ala Leu Val Lys Gln Tyr Met Thr Pro Thr Leu Thr Pro Gly Glu Gly
        115                 120                 125

Tyr Met Gln Gly Phe Tyr Lys Gly Leu Thr Phe Thr Asn His Leu Asp
    130                 135                 140

Ile His Arg Pro Leu Thr Gln Ile Ile Ser Asp
145                 150                 155


<210> 2485
<211> 735
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(712)
<223> RXA01907

<400> 2485
ttcgttttac ccacaccagc acgtcaccct cttgcatcac gccgagaggg tgacgtgctt 60

ttttcctact tttcctcata actacagaag ggacgccctc atg tct gct ttt gat   115
                                              Met Ser Ala Phe Asp
                                                1               5

gaa ctc cgc aag aac tac cgc tac aag ttc act gac acc tgg ccg gcc   163
Glu Leu Arg Lys Asn Tyr Arg Tyr Lys Phe Thr Asp Thr Trp Pro Ala
                10                  15                  20

aac gct gtt acc ggc acc ggc tac tac gcc aac cca gct ttt atc atc   211
Asn Ala Val Thr Gly Thr Gly Tyr Tyr Ala Asn Pro Ala Phe Ile Ile
            25                  30                  35

atc tcc gct gat gcc atg acg cag aac acc cat gcc gat tcc aat ctc   259
Ile Ser Ala Asp Ala Met Thr Gln Asn Thr His Ala Asp Ser Asn Leu
        40                  45                  50

atc acg gtt aaa gag cac ctt aac acc ctg ttt ccg tac agc gta caa   307
Ile Thr Val Lys Glu His Leu Asn Thr Leu Phe Pro Tyr Ser Val Gln
    55                  60                  65

cgc aag gat cgt gcc ttt gtc tct gag atc tac acc cct att aac ctg   355
Arg Lys Asp Arg Ala Phe Val Ser Glu Ile Tyr Thr Pro Ile Asn Leu
70                  75                  80                  85

ctc gaa gat aat cca gaa cta gct caa gaa ata ctc gat gtg ctc gac   403
Leu Glu Asp Asn Pro Glu Leu Ala Gln Glu Ile Leu Asp Val Leu Asp
                90                  95                  100

acc ctg agc aac aac gct gtt ttt aac gat gcg cac tac agc gag ctt   451
Thr Leu Ser Asn Asn Ala Val Phe Asn Asp Ala His Tyr Ser Glu Leu
            105                 110                 115

gaa cta gag cgc ctc aat gaa tat gtc atc gac acc ttg gcc tat gac   499
Glu Leu Glu Arg Leu Asn Glu Tyr Val Ile Asp Thr Leu Ala Tyr Asp
        120                 125                 130

atg aag tcc gac atg atg cgc gcc ctc gtt aag gcc cga cca gag gcc   547
Met Lys Ser Asp Met Met Arg Ala Leu Val Lys Ala Arg Pro Glu Ala
```

```
    135                 140                 145

gat ctt gag gcg atg gaa gaa ctc gac att gcc aat atc cag agc tgg   595
Asp Leu Glu Ala Met Glu Glu Leu Asp Ile Ala Asn Ile Gln Ser Trp
150                 155                 160                 165

att aat ctc cac tcc tcc act gtg agc gaa cac aac gat ggc agc gtt   643
Ile Asn Leu His Ser Ser Thr Val Ser Glu His Asn Asp Gly Ser Val
                170                 175                 180

gat gat gca ccg ttt aat tct ctc gca tta gct gag att tat ttg caa   691
Asp Asp Ala Pro Phe Asn Ser Leu Ala Leu Ala Glu Ile Tyr Leu Gln
            185                 190                 195

cag ctt gca gac cac act gtc taagcacgct gtgtaactac cac            735
Gln Leu Ala Asp His Thr Val
        200
```

<210> 2486
<211> 204
<212> PRT
<213> Corynebacterium glutamicum

<400> 2486

```
Met Ser Ala Phe Asp Glu Leu Arg Lys Asn Tyr Arg Tyr Lys Phe Thr
  1               5                  10                  15

Asp Thr Trp Pro Ala Asn Ala Val Thr Gly Thr Gly Tyr Tyr Ala Asn
             20                  25                  30

Pro Ala Phe Ile Ile Ile Ser Ala Asp Ala Met Thr Gln Asn Thr His
         35                  40                  45

Ala Asp Ser Asn Leu Ile Thr Val Lys Glu His Leu Asn Thr Leu Phe
     50                  55                  60

Pro Tyr Ser Val Gln Arg Lys Asp Arg Ala Phe Val Ser Glu Ile Tyr
 65                  70                  75                  80

Thr Pro Ile Asn Leu Leu Glu Asp Asn Pro Glu Leu Ala Gln Glu Ile
                 85                  90                  95

Leu Asp Val Leu Asp Thr Leu Ser Asn Asn Ala Val Phe Asn Asp Ala
            100                 105                 110

His Tyr Ser Glu Leu Glu Leu Glu Arg Leu Asn Glu Tyr Val Ile Asp
        115                 120                 125

Thr Leu Ala Tyr Asp Met Lys Ser Asp Met Met Arg Ala Leu Val Lys
    130                 135                 140

Ala Arg Pro Glu Ala Asp Leu Glu Ala Met Glu Glu Leu Asp Ile Ala
145                 150                 155                 160

Asn Ile Gln Ser Trp Ile Asn Leu His Ser Ser Thr Val Ser Glu His
                165                 170                 175

Asn Asp Gly Ser Val Asp Asp Ala Pro Phe Asn Ser Leu Ala Leu Ala
            180                 185                 190
```

```
Glu Ile Tyr Leu Gln Gln Leu Ala Asp His Thr Val
        195                 200


<210> 2487
<211> 529
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(529)
<223> RXA01923

<400> 2487
ccaaagtgaa taccccgact gcagcagcgc aaaagttcaa gtactttggg atgcaaatct 60

agtagcacgt cccatgtttc tcacactctc aggagctgac atg tct gca ctt att   115
                                            Met Ser Ala Leu Ile
                                              1               5

aaa ggt tca gga cct cat cat gtg gtt gtc tta aat ggt tgg ttt ggt   163
Lys Gly Ser Gly Pro His His Val Val Val Leu Asn Gly Trp Phe Gly
                 10                  15                  20

cat gct gcg ggc tgg gga gct ttc gct gac tat ctt gac ctc ggc aac   211
His Ala Ala Gly Trp Gly Ala Phe Ala Asp Tyr Leu Asp Leu Gly Asn
             25                  30                  35

tac acc tgg cac ttt tgg gat tac cga ggt tac ggc aac aga aaa gac   259
Tyr Thr Trp His Phe Trp Asp Tyr Arg Gly Tyr Gly Asn Arg Lys Asp
         40                  45                  50

gac gca gga gaa ttt act ctg gag gaa att tca gcg gat atc gtt gca   307
Asp Ala Gly Glu Phe Thr Leu Glu Glu Ile Ser Ala Asp Ile Val Ala
     55                  60                  65

tac atc gac tcg att gag gca gaa aag gtt tcc atc ctg ggc cat tcc   355
Tyr Ile Asp Ser Ile Glu Ala Glu Lys Val Ser Ile Leu Gly His Ser
 70                  75                  80                  85

atg ggt gga gtg ttc atg cag aaa gtc ctt gca gac agc gcc acc ccc   403
Met Gly Gly Val Phe Met Gln Lys Val Leu Ala Asp Ser Ala Thr Pro
                 90                  95                 100

atc gct tca ctg gtt gga att tct gcc gtt gct gca gct gga aca cca   451
Ile Ala Ser Leu Val Gly Ile Ser Ala Val Ala Ala Ala Gly Thr Pro
            105                 110                 115

ttc gat gag gat tct cgg aag ctt ttc acc tca gca ggg cac aac ccg   499
Phe Asp Glu Asp Ser Arg Lys Leu Phe Thr Ser Ala Gly His Asn Pro
        120                 125                 130

gac tcg agg cga gcc atc atc gat ttc acc                          529
Asp Ser Arg Arg Ala Ile Ile Asp Phe Thr
    135                 140


<210> 2488
<211> 143
<212> PRT
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<213> Corynebacterium glutamicum

<400> 2488

```
Met Ser Ala Leu Ile Lys Gly Ser Gly Pro His His Val Val Val Leu
  1               5                  10                  15

Asn Gly Trp Phe Gly His Ala Ala Gly Trp Gly Ala Phe Ala Asp Tyr
             20                  25                  30

Leu Asp Leu Gly Asn Tyr Thr Trp His Phe Trp Asp Tyr Arg Gly Tyr
         35                  40                  45

Gly Asn Arg Lys Asp Asp Ala Gly Glu Phe Thr Leu Glu Glu Ile Ser
     50                  55                  60

Ala Asp Ile Val Ala Tyr Ile Asp Ser Ile Glu Ala Glu Lys Val Ser
 65                  70                  75                  80

Ile Leu Gly His Ser Met Gly Gly Val Phe Met Gln Lys Val Leu Ala
                 85                  90                  95

Asp Ser Ala Thr Pro Ile Ala Ser Leu Val Gly Ile Ser Ala Val Ala
            100                 105                 110

Ala Ala Gly Thr Pro Phe Asp Glu Asp Ser Arg Lys Leu Phe Thr Ser
        115                 120                 125

Ala Gly His Asn Pro Asp Ser Arg Arg Ala Ile Ile Asp Phe Thr
    130                 135                 140
```

<210> 2489
<211> 777
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(754)
<223> RXA01931

<400> 2489

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tcgataggca tggcgccgat tctaggtcga actgatctaa agtcccacca cgcaaaagta 60

accaaggcgt acatctaccc ggcactttaa gatcagtggc atg agc act tct ttt   115
                                            Met Ser Thr Ser Phe
                                              1               5

gag tcc att ccc gga gtt act atc tcc gct cga aaa gcc ttg agc act   163
Glu Ser Ile Pro Gly Val Thr Ile Ser Ala Arg Lys Ala Leu Ser Thr
                 10                  15                  20

gcg ggg ttt aaa gat ctg gaa tcg ctt gca ggt acc aat tac gaa gaa   211
Ala Gly Phe Lys Asp Leu Glu Ser Leu Ala Gly Thr Asn Tyr Glu Glu
             25                  30                  35

gtg gct ggt ctg tca gga att ggc gca cgt act ttg gag cga ttg caa   259
Val Ala Gly Leu Ser Gly Ile Gly Ala Arg Thr Leu Glu Arg Leu Gln
         40                  45                  50

gca gcg ctg gtg gag aag aga atg agc ttt ggc ggt aaa gtg cca gag   307
```

```
Ala Ala Leu Val Glu Lys Arg Met Ser Phe Gly Gly Lys Val Pro Glu
     55                  60                  65

gca gaa cag cgc acc gcg acg tgg aca acg cta gat tct gca gca cca   355
Ala Glu Gln Arg Thr Ala Thr Trp Thr Thr Leu Asp Ser Ala Ala Pro
 70                  75                  80                  85

gag gca aca gaa acc tca gaa tcc cca gag tac ttc att caa aac cta   403
Glu Ala Thr Glu Thr Ser Glu Ser Pro Glu Tyr Phe Ile Gln Asn Leu
                90                  95                 100

gac att cct cgc aga att acc cac ggc cgg ttg ttg ttg gaa att ttc   451
Asp Ile Pro Arg Arg Ile Thr His Gly Arg Leu Leu Leu Glu Ile Phe
            105                 110                 115

aac aga gcg aca ggc cag aaa cct tat gta gca ggg tct tcg att gtt   499
Asn Arg Ala Thr Gly Gln Lys Pro Tyr Val Ala Gly Ser Ser Ile Val
        120                 125                 130

ggt tat ggg cga gtt cat tat cgc tat gcc acg ggt agg gaa ggg atc   547
Gly Tyr Gly Arg Val His Tyr Arg Tyr Ala Thr Gly Arg Glu Gly Ile
    135                 140                 145

act att cgt gtg ggt ttc agt ccg cga aag gca aag att tca ctt tat   595
Thr Ile Arg Val Gly Phe Ser Pro Arg Lys Ala Lys Ile Ser Leu Tyr
150                 155                 160                 165

gga cta acc agt gcg cct gcg tct cga gaa ctt ctg aag aaa ttg ggt   643
Gly Leu Thr Ser Ala Pro Ala Ser Arg Glu Leu Leu Lys Lys Leu Gly
                170                 175                 180

aag cat tct gtt ggt gtg tcc tgc cta tat atc aac aaa cca gag gat   691
Lys His Ser Val Gly Val Ser Cys Leu Tyr Ile Asn Lys Pro Glu Asp
            185                 190                 195

gtt gat ctt gag gtg ctt gag gaa atg atc cgt att tct tgg gaa gcg   739
Val Asp Leu Glu Val Leu Glu Glu Met Ile Arg Ile Ser Trp Glu Ala
        200                 205                 210

gaa cct ggc gaa tgt taaatctcaa cctttaacaa agt                    777
Glu Pro Gly Glu Cys
    215
```

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<210> 2490
<211> 218
<212> PRT
<213> Corynebacterium glutamicum

<400> 2490

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Met Ser Thr Ser Phe Glu Ser Ile Pro Gly Val Thr Ile Ser Ala Arg
  1               5                  10                  15

Lys Ala Leu Ser Thr Ala Gly Phe Lys Asp Leu Glu Ser Leu Ala Gly
             20                  25                  30

Thr Asn Tyr Glu Glu Val Ala Gly Leu Ser Gly Ile Gly Ala Arg Thr
         35                  40                  45

Leu Glu Arg Leu Gln Ala Ala Leu Val Glu Lys Arg Met Ser Phe Gly
     50                  55                  60
```

```
Gly Lys Val Pro Glu Ala Glu Gln Arg Thr Ala Thr Trp Thr Thr Leu
 65                  70                  75                  80

Asp Ser Ala Ala Pro Glu Ala Thr Glu Thr Ser Glu Ser Pro Glu Tyr
                 85                  90                  95

Phe Ile Gln Asn Leu Asp Ile Pro Arg Arg Ile Thr His Gly Arg Leu
            100                 105                 110

Leu Leu Glu Ile Phe Asn Arg Ala Thr Gly Gln Lys Pro Tyr Val Ala
        115                 120                 125

Gly Ser Ser Ile Val Gly Tyr Gly Arg Val His Tyr Arg Tyr Ala Thr
    130                 135                 140

Gly Arg Glu Gly Ile Thr Ile Arg Val Gly Phe Ser Pro Arg Lys Ala
145                 150                 155                 160

Lys Ile Ser Leu Tyr Gly Leu Thr Ser Ala Pro Ala Ser Arg Glu Leu
                165                 170                 175

Leu Lys Lys Leu Gly Lys His Ser Val Gly Val Ser Cys Leu Tyr Ile
            180                 185                 190

Asn Lys Pro Glu Asp Val Asp Leu Glu Val Leu Glu Glu Met Ile Arg
        195                 200                 205

Ile Ser Trp Glu Ala Glu Pro Gly Glu Cys
    210                 215


<210> 2491
<211> 558
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(535)
<223> RXA01941

<400> 2491
ccggacttgc cgctggttta gtcacttttt gctcacgacg gtatttattg gtcgatttca 60

ccagcgcagc gttgaaaaac gttgggcgcc agtcacccac atg gcc ttg act tca   115
                                              Met Ala Leu Thr Ser
                                                1               5

ctt ttg cac cag ctt gca gat aaa aaa cac agt gac ctc agc cgg gaa   163
Leu Leu His Gln Leu Ala Asp Lys Lys His Ser Asp Leu Ser Arg Glu
                10                  15                  20

gac atc gta ccg cgg gcc ttt act gtc ccg acc tct act gac gcc cac   211
Asp Ile Val Pro Arg Ala Phe Thr Val Pro Thr Ser Thr Asp Ala His
            25                  30                  35

gct att cat caa gac ttg gaa aaa ctc cga aac tcc gta ctc aaa gag   259
Ala Ile His Gln Asp Leu Glu Lys Leu Arg Asn Ser Val Leu Lys Glu
        40                  45                  50
```

```
caa aat cac cta acc act gtg ttg gga act tgg tca gaa ttc ctc acc   307
Gln Asn His Leu Thr Thr Val Leu Gly Thr Trp Ser Glu Phe Leu Thr
     55                  60                  65

tcc aac agc gat aac tcc gac att ttg cgt tcc tcc gct gaa ctt ggg   355
Ser Asn Ser Asp Asn Ser Asp Ile Leu Arg Ser Ser Ala Glu Leu Gly
 70                  75                  80                  85

ctc caa ttg gag cag gtc cgc gat aaa gca ctc gaa gtg gaa cag cgt   403
Leu Gln Leu Glu Gln Val Arg Asp Lys Ala Leu Glu Val Glu Gln Arg
                 90                  95                 100

atc aaa gcc tct gct cag gtg gat ctt acg gac ctg gct cat gag att   451
Ile Lys Ala Ser Ala Gln Val Asp Leu Thr Asp Leu Ala His Glu Ile
            105                 110                 115

gag atc tgc aat caa cac cac gca acc ctc atc agt gcg att cag gta   499
Glu Ile Cys Asn Gln His His Ala Thr Leu Ile Ser Ala Ile Gln Val
        120                 125                 130

aga ctg caa tcg cat act gct gag ctt cgg gct ggg tgatttctta        545
Arg Leu Gln Ser His Thr Ala Glu Leu Arg Ala Gly
    135                 140                 145

agactgacct agt                                                    558


<210> 2492
<211> 145
<212> PRT
<213> Corynebacterium glutamicum

<400> 2492
Met Ala Leu Thr Ser Leu Leu His Gln Leu Ala Asp Lys Lys His Ser
  1               5                  10                  15

Asp Leu Ser Arg Glu Asp Ile Val Pro Arg Ala Phe Thr Val Pro Thr
             20                  25                  30

Ser Thr Asp Ala His Ala Ile His Gln Asp Leu Glu Lys Leu Arg Asn
         35                  40                  45

Ser Val Leu Lys Glu Gln Asn His Leu Thr Thr Val Leu Gly Thr Trp
     50                  55                  60

Ser Glu Phe Leu Thr Ser Asn Ser Asp Asn Ser Asp Ile Leu Arg Ser
 65                  70                  75                  80

Ser Ala Glu Leu Gly Leu Gln Leu Glu Gln Val Arg Asp Lys Ala Leu
                 85                  90                  95

Glu Val Glu Gln Arg Ile Lys Ala Ser Ala Gln Val Asp Leu Thr Asp
            100                 105                 110

Leu Ala His Glu Ile Glu Ile Cys Asn Gln His His Ala Thr Leu Ile
        115                 120                 125

Ser Ala Ile Gln Val Arg Leu Gln Ser His Thr Ala Glu Leu Arg Ala
    130                 135                 140

Gly
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145

<210> 2493
<211> 723
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(700)
<223> RXA01942

<400> 2493
gccgcgaaat tcggtgaaat tgaaggtatt cctgcagatc aggcaaattc ttccacgact 60

gtgatcaagg tcaacggcaa gaacgagtaa cctgggatcc atg ttg cgc att gga 115
Met Leu Arg Ile Gly
1 5

cta aca gga ggg atc ggc agc ggt aaa tct acc gtt gcc gat ctt ttg 163
Leu Thr Gly Gly Ile Gly Ser Gly Lys Ser Thr Val Ala Asp Leu Leu
10 15 20

tca tct gaa gga ttt ctc atc gtc gac gcg gac caa gtt gcc cgc gat 211
Ser Ser Glu Gly Phe Leu Ile Val Asp Ala Asp Gln Val Ala Arg Asp
25 30 35

atc gtc gaa ccc gga caa ccg gca tta gca gag cta gct gaa gct ttt 259
Ile Val Glu Pro Gly Gln Pro Ala Leu Ala Glu Leu Ala Glu Ala Phe
40 45 50

ggc caa gac atc tta aaa ccc gac ggc act cta gac cgc gcg gga tta 307
Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu Asp Arg Ala Gly Leu
55 60 65

gca gcc aaa gca ttt gtc agc gaa gaa caa aca gcg ctg ctc aat gcc 355
Ala Ala Lys Ala Phe Val Ser Glu Glu Gln Thr Ala Leu Leu Asn Ala
70 75 80 85

att acc cac cct cgt atc gcc gaa gag tca gct cgt cga ttc aac gaa 403
Ile Thr His Pro Arg Ile Ala Glu Glu Ser Ala Arg Arg Phe Asn Glu
90 95 100

gcc gaa gat caa ggc gcc aaa gtt gcg gtt tat gac atg cct ttg ctt 451
Ala Glu Asp Gln Gly Ala Lys Val Ala Val Tyr Asp Met Pro Leu Leu
105 110 115

gta gaa aaa ggc ctt gac cgc aag atg gac ctt gtc gtc gta gtt gat 499
Val Glu Lys Gly Leu Asp Arg Lys Met Asp Leu Val Val Val Val Asp
120 125 130

gtt gac gta gag gaa cgc gtc cgc aga ctt gtg gaa aaa cgt ggc ctc 547
Val Asp Val Glu Glu Arg Val Arg Arg Leu Val Glu Lys Arg Gly Leu
135 140 145

aca gag gac gac gtg cgg cgt cga atc gct tct caa gtg ccc gac gac 595
Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser Gln Val Pro Asp Asp
150 155 160 165

gtc aga ctt aaa gcc gct gac atc gtt gtg gac aat aac ggc acg cta 643

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Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp Asn Asn Gly Thr Leu
                170                 175                 180

gag gac ctt cat gct gaa gca agc aag ctg att gct gag att ctt agt   691
Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile Ala Glu Ile Leu Ser
            185                 190                 195

cgc gtg aat tagcactaaa acatcgtcaa agt                             723
Arg Val Asn
        200


<210> 2494
<211> 200
<212> PRT
<213> Corynebacterium glutamicum

<400> 2494
Met Leu Arg Ile Gly Leu Thr Gly Gly Ile Gly Ser Gly Lys Ser Thr
  1               5                  10                  15

Val Ala Asp Leu Leu Ser Ser Glu Gly Phe Leu Ile Val Asp Ala Asp
             20                  25                  30

Gln Val Ala Arg Asp Ile Val Glu Pro Gly Gln Pro Ala Leu Ala Glu
         35                  40                  45

Leu Ala Glu Ala Phe Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu
     50                  55                  60

Asp Arg Ala Gly Leu Ala Ala Lys Ala Phe Val Ser Glu Glu Gln Thr
 65                  70                  75                  80

Ala Leu Leu Asn Ala Ile Thr His Pro Arg Ile Ala Glu Glu Ser Ala
                 85                  90                  95

Arg Arg Phe Asn Glu Ala Glu Asp Gln Gly Ala Lys Val Ala Val Tyr
            100                 105                 110

Asp Met Pro Leu Leu Val Glu Lys Gly Leu Asp Arg Lys Met Asp Leu
        115                 120                 125

Val Val Val Val Asp Val Asp Val Glu Glu Arg Val Arg Arg Leu Val
    130                 135                 140

Glu Lys Arg Gly Leu Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser
145                 150                 155                 160

Gln Val Pro Asp Asp Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp
                165                 170                 175

Asn Asn Gly Thr Leu Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile
            180                 185                 190

Ala Glu Ile Leu Ser Arg Val Asn
        195                 200


<210> 2495
<211> 585
<212> DNA
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<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(562)
<223> RXA01957

<400> 2495
acctcaactc cacagagcgt tgttatcaga tgctgatatg gctcgccttg cagcacaact 60

gaccgacaaa cactaaaacc tccacaacaa ggacatcatc atg act act cgc acc 115
Met Thr Thr Arg Thr
1 5

gta tct act tct gca ccc cat gtc act gtc aac atc aat acc gcg cac 163
Val Ser Thr Ser Ala Pro His Val Thr Val Asn Ile Asn Thr Ala His
10 15 20

aac aaa aca cgc act gtt acc aat ggc gcc aga aaa act aat gca gag 211
Asn Lys Thr Arg Thr Val Thr Asn Gly Ala Arg Lys Thr Asn Ala Glu
25 30 35

cgt ggc aag agc tgc atc tca ttt cgt gta ggg cca gaa ttg ttt gat 259
Arg Gly Lys Ser Cys Ile Ser Phe Arg Val Gly Pro Glu Leu Phe Asp
40 45 50

gaa ttc aaa gcg acc tgc atc gac aac gat att tcc atg acc aag gcg 307
Glu Phe Lys Ala Thr Cys Ile Asp Asn Asp Ile Ser Met Thr Lys Ala
55 60 65

ttt gag aaa gag ctt cgc acc tgg gtt gat gag cac aac gct ggt gca 355
Phe Glu Lys Glu Leu Arg Thr Trp Val Asp Glu His Asn Ala Gly Ala
70 75 80 85

aca aag aaa aga aac acc cat cgc acc tac gta caa gca ccc gtt ggt 403
Thr Lys Lys Arg Asn Thr His Arg Thr Tyr Val Gln Ala Pro Val Gly
90 95 100

act gtc gcc acc agc tct att cca ggt ctt ggg tta ttt act gtg ttc 451
Thr Val Ala Thr Ser Ser Ile Pro Gly Leu Gly Leu Phe Thr Val Phe
105 110 115

aag aag agc tct gat cag atg tgg tac gac ctg gaa agc agc ccg ctg 499
Lys Lys Ser Ser Asp Gln Met Trp Tyr Asp Leu Glu Ser Ser Pro Leu
120 125 130

atc gca caa gag ccc atg tcg aat atg gac atg cat cgt aac ggc tct 547
Ile Ala Gln Glu Pro Met Ser Asn Met Asp Met His Arg Asn Gly Ser
135 140 145

ttt gag ctg cac ctg tagatctctc tctcgaccac aca 585
Phe Glu Leu His Leu
150

<210> 2496
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 2496

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Met Thr Thr Arg Thr Val Ser Thr Ser Ala Pro His Val Thr Val Asn
  1               5                  10                  15

Ile Asn Thr Ala His Asn Lys Thr Arg Thr Val Thr Asn Gly Ala Arg
             20                  25                  30

Lys Thr Asn Ala Glu Arg Gly Lys Ser Cys Ile Ser Phe Arg Val Gly
         35                  40                  45

Pro Glu Leu Phe Asp Glu Phe Lys Ala Thr Cys Ile Asp Asn Asp Ile
     50                  55                  60

Ser Met Thr Lys Ala Phe Glu Lys Glu Leu Arg Thr Trp Val Asp Glu
 65                  70                  75                  80

His Asn Ala Gly Ala Thr Lys Lys Arg Asn Thr His Arg Thr Tyr Val
                 85                  90                  95

Gln Ala Pro Val Gly Thr Val Ala Thr Ser Ser Ile Pro Gly Leu Gly
            100                 105                 110

Leu Phe Thr Val Phe Lys Lys Ser Ser Asp Gln Met Trp Tyr Asp Leu
        115                 120                 125

Glu Ser Ser Pro Leu Ile Ala Gln Glu Pro Met Ser Asn Met Asp Met
    130                 135                 140

His Arg Asn Gly Ser Phe Glu Leu His Leu
145                 150


<210> 2497
<211> 630
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(607)
<223> RXA01958

<400> 2497
atatggacat gcatcgtaac ggctcttttg agctgcacct gtagatctct ctctcgacca 60

cacacagctc tcaccacctc ctagaaagga cggtttcacc atg tct aaa aaa cgc   115
                                            Met Ser Lys Lys Arg
                                              1               5

gac cac ctc acc gtc att cct gac ctt gag tca cgc acc cat cac agc   163
Asp His Leu Thr Val Ile Pro Asp Leu Glu Ser Arg Thr His His Ser
                 10                  15                  20

cgc agt aca caa ccg cca act acg ctg ccc gca cca cag ctg act att   211
Arg Ser Thr Gln Pro Pro Thr Thr Leu Pro Ala Pro Gln Leu Thr Ile
             25                  30                  35

atc acc gca cca gac aag cat caa cca cag ctt cgg gtt gtt aaa aac   259
Ile Thr Ala Pro Asp Lys His Gln Pro Gln Leu Arg Val Val Lys Asn
         40                  45                  50

acc acc acc cca tct tct gtg cag ccc tcg ccg atc aac tac agc ttt   307
```

```
Thr Thr Thr Pro Ser Ser Val Gln Pro Ser Pro Ile Asn Tyr Ser Phe
     55                  60                  65

act gat cct gta ctt cgc gag gct cac tat gca ttc cag cac agc gaa   355
Thr Asp Pro Val Leu Arg Glu Ala His Tyr Ala Phe Gln His Ser Glu
 70                  75                  80                  85

ctt gcc agg cca aca gtc ctg gac tca cac tgg gtt cgt cgc gca caa   403
Leu Ala Arg Pro Thr Val Leu Asp Ser His Trp Val Arg Arg Ala Gln
                90                  95                 100

gaa gaa ttc gac act gag cat aat gct gcc tat gtc cgt gcc gct gac   451
Glu Glu Phe Asp Thr Glu His Asn Ala Ala Tyr Val Arg Ala Ala Asp
            105                 110                 115

cag ctc tta tcc cct ttt gat gcc tac atc ctc gac aac ggc gat gtt   499
Gln Leu Leu Ser Pro Phe Asp Ala Tyr Ile Leu Asp Asn Gly Asp Val
        120                 125                 130

tac acc aag acc cca cgt gcc atc agt gct gct gaa caa gaa gaa ata   547
Tyr Thr Lys Thr Pro Arg Ala Ile Ser Ala Ala Glu Gln Glu Glu Ile
    135                 140                 145

ctt gag cac ttg cac gaa cac cat atc tgc tgg gac gaa gaa gct gaa   595
Leu Glu His Leu His Glu His His Ile Cys Trp Asp Glu Glu Ala Glu
150                 155                 160                 165

ttc ctg ctg cgc taaaggttgc cactggtttc agg                        630
Phe Leu Leu Arg
```

<210> 2498
<211> 169
<212> PRT
<213> Corynebacterium glutamicum

<400> 2498

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Met Ser Lys Lys Arg Asp His Leu Thr Val Ile Pro Asp Leu Glu Ser
  1               5                  10                  15

Arg Thr His His Ser Arg Ser Thr Gln Pro Pro Thr Thr Leu Pro Ala
             20                  25                  30

Pro Gln Leu Thr Ile Ile Thr Ala Pro Asp Lys His Gln Pro Gln Leu
         35                  40                  45

Arg Val Val Lys Asn Thr Thr Thr Pro Ser Ser Val Gln Pro Ser Pro
     50                  55                  60

Ile Asn Tyr Ser Phe Thr Asp Pro Val Leu Arg Glu Ala His Tyr Ala
 65                  70                  75                  80

Phe Gln His Ser Glu Leu Ala Arg Pro Thr Val Leu Asp Ser His Trp
                 85                  90                  95

Val Arg Arg Ala Gln Glu Glu Phe Asp Thr Glu His Asn Ala Ala Tyr
            100                 105                 110

Val Arg Ala Ala Asp Gln Leu Leu Ser Pro Phe Asp Ala Tyr Ile Leu
        115                 120                 125
```

```
Asp Asn Gly Asp Val Tyr Thr Lys Thr Pro Arg Ala Ile Ser Ala Ala
    130                 135                 140

Glu Gln Glu Glu Ile Leu Glu His Leu His Glu His His Ile Cys Trp
145                 150                 155                 160

Asp Glu Glu Ala Glu Phe Leu Leu Arg
                165
```

<210> 2499
<211> 481
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(481)
<223> RXA01959

<400> 2499

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cccaactact atgcacagcc cgtaaccatc gagccggcta aaatctatca acagaaaaac 60

cactgcctat ttgaccattc ttgtgcaaga aagtacacct atg ccc cac gac gtt   115
                                            Met Pro His Asp Val
                                              1               5

tac gat gtc gaa cac atc att tcc aag caa cct ttc tgc tcc atc ttt   163
Tyr Asp Val Glu His Ile Ile Ser Lys Gln Pro Phe Cys Ser Ile Phe
                 10                  15                  20

ttc cag ctc ccc gct gca gcg ctg aaa cct act att caa aaa gct gcc   211
Phe Gln Leu Pro Ala Ala Ala Leu Lys Pro Thr Ile Gln Lys Ala Ala
             25                  30                  35

acc aac cgc gac ctt act aag ctc aac acc gaa cag atc gct gag aac   259
Thr Asn Arg Asp Leu Thr Lys Leu Asn Thr Glu Gln Ile Ala Glu Asn
         40                  45                  50

cta cag cgc tac ctc gac acc tac agt gtc atg tct cac cag cgt gtc   307
Leu Gln Arg Tyr Leu Asp Thr Tyr Ser Val Met Ser His Gln Arg Val
     55                  60                  65

acc att gaa gag gtc act cat gtg cgc aac cct cat gag cct gat tat   355
Thr Ile Glu Glu Val Thr His Val Arg Asn Pro His Glu Pro Asp Tyr
 70                  75                  80                  85

gag ttt tca cca cag tac ggt gca cat atc tcg ctc atc ggt gag tct   403
Glu Phe Ser Pro Gln Tyr Gly Ala His Ile Ser Leu Ile Gly Glu Ser
                 90                  95                 100

tat gct gtg aac acg gcc acc aac gag cct tat gcc acc gac tcc gag   451
Tyr Ala Val Asn Thr Ala Thr Asn Glu Pro Tyr Ala Thr Asp Ser Glu
            105                 110                 115

ggc cat cct ctc gca ctg tat ttt gaa atg                          481
Gly His Pro Leu Ala Leu Tyr Phe Glu Met
        120                 125
```

<210> 2500
<211> 127
<212> PRT
<213> Corynebacterium glutamicum

<400> 2500
Met Pro His Asp Val Tyr Asp Val Glu His Ile Ile Ser Lys Gln Pro
1 5 10 15

Phe Cys Ser Ile Phe Phe Gln Leu Pro Ala Ala Ala Leu Lys Pro Thr
20 25 30

Ile Gln Lys Ala Ala Thr Asn Arg Asp Leu Thr Lys Leu Asn Thr Glu
35 40 45

Gln Ile Ala Glu Asn Leu Gln Arg Tyr Leu Asp Thr Tyr Ser Val Met
50 55 60

Ser His Gln Arg Val Thr Ile Glu Glu Val Thr His Val Arg Asn Pro
65 70 75 80

His Glu Pro Asp Tyr Glu Phe Ser Pro Gln Tyr Gly Ala His Ile Ser
85 90 95

Leu Ile Gly Glu Ser Tyr Ala Val Asn Thr Ala Thr Asn Glu Pro Tyr
100 105 110

Ala Thr Asp Ser Glu Gly His Pro Leu Ala Leu Tyr Phe Glu Met
115 120 125

<210> 2501
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(580)
<223> RXA01961

<400> 2501
aacacccagc tagtgcctgt gcttgagcta ccaaagttca atccttttga ggcacttgct 60

atccaccttg aagccgccaa caactaagaa agcatccttc atg act gac aac gct 115
Met Thr Asp Asn Ala
1 5

gac aac acc aca gat aac gta acc aat aac tca gac acc aat ctc gat 163
Asp Asn Thr Thr Asp Asn Val Thr Asn Asn Ser Asp Thr Asn Leu Asp
10 15 20

tac agc ttc gac ccg ctc cct gac gag ccc tat gcc tac ggc ttt gaa 211
Tyr Ser Phe Asp Pro Leu Pro Asp Glu Pro Tyr Ala Tyr Gly Phe Glu
25 30 35

ctg gtc gct gct gat gca cac tct gac tca aca aca acc agc acc gat 259
Leu Val Ala Ala Asp Ala His Ser Asp Ser Thr Thr Thr Ser Thr Asp
40 45 50

acc cca gag act gtc gct gtg gca ctt aaa acc cgc gag gac act atc 307

```
Thr Pro Glu Thr Val Ala Val Ala Leu Lys Thr Arg Glu Asp Thr Ile
     55                  60                  65

aac tgg gtc aac acc cag cgt gcc gaa ggt aaa ccc gat gaa att cgt   355
Asn Trp Val Asn Thr Gln Arg Ala Glu Gly Lys Pro Asp Glu Ile Arg
 70                  75                  80                  85

atc aat aac cca att cga tca gag cgt att gct gag ttt gtc cac gaa   403
Ile Asn Asn Pro Ile Arg Ser Glu Arg Ile Ala Glu Phe Val His Glu
                 90                  95                 100

atg atc atg cat cac ggc ctc gta gcc tgc atg gaa gat ctc gca ata   451
Met Ile Met His His Gly Leu Val Ala Cys Met Glu Asp Leu Ala Ile
            105                 110                 115

ctt atc aag cgc gac aag ctc acc cag ctg gaa gcc gaa aac gct atc   499
Leu Ile Lys Arg Asp Lys Leu Thr Gln Leu Glu Ala Glu Asn Ala Ile
        120                 125                 130

aca gcc tgg cac aac ctc acc aaa gaa tcc ctt ggt cag atc atg ggg   547
Thr Ala Trp His Asn Leu Thr Lys Glu Ser Leu Gly Gln Ile Met Gly
    135                 140                 145

ctc ttc tat cag tac gtc gaa aac aac aca aaa taggaaagaa gaaacaccat 600
Leu Phe Tyr Gln Tyr Val Glu Asn Asn Thr Lys
150                 155                 160

cat                                                               603


<210> 2502
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 2502
Met Thr Asp Asn Ala Asp Asn Thr Thr Asp Asn Val Thr Asn Asn Ser
  1               5                  10                  15

Asp Thr Asn Leu Asp Tyr Ser Phe Asp Pro Leu Pro Asp Glu Pro Tyr
             20                  25                  30

Ala Tyr Gly Phe Glu Leu Val Ala Ala Asp Ala His Ser Asp Ser Thr
         35                  40                  45

Thr Thr Ser Thr Asp Thr Pro Glu Thr Val Ala Val Ala Leu Lys Thr
     50                  55                  60

Arg Glu Asp Thr Ile Asn Trp Val Asn Thr Gln Arg Ala Glu Gly Lys
 65                  70                  75                  80

Pro Asp Glu Ile Arg Ile Asn Asn Pro Ile Arg Ser Glu Arg Ile Ala
                 85                  90                  95

Glu Phe Val His Glu Met Ile Met His His Gly Leu Val Ala Cys Met
            100                 105                 110

Glu Asp Leu Ala Ile Leu Ile Lys Arg Asp Lys Leu Thr Gln Leu Glu
        115                 120                 125

Ala Glu Asn Ala Ile Thr Ala Trp His Asn Leu Thr Lys Glu Ser Leu
```

```
    130                 135                 140

Gly Gln Ile Met Gly Leu Phe Tyr Gln Tyr Val Glu Asn Asn Thr Lys
145                 150                 155                 160
```

<210> 2503
<211> 693
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(670)
<223> RXA01962

<400> 2503

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agcctggcac aacctcacca aagaatccct tggtcagatc atggggctct tctatcagta 60

cgtcgaaaac aacacaaaat aggaaagaag aaacaccatc atg tct gac aac act   115
                                              Met Ser Asp Asn Thr
                                                1               5

cag gac aac cct ttc tcc atc cgc tac gca cac cct gac cac cag ctc   163
Gln Asp Asn Pro Phe Ser Ile Arg Tyr Ala His Pro Asp His Gln Leu
                10                  15                  20

gct ctt aat gag ctt gtt gat act gcc gat cta cct gca cca aca agc   211
Ala Leu Asn Glu Leu Val Asp Thr Ala Asp Leu Pro Ala Pro Thr Ser
            25                  30                  35

tat atg aaa aat ccc tgg tcc ggg gac aac acg cct atc gcc gag tgg   259
Tyr Met Lys Asn Pro Trp Ser Gly Asp Asn Thr Pro Ile Ala Glu Trp
        40                  45                  50

cga cgc gag cgc atc acc cag tgg cag cgc acc gag atc att gtc aat   307
Arg Arg Glu Arg Ile Thr Gln Trp Gln Arg Thr Glu Ile Ile Val Asn
    55                  60                  65

caa cgc gat gat gac gat ctc att cac gtc agc ttc ccg aag ctc ggc   355
Gln Arg Asp Asp Asp Asp Leu Ile His Val Ser Phe Pro Lys Leu Gly
70                  75                  80                  85

cag cac att cag ctc aac acc gac gat att ctc gca ttg gtc gca gcc   403
Gln His Ile Gln Leu Asn Thr Asp Asp Ile Leu Ala Leu Val Ala Ala
                90                  95                  100

tgc gtc aca ccc act gct aac gac att gag gca act atc gaa gaa aat   451
Cys Val Thr Pro Thr Ala Asn Asp Ile Glu Ala Thr Ile Glu Glu Asn
            105                 110                 115

ctc cac tca tat ccg cac gat acg gtc atc atg ttt aac gca gat gat   499
Leu His Ser Tyr Pro His Asp Thr Val Ile Met Phe Asn Ala Asp Asp
        120                 125                 130

cta gat gat gcc ctt ggt ctc gtt gtt gcc gtc aaa gac gcg agc ggg   547
Leu Asp Asp Ala Leu Gly Leu Val Val Ala Val Lys Asp Ala Ser Gly
    135                 140                 145
```

```
gaa cac tca ccg cgc gct gtc tgg cgc acc aac acc gat cat gga gct   595
Glu His Ser Pro Arg Ala Val Trp Arg Thr Asn Thr Asp His Gly Ala
150                 155                 160                 165

ctt gac gag act gaa ctc gcg cgg ctc att ctc aaa ttc ggt ggc agc   643
Leu Asp Glu Thr Glu Leu Ala Arg Leu Ile Leu Lys Phe Gly Gly Ser
                170                 175                 180

ttc gat gac tac ggc gtg ctg caa cat taaaccgact cactaagcac         690
Phe Asp Asp Tyr Gly Val Leu Gln His
            185                 190

cgc                                                               693
```

<210> 2504
<211> 190
<212> PRT
<213> Corynebacterium glutamicum

<400> 2504

```
Met Ser Asp Asn Thr Gln Asp Asn Pro Phe Ser Ile Arg Tyr Ala His
  1               5                  10                  15

Pro Asp His Gln Leu Ala Leu Asn Glu Leu Val Asp Thr Ala Asp Leu
             20                  25                  30

Pro Ala Pro Thr Ser Tyr Met Lys Asn Pro Trp Ser Gly Asp Asn Thr
         35                  40                  45

Pro Ile Ala Glu Trp Arg Arg Glu Arg Ile Thr Gln Trp Gln Arg Thr
     50                  55                  60

Glu Ile Ile Val Asn Gln Arg Asp Asp Asp Asp Leu Ile His Val Ser
 65                  70                  75                  80

Phe Pro Lys Leu Gly Gln His Ile Gln Leu Asn Thr Asp Asp Ile Leu
                 85                  90                  95

Ala Leu Val Ala Ala Cys Val Thr Pro Thr Ala Asn Asp Ile Glu Ala
            100                 105                 110

Thr Ile Glu Glu Asn Leu His Ser Tyr Pro His Asp Thr Val Ile Met
        115                 120                 125

Phe Asn Ala Asp Asp Leu Asp Asp Ala Leu Gly Leu Val Val Ala Val
    130                 135                 140

Lys Asp Ala Ser Gly Glu His Ser Pro Arg Ala Val Trp Arg Thr Asn
145                 150                 155                 160

Thr Asp His Gly Ala Leu Asp Glu Thr Glu Leu Ala Arg Leu Ile Leu
                165                 170                 175

Lys Phe Gly Gly Ser Phe Asp Asp Tyr Gly Val Leu Gln His
            180                 185                 190
```

<210> 2505
<211> 784

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(784)
<223> RXA01963

<400> 2505
cagattttct ctgtgtgagc tggggttttc tgcatttccc acttgttttt ctccaacact 60

ccacacacac accttcaaag aagaaagttc gaaagattct atg aaa aac cgt aaa 115
Met Lys Asn Arg Lys
1 5

aaa atc atg tct acc ctc acc act gtc tgc gcc gta ctg ggt ata gtt 163
Lys Ile Met Ser Thr Leu Thr Thr Val Cys Ala Val Leu Gly Ile Val
10 15 20

gca gct cat cca ttc cac gcc tct gct gtc atc ggc ggc tct gtc cca 211
Ala Ala His Pro Phe His Ala Ser Ala Val Ile Gly Gly Ser Val Pro
25 30 35

tca act gat tcc gtt gcc aac gct gtc gca aaa atc gga cca ggc gca 259
Ser Thr Asp Ser Val Ala Asn Ala Val Ala Lys Ile Gly Pro Gly Ala
40 45 50

ttg aac tgc agc ggt gtc atg atc tca cca tcg tgg gca ctc acc gca 307
Leu Asn Cys Ser Gly Val Met Ile Ser Pro Ser Trp Ala Leu Thr Ala
55 60 65

cgc cac tgt gtc gat gac atc aac ata ctc ggc gac atc gac acc atc 355
Arg His Cys Val Asp Asp Ile Asn Ile Leu Gly Asp Ile Asp Thr Ile
70 75 80 85

acg cct att act cca ggt att cat cgc aat gaa ggt aac tat atg ggt 403
Thr Pro Ile Thr Pro Gly Ile His Arg Asn Glu Gly Asn Tyr Met Gly
90 95 100

gag gtt tac cgc gca ccg tcc ggt gat cta gcg ctc att aat atc aac 451
Glu Val Tyr Arg Ala Pro Ser Gly Asp Leu Ala Leu Ile Asn Ile Asn
105 110 115

ggc gtg cac aag ggc acc att gcg cag ctc ccc aca caa gaa tat cca 499
Gly Val His Lys Gly Thr Ile Ala Gln Leu Pro Thr Gln Glu Tyr Pro
120 125 130

ctg gga acc gct gca cag tca gtc ggt ttt ggt ggc ggt ggt gtc aat 547
Leu Gly Thr Ala Ala Gln Ser Val Gly Phe Gly Gly Gly Gly Val Asn
135 140 145

atc cgc acc gct gaa tcg gtc aac atg att ctc acc gac ata tat agc 595
Ile Arg Thr Ala Glu Ser Val Asn Met Ile Leu Thr Asp Ile Tyr Ser
150 155 160 165

gtg agg tca ggg aaa ttc cat cac ggt gtc ggt cga tca cac tat ctc 643
Val Arg Ser Gly Lys Phe His His Gly Val Gly Arg Ser His Tyr Leu
170 175 180

ctc ttt gat tat gac agt gct gaa act ggt cga atc cac aaa ggt gat 691
Leu Phe Asp Tyr Asp Ser Ala Glu Thr Gly Arg Ile His Lys Gly Asp

```
            185                 190                 195

tct ggg ggc ccc atc ttc att ggt gac gag gtt gtg ggc att atg tct   739
Ser Gly Gly Pro Ile Phe Ile Gly Asp Glu Val Val Gly Ile Met Ser
        200                 205                 210

cac ggc aca ata aat aag aac gac ggg tct ttt gat gac gaa tcc       784
His Gly Thr Ile Asn Lys Asn Asp Gly Ser Phe Asp Asp Glu Ser
    215                 220                 225


<210> 2506
<211> 228
<212> PRT
<213> Corynebacterium glutamicum

<400> 2506
Met Lys Asn Arg Lys Lys Ile Met Ser Thr Leu Thr Thr Val Cys Ala
  1               5                  10                  15

Val Leu Gly Ile Val Ala Ala His Pro Phe His Ala Ser Ala Val Ile
             20                  25                  30

Gly Gly Ser Val Pro Ser Thr Asp Ser Val Ala Asn Ala Val Ala Lys
         35                  40                  45

Ile Gly Pro Gly Ala Leu Asn Cys Ser Gly Val Met Ile Ser Pro Ser
     50                  55                  60

Trp Ala Leu Thr Ala Arg His Cys Val Asp Asp Ile Asn Ile Leu Gly
 65                  70                  75                  80

Asp Ile Asp Thr Ile Thr Pro Ile Thr Pro Gly Ile His Arg Asn Glu
                 85                  90                  95

Gly Asn Tyr Met Gly Glu Val Tyr Arg Ala Pro Ser Gly Asp Leu Ala
            100                 105                 110

Leu Ile Asn Ile Asn Gly Val His Lys Gly Thr Ile Ala Gln Leu Pro
        115                 120                 125

Thr Gln Glu Tyr Pro Leu Gly Thr Ala Ala Gln Ser Val Gly Phe Gly
    130                 135                 140

Gly Gly Gly Val Asn Ile Arg Thr Ala Glu Ser Val Asn Met Ile Leu
145                 150                 155                 160

Thr Asp Ile Tyr Ser Val Arg Ser Gly Lys Phe His His Gly Val Gly
                165                 170                 175

Arg Ser His Tyr Leu Leu Phe Asp Tyr Asp Ser Ala Glu Thr Gly Arg
            180                 185                 190

Ile His Lys Gly Asp Ser Gly Gly Pro Ile Phe Ile Gly Asp Glu Val
        195                 200                 205

Val Gly Ile Met Ser His Gly Thr Ile Asn Lys Asn Asp Gly Ser Phe
    210                 215                 220

Asp Asp Glu Ser
225
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<210> 2507
<211> 1426
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1426)
<223> RXA01964

<400> 2507
agagccagat gatggctttg atatggatga tgtcatgggc caagcgttcg gtcgctagct 60

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cataccttgt tacaacgaca ctttttaagg gaagaagatt atg acc agc gct gtg   115
                                            Met Thr Ser Ala Val
                                              1               5

aat gtg cag aag aag acc aca cag aaa gta ctt aag ccc att aat acg   163
Asn Val Gln Lys Lys Thr Thr Gln Lys Val Leu Lys Pro Ile Asn Thr
                 10                  15                  20

aag aat tac tct gcg aca gat gca gta cag aca ggc cag cac gga tct   211
Lys Asn Tyr Ser Ala Thr Asp Ala Val Gln Thr Gly Gln His Gly Ser
             25                  30                  35

gct tta ggc tcg aat atc ggt gtc tac acc tat acc gct gga ctc gat   259
Ala Leu Gly Ser Asn Ile Gly Val Tyr Thr Tyr Thr Ala Gly Leu Asp
         40                  45                  50

att gga aac ggt tat gtc aag ggc att atc gag gca acc ggt gat acg   307
Ile Gly Asn Gly Tyr Val Lys Gly Ile Ile Glu Ala Thr Gly Asp Thr
     55                  60                  65

act ggc acg tct gtt gat gtt att gat atg ccc tct gca gca acg cgc   355
Thr Gly Thr Ser Val Asp Val Ile Asp Met Pro Ser Ala Ala Thr Arg
 70                  75                  80                  85

atg agc cgg cca acg gaa gtt ccc gaa cca gat gac acc gct gtt gct   403
Met Ser Arg Pro Thr Glu Val Pro Glu Pro Asp Asp Thr Ala Val Ala
                 90                  95                 100

gtc acc ggt gcg gat ttc ttc aac cac att gat acc aat ttc aat tcg   451
Val Thr Gly Ala Asp Phe Phe Asn His Ile Asp Thr Asn Phe Asn Ser
             105                 110                 115

cct atg gtg aaa ggt aat tat cgt tac ctt tgt ggc acg cgc agc ttg   499
Pro Met Val Lys Gly Asn Tyr Arg Tyr Leu Cys Gly Thr Arg Ser Leu
         120                 125                 130

tct gca cga ggt agc ttg gag gaa ttt gat ctg gtg ggt aac cgc tcc   547
Ser Ala Arg Gly Ser Leu Glu Glu Phe Asp Leu Val Gly Asn Arg Ser
    135                 140                 145

aag gcg gaa caa gaa ctg agc aag gtg ctg gtc atg gca gta ctt gcg   595
Lys Ala Glu Gln Glu Leu Ser Lys Val Leu Val Met Ala Val Leu Ala
150                 155                 160                 165

gcc aag gct gtg aaa gac ttt gtg gca gca cat ggt cga atc cca cag   643
Ala Lys Ala Val Lys Asp Phe Val Ala Ala His Gly Arg Ile Pro Gln
```

```
                170                 175                 180

gtt gct gtt gag ggt gat ccc ggt gtg ctg cgt gtg cat acg tat ctt   691
Val Ala Val Glu Gly Asp Pro Gly Val Leu Arg Val His Thr Tyr Leu
            185                 190                 195

gca ctt gcg tta ccg att aat gaa tat gtg ggt cac cgt cat ggg tat   739
Ala Leu Ala Leu Pro Ile Asn Glu Tyr Val Gly His Arg His Gly Tyr
        200                 205                 210

aag gca cag ttt atg ggt gat ggg gca gcg aac ccg gct gtg cat gtg   787
Lys Ala Gln Phe Met Gly Asp Gly Ala Ala Asn Pro Ala Val His Val
    215                 220                 225

gtg acg gtt aac aac ttt gaa acc cca gca acg gtg cag ctc atc ttt   835
Val Thr Val Asn Asn Phe Glu Thr Pro Ala Thr Val Gln Leu Ile Phe
230                 235                 240                 245

gag cgt gtc gag gtc att gcc gag ggc gca tcg gca cag tat gcc att   883
Glu Arg Val Glu Val Ile Ala Glu Gly Ala Ser Ala Gln Tyr Ala Ile
                250                 255                 260

acc gca ggt ggc gaa gta ctt atg aac gga atg ctc gcc gat gta cgc   931
Thr Ala Gly Gly Glu Val Leu Met Asn Gly Met Leu Ala Asp Val Arg
            265                 270                 275

tcc aaa ggg ctt gct cta gag ggc gtg aca gca ggt gat gtg cta caa   979
Ser Lys Gly Leu Ala Leu Glu Gly Val Thr Ala Gly Asp Val Leu Gln
        280                 285                 290

gct cgc cac aca atc ggt gtg gat gtg ggt gaa ggt act gtg aat ttc   1027
Ala Arg His Thr Ile Gly Val Asp Val Gly Glu Gly Thr Val Asn Phe
    295                 300                 305

cca gtc ttt acg gat ggg cgg ttt aat cat gat gct tca cgc gcc tat   1075
Pro Val Phe Thr Asp Gly Arg Phe Asn His Asp Ala Ser Arg Ala Tyr
310                 315                 320                 325

gac aag ggt tat ggc acc gtc ttg gag tcg gcg att cag gct atg gac   1123
Asp Lys Gly Tyr Gly Thr Val Leu Glu Ser Ala Ile Gln Ala Met Asp
                330                 335                 340

gat gct ggg ttg gca cac aac ttt aac tcg cgt aag cag ttg gct gat   1171
Asp Ala Gly Leu Ala His Asn Phe Asn Ser Arg Lys Gln Leu Ala Asp
            345                 350                 355

tat ttg cag cga cca ccg agt gca ctc aag cgg aat ttc tat acc cgc   1219
Tyr Leu Gln Arg Pro Pro Ser Ala Leu Lys Arg Asn Phe Tyr Thr Arg
        360                 365                 370

gtg gaa cag cat gtt gat cag gag gca gtg ttc ttt gtt cag gat gtg   1267
Val Glu Gln His Val Asp Gln Glu Ala Val Phe Phe Val Gln Asp Val
    375                 380                 385

gct gca gag ttc gca cga gtg ttg agc gac gtg ggt gct ctt acc gaa   1315
Ala Ala Glu Phe Ala Arg Val Leu Ser Asp Val Gly Ala Leu Thr Glu
390                 395                 400                 405

gta gcc ttt gtc tac ggc ggt ggt tcc ggc ccg ctg cgt gat cga ctg   1363
Val Ala Phe Val Tyr Gly Gly Gly Ser Gly Pro Leu Arg Asp Arg Leu
                410                 415                 420
```

```
cat gaa gcg ttg ctg att aag gca gcg gag atg ggt tcg gaa gat acg   1411
His Glu Ala Leu Leu Ile Lys Ala Ala Glu Met Gly Ser Glu Asp Thr
            425                 430                 435

ttc ccg gtg ctg tat                                             1426
Phe Pro Val Leu Tyr
        440
```

<210> 2508
<211> 442
<212> PRT
<213> Corynebacterium glutamicum

<400> 2508

```
Met Thr Ser Ala Val Asn Val Gln Lys Lys Thr Thr Gln Lys Val Leu
  1               5                  10                  15

Lys Pro Ile Asn Thr Lys Asn Tyr Ser Ala Thr Asp Ala Val Gln Thr
             20                  25                  30

Gly Gln His Gly Ser Ala Leu Gly Ser Asn Ile Gly Val Tyr Thr Tyr
         35                  40                  45

Thr Ala Gly Leu Asp Ile Gly Asn Gly Tyr Val Lys Gly Ile Ile Glu
     50                  55                  60

Ala Thr Gly Asp Thr Thr Gly Thr Ser Val Asp Val Ile Asp Met Pro
 65                  70                  75                  80

Ser Ala Ala Thr Arg Met Ser Arg Pro Thr Glu Val Pro Glu Pro Asp
                 85                  90                  95

Asp Thr Ala Val Ala Val Thr Gly Ala Asp Phe Phe Asn His Ile Asp
            100                 105                 110

Thr Asn Phe Asn Ser Pro Met Val Lys Gly Asn Tyr Arg Tyr Leu Cys
        115                 120                 125

Gly Thr Arg Ser Leu Ser Ala Arg Gly Ser Leu Glu Glu Phe Asp Leu
    130                 135                 140

Val Gly Asn Arg Ser Lys Ala Glu Gln Glu Leu Ser Lys Val Leu Val
145                 150                 155                 160

Met Ala Val Leu Ala Ala Lys Ala Val Lys Asp Phe Val Ala Ala His
                165                 170                 175

Gly Arg Ile Pro Gln Val Ala Val Glu Gly Asp Pro Gly Val Leu Arg
            180                 185                 190

Val His Thr Tyr Leu Ala Leu Ala Leu Pro Ile Asn Glu Tyr Val Gly
        195                 200                 205

His Arg His Gly Tyr Lys Ala Gln Phe Met Gly Asp Gly Ala Ala Asn
    210                 215                 220

Pro Ala Val His Val Val Thr Val Asn Asn Phe Glu Thr Pro Ala Thr
225                 230                 235                 240
```

```
Val Gln Leu Ile Phe Glu Arg Val Glu Val Ile Ala Glu Gly Ala Ser
                245                 250                 255

Ala Gln Tyr Ala Ile Thr Ala Gly Gly Glu Val Leu Met Asn Gly Met
            260                 265                 270

Leu Ala Asp Val Arg Ser Lys Gly Leu Ala Leu Glu Gly Val Thr Ala
        275                 280                 285

Gly Asp Val Leu Gln Ala Arg His Thr Ile Gly Val Asp Val Gly Glu
    290                 295                 300

Gly Thr Val Asn Phe Pro Val Phe Thr Asp Gly Arg Phe Asn His Asp
305                 310                 315                 320

Ala Ser Arg Ala Tyr Asp Lys Gly Tyr Gly Thr Val Leu Glu Ser Ala
                325                 330                 335

Ile Gln Ala Met Asp Asp Ala Gly Leu Ala His Asn Phe Asn Ser Arg
            340                 345                 350

Lys Gln Leu Ala Asp Tyr Leu Gln Arg Pro Pro Ser Ala Leu Lys Arg
        355                 360                 365

Asn Phe Tyr Thr Arg Val Glu Gln His Val Asp Gln Glu Ala Val Phe
    370                 375                 380

Phe Val Gln Asp Val Ala Ala Glu Phe Ala Arg Val Leu Ser Asp Val
385                 390                 395                 400

Gly Ala Leu Thr Glu Val Ala Phe Val Tyr Gly Gly Gly Ser Gly Pro
                405                 410                 415

Leu Arg Asp Arg Leu His Glu Ala Leu Leu Ile Lys Ala Ala Glu Met
            420                 425                 430

Gly Ser Glu Asp Thr Phe Pro Val Leu Tyr
        435                 440


<210> 2509
<211> 684
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(661)
<223> RXA01965

<400> 2509
acttctatgt tactattaaa ttagtcaata acgttagtca taaacaatgc agttattgaa 60

gagaaacttc ccgacacaat gtacgaaatg ggggtcacac atg gct caa aaa cag   115
                                            Met Ala Gln Lys Gln
                                              1               5

gac acg aca cat gta tca gag gac gat gcc ccg tgg cgt aat gtg cgt   163
Asp Thr Thr His Val Ser Glu Asp Asp Ala Pro Trp Arg Asn Val Arg
                 10                  15                  20
```

```
atg cgc ttc cca gaa aca gac gct atc gtt gag cgg ttt ttg gaa aca   211
Met Arg Phe Pro Glu Thr Asp Ala Ile Val Glu Arg Phe Leu Glu Thr
             25                  30                  35

cag ggt gct cgt ggc atc tcg ctt gcg atg cga cag ctg atc tat ttg   259
Gln Gly Ala Arg Gly Ile Ser Leu Ala Met Arg Gln Leu Ile Tyr Leu
         40                  45                  50

ttt gtc gct gaa tac ggt gat gta gag gtt gct acc gtt att ggc ctc   307
Phe Val Ala Glu Tyr Gly Asp Val Glu Val Ala Thr Val Ile Gly Leu
     55                  60                  65

aag ctg gtg gaa agc ctg cag gca ggg gct gag ggt agt gat ctt ttt   355
Lys Leu Val Glu Ser Leu Gln Ala Gly Ala Glu Gly Ser Asp Leu Phe
 70                  75                  80                  85

gct cag ctc gcg gcc ggg gtt gct gac gta gac gct gtg act aca cgc   403
Ala Gln Leu Ala Ala Gly Val Ala Asp Val Asp Ala Val Thr Thr Arg
                 90                  95                 100

aag aag gca ccg cag cag ata gca ccg cca tcg acc aca acc cgt gca   451
Lys Lys Ala Pro Gln Gln Ile Ala Pro Pro Ser Thr Thr Thr Arg Ala
            105                 110                 115

cct gat cag gta aat gag ttt gtt gcc gag gcg gag agt cag ccg gtt   499
Pro Asp Gln Val Asn Glu Phe Val Ala Glu Ala Glu Ser Gln Pro Val
        120                 125                 130

gag gag tca gtt gtt gag gcc aaa gta ccc aag cag cag gta gca cca   547
Glu Glu Ser Val Val Glu Ala Lys Val Pro Lys Gln Gln Val Ala Pro
    135                 140                 145

cag ccg gca cag aag ccg gag caa aaa cca gaa caa aag tcg gcg caa   595
Gln Pro Ala Gln Lys Pro Glu Gln Lys Pro Glu Gln Lys Ser Ala Gln
150                 155                 160                 165

cca gca cag tca gag cca gat gat ggc ttt gat atg gat gat gtc atg   643
Pro Ala Gln Ser Glu Pro Asp Asp Gly Phe Asp Met Asp Asp Val Met
                170                 175                 180

ggc caa gcg ttc ggt cgc tagctcatac cttgttacaa cga                684
Gly Gln Ala Phe Gly Arg
            185
```

<210> 2510
<211> 187
<212> PRT
<213> Corynebacterium glutamicum

<400> 2510

```
Met Ala Gln Lys Gln Asp Thr Thr His Val Ser Glu Asp Asp Ala Pro
  1               5                  10                  15

Trp Arg Asn Val Arg Met Arg Phe Pro Glu Thr Asp Ala Ile Val Glu
             20                  25                  30

Arg Phe Leu Glu Thr Gln Gly Ala Arg Gly Ile Ser Leu Ala Met Arg
         35                  40                  45

Gln Leu Ile Tyr Leu Phe Val Ala Glu Tyr Gly Asp Val Glu Val Ala
```

```
     50                  55                  60

Thr Val Ile Gly Leu Lys Leu Val Glu Ser Leu Gln Ala Gly Ala Glu
 65                  70                  75                  80

Gly Ser Asp Leu Phe Ala Gln Leu Ala Ala Gly Val Ala Asp Val Asp
                85                  90                  95

Ala Val Thr Thr Arg Lys Lys Ala Pro Gln Gln Ile Ala Pro Pro Ser
            100                 105                 110

Thr Thr Thr Arg Ala Pro Asp Gln Val Asn Glu Phe Val Ala Glu Ala
        115                 120                 125

Glu Ser Gln Pro Val Glu Glu Ser Val Val Glu Ala Lys Val Pro Lys
    130                 135                 140

Gln Gln Val Ala Pro Gln Pro Ala Gln Lys Pro Glu Gln Lys Pro Glu
145                 150                 155                 160

Gln Lys Ser Ala Gln Pro Ala Gln Ser Glu Pro Asp Asp Gly Phe Asp
                165                 170                 175

Met Asp Asp Val Met Gly Gln Ala Phe Gly Arg
            180                 185


<210> 2511
<211> 726
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (47)..(703)
<223> RXA01966

<400> 2511
ccctgttatg ggctgggttt ataagaagat gggttagttt ttaaaagtg tct gaa tct 58
                                                    Val Ser Glu Ser
                                                      1

gaa aac aac aca aca cca gca gtc gca gct cgc gat gac cgt ctg gtc   106
Glu Asn Asn Thr Thr Pro Ala Val Ala Ala Arg Asp Asp Arg Leu Val
  5                  10                  15                  20

tgg gtc gat ctg gaa atg act ggt cta gat ttg aag cgc cac gtg atc   154
Trp Val Asp Leu Glu Met Thr Gly Leu Asp Leu Lys Arg His Val Ile
                25                  30                  35

gtg gag gtt gcg gcg ttg gtc act gac gct aac ctc aac gtt ttg ggc   202
Val Glu Val Ala Ala Leu Val Thr Asp Ala Asn Leu Asn Val Leu Gly
            40                  45                  50

gag ggc gtg gac ttg gtt gtt cac gca act gaa gaa gag ctc gcg cag   250
Glu Gly Val Asp Leu Val Val His Ala Thr Glu Glu Glu Leu Ala Gln
        55                  60                  65

atg gat gat ttt gtc acc aac atg cac gaa tcc tct ggg ctg act gag   298
Met Asp Asp Phe Val Thr Asn Met His Glu Ser Ser Gly Leu Thr Glu
    70                  75                  80
```

```
cag atc cgg gaa tcc gcg gtc acg ttg aag gaa gcc gaa gat gct gtg   346
Gln Ile Arg Glu Ser Ala Val Thr Leu Lys Glu Ala Glu Asp Ala Val
 85                  90                  95                 100

ctc gca ttg att gaa aag cac tgc gat cca gcc cat cct gca ccg cta   394
Leu Ala Leu Ile Glu Lys His Cys Asp Pro Ala His Pro Ala Pro Leu
                105                 110                 115

gct ggt aac tcc att gcc act gac cgc gcg ttt atc cgc gaa cat atg   442
Ala Gly Asn Ser Ile Ala Thr Asp Arg Ala Phe Ile Arg Glu His Met
            120                 125                 130

cca cgt ctt gat gag gcc ctg cat tac cgc atg gtg gat gtg tcc tcg   490
Pro Arg Leu Asp Glu Ala Leu His Tyr Arg Met Val Asp Val Ser Ser
        135                 140                 145

gtg aag gaa ttg gcg cgt cgc tgg tac cca cgc gtg tac tac aag cag   538
Val Lys Glu Leu Ala Arg Arg Trp Tyr Pro Arg Val Tyr Tyr Lys Gln
    150                 155                 160

ccg gag aag ggt ttg gcg cac cgc gcg ttg gcg gac att gtg gag tcg   586
Pro Glu Lys Gly Leu Ala His Arg Ala Leu Ala Asp Ile Val Glu Ser
165                 170                 175                 180

att cgg gag ttg gat tac tac cgt cgc tca ttt ttt gtt gca gag cct   634
Ile Arg Glu Leu Asp Tyr Tyr Arg Arg Ser Phe Phe Val Ala Glu Pro
                185                 190                 195

ggt cct acc tct gag cag tgc gca gat gat gcg cag gca gcg gtg gac   682
Gly Pro Thr Ser Glu Gln Cys Ala Asp Asp Ala Gln Ala Ala Val Asp
            200                 205                 210

cgt ttt gca ccc tac ttt gat tagagggttt taagcagcct ggt            726
Arg Phe Ala Pro Tyr Phe Asp
        215
```

Replacement Sheet

<210> 2512
<211> 219
<212> PRT
<213> Corynebacterium glutamicum

<400> 2512

```
Val Ser Glu Ser Glu Asn Asn Thr Thr Pro Ala Val Ala Ala Arg Asp
  1               5                  10                  15

Asp Arg Leu Val Trp Val Asp Leu Glu Met Thr Gly Leu Asp Leu Lys
             20                  25                  30

Arg His Val Ile Val Glu Val Ala Ala Leu Val Thr Asp Ala Asn Leu
         35                  40                  45

Asn Val Leu Gly Glu Gly Val Asp Leu Val Val His Ala Thr Glu Glu
     50                  55                  60

Glu Leu Ala Gln Met Asp Asp Phe Val Thr Asn Met His Glu Ser Ser
 65                  70                  75                  80

Gly Leu Thr Glu Gln Ile Arg Glu Ser Ala Val Thr Leu Lys Glu Ala
                 85                  90                  95
```

```
Glu Asp Ala Val Leu Ala Leu Ile Glu Lys His Cys Asp Pro Ala His
            100                 105                 110

Pro Ala Pro Leu Ala Gly Asn Ser Ile Ala Thr Asp Arg Ala Phe Ile
        115                 120                 125

Arg Glu His Met Pro Arg Leu Asp Glu Ala Leu His Tyr Arg Met Val
    130                 135                 140

Asp Val Ser Ser Val Lys Glu Leu Ala Arg Arg Trp Tyr Pro Arg Val
145                 150                 155                 160

Tyr Tyr Lys Gln Pro Glu Lys Gly Leu Ala His Arg Ala Leu Ala Asp
                165                 170                 175

Ile Val Glu Ser Ile Arg Glu Leu Asp Tyr Tyr Arg Arg Ser Phe Phe
            180                 185                 190

Val Ala Glu Pro Gly Pro Thr Ser Glu Gln Cys Ala Asp Asp Ala Gln
        195                 200                 205

Ala Ala Val Asp Arg Phe Ala Pro Tyr Phe Asp
    210                 215


<210> 2513
<211> 1281
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1258)
<223> RXA01968

<400> 2513
gaactggcgc tttttaagtt gtggcaattt tgccagaagg gcgtaacagg tgcgggtttt 60

tcgtggtagg cgcggagcag tagcaggatc ttttcttgca gtg ctg gca att ggt   115
                                              Val Leu Ala Ile Gly
                                                1               5

tca ctg gcg ctt acg ggt tgc aca att gaa cga agc gat gcg cag gag   163
Ser Leu Ala Leu Thr Gly Cys Thr Ile Glu Arg Ser Asp Ala Gln Glu
                10                  15                  20

caa tcc tcg cag caa agt aca gaa gtt gaa gct gaa gaa gct caa gct   211
Gln Ser Ser Gln Gln Ser Thr Glu Val Glu Ala Glu Glu Ala Gln Ala
            25                  30                  35

cct gtg att tct gtt gat gat ggt gat gag gat gtg gac cct tcg gaa   259
Pro Val Ile Ser Val Asp Asp Gly Asp Glu Asp Val Asp Pro Ser Glu
        40                  45                  50

tct gtc atc gta aag tcg atg ggt gac ggt ctg agc aag gtc acc atg   307
Ser Val Ile Val Lys Ser Met Gly Asp Gly Leu Ser Lys Val Thr Met
    55                  60                  65

act aat gaa gaa ggc tat gag gtt gag tca gag ctt tct gac gat ggc   355
Thr Asn Glu Glu Gly Tyr Glu Val Glu Ser Glu Leu Ser Asp Asp Gly
```

```
 70                  75                  80                  85

cgt agc tgg acc act gcg gaa acc ctt ggc tac aac cgc acg tac acc   403
Arg Ser Trp Thr Thr Ala Glu Thr Leu Gly Tyr Asn Arg Thr Tyr Thr
                 90                  95                 100

att aag gca acc gat aag aac ggc gag acc gct act gcg tct ttt agt   451
Ile Lys Ala Thr Asp Lys Asn Gly Glu Thr Ala Thr Ala Ser Phe Ser
            105                 110                 115

act gca acc cct gca gct acc aca aac gtg gcg ctt tct ccg ctg gct   499
Thr Ala Thr Pro Ala Ala Thr Thr Asn Val Ala Leu Ser Pro Leu Ala
        120                 125                 130

gat tct gtc gtt ggt gtt ggc cag act atc ggt ttc cgt ttt ggt tcc   547
Asp Ser Val Val Gly Val Gly Gln Thr Ile Gly Phe Arg Phe Gly Ser
    135                 140                 145

cct gtg aag gat cgc aag gcg gct cag gat gct att act gtg aca act   595
Pro Val Lys Asp Arg Lys Ala Ala Gln Asp Ala Ile Thr Val Thr Thr
150                 155                 160                 165

tca cca aag gtg gag ggt ggc ttt tac tgg ttg aac aac agt gag ttg   643
Ser Pro Lys Val Glu Gly Gly Phe Tyr Trp Leu Asn Asn Ser Glu Leu
                170                 175                 180

cgc tgg cgt cca gcg gag tac tgg gag cca ggt act gaa gtt acg gtc   691
Arg Trp Arg Pro Ala Glu Tyr Trp Glu Pro Gly Thr Glu Val Thr Val
            185                 190                 195

gag gct gac att tac ggc aag gat ctc ggc ggc ggt gtc tgg ggc gaa   739
Glu Ala Asp Ile Tyr Gly Lys Asp Leu Gly Gly Gly Val Trp Gly Glu
        200                 205                 210

act gat aac gcc acc aac ttc acc att ggt gac aag gtt gag gct gtg   787
Thr Asp Asn Ala Thr Asn Phe Thr Ile Gly Asp Lys Val Glu Ala Val
    215                 220                 225

gca gat gat gcc acc aag acc atg agt gtg tac aag aac ggt gag ttg   835
Ala Asp Asp Ala Thr Lys Thr Met Ser Val Tyr Lys Asn Gly Glu Leu
230                 235                 240                 245

ctg cgc act atg ccg gta tcc ttt ggt cgt gac acc tct gag tgg gca   883
Leu Arg Thr Met Pro Val Ser Phe Gly Arg Asp Thr Ser Glu Trp Ala
                250                 255                 260

acg cca aac ggt acc tac atc att ggt gat cgc aat gag tcg atg atc   931
Thr Pro Asn Gly Thr Tyr Ile Ile Gly Asp Arg Asn Glu Ser Met Ile
            265                 270                 275

atg gac tcc acc acc ttc ggt ctg gga tat gag gag ggt ggc tac cgc   979
Met Asp Ser Thr Thr Phe Gly Leu Gly Tyr Glu Glu Gly Gly Tyr Arg
        280                 285                 290

act ccg gtg aag tac gcg acc cag atg tcc tat tct gga att tac gtg   1027
Thr Pro Val Lys Tyr Ala Thr Gln Met Ser Tyr Ser Gly Ile Tyr Val
    295                 300                 305

cac gca gca ccg tgg tct gta ggt gcg caa ggt agc tac aac acc tca   1075
His Ala Ala Pro Trp Ser Val Gly Ala Gln Gly Ser Tyr Asn Thr Ser
310                 315                 320                 325
```

```
cat ggt tgc atc aat gta tcc acc gaa aat gct cag tgg ttc cag gag   1123
His Gly Cys Ile Asn Val Ser Thr Glu Asn Ala Gln Trp Phe Gln Glu
                330                 335                 340

gcc gtg aag cgc ggt gac att gtg acc gtg aaa aac acc atc ggt gag   1171
Ala Val Lys Arg Gly Asp Ile Val Thr Val Lys Asn Thr Ile Gly Glu
            345                 350                 355

act ttg agt ggc tac gac gga ctg ggg gac tgg aac att cca tgg tct   1219
Thr Leu Ser Gly Tyr Asp Gly Leu Gly Asp Trp Asn Ile Pro Trp Ser
        360                 365                 370

gaa tgg agc aag ggg aac gcg gat caa act tcg gcg tgg taactgcgga    1268
Glu Trp Ser Lys Gly Asn Ala Asp Gln Thr Ser Ala Trp
    375                 380                 385

agtcgcaggt aaa                                                   1281
```

<210> 2514
<211> 386
<212> PRT
<213> Corynebacterium glutamicum

<400> 2514

```
Val Leu Ala Ile Gly Ser Leu Ala Leu Thr Gly Cys Thr Ile Glu Arg
  1               5                  10                  15

Ser Asp Ala Gln Glu Gln Ser Ser Gln Gln Ser Thr Glu Val Glu Ala
             20                  25                  30

Glu Glu Ala Gln Ala Pro Val Ile Ser Val Asp Asp Gly Asp Glu Asp
         35                  40                  45

Val Asp Pro Ser Glu Ser Val Ile Val Lys Ser Met Gly Asp Gly Leu
     50                  55                  60

Ser Lys Val Thr Met Thr Asn Glu Glu Gly Tyr Glu Val Glu Ser Glu
 65                  70                  75                  80

Leu Ser Asp Asp Gly Arg Ser Trp Thr Thr Ala Glu Thr Leu Gly Tyr
                 85                  90                  95

Asn Arg Thr Tyr Thr Ile Lys Ala Thr Asp Lys Asn Gly Glu Thr Ala
            100                 105                 110

Thr Ala Ser Phe Ser Thr Ala Thr Pro Ala Ala Thr Thr Asn Val Ala
        115                 120                 125

Leu Ser Pro Leu Ala Asp Ser Val Val Gly Val Gly Gln Thr Ile Gly
    130                 135                 140

Phe Arg Phe Gly Ser Pro Val Lys Asp Arg Lys Ala Ala Gln Asp Ala
145                 150                 155                 160

Ile Thr Val Thr Thr Ser Pro Lys Val Glu Gly Gly Phe Tyr Trp Leu
                165                 170                 175

Asn Asn Ser Glu Leu Arg Trp Arg Pro Ala Glu Tyr Trp Glu Pro Gly
            180                 185                 190
```

```
Thr Glu Val Thr Val Glu Ala Asp Ile Tyr Gly Lys Asp Leu Gly Gly
        195                 200                 205

Gly Val Trp Gly Glu Thr Asp Asn Ala Thr Asn Phe Thr Ile Gly Asp
    210                 215                 220

Lys Val Glu Ala Val Ala Asp Asp Ala Thr Lys Thr Met Ser Val Tyr
225                 230                 235                 240

Lys Asn Gly Glu Leu Leu Arg Thr Met Pro Val Ser Phe Gly Arg Asp
                245                 250                 255

Thr Ser Glu Trp Ala Thr Pro Asn Gly Thr Tyr Ile Ile Gly Asp Arg
            260                 265                 270

Asn Glu Ser Met Ile Met Asp Ser Thr Thr Phe Gly Leu Gly Tyr Glu
        275                 280                 285

Glu Gly Gly Tyr Arg Thr Pro Val Lys Tyr Ala Thr Gln Met Ser Tyr
    290                 295                 300

Ser Gly Ile Tyr Val His Ala Ala Pro Trp Ser Val Gly Ala Gln Gly
305                 310                 315                 320

Ser Tyr Asn Thr Ser His Gly Cys Ile Asn Val Ser Thr Glu Asn Ala
                325                 330                 335

Gln Trp Phe Gln Glu Ala Val Lys Arg Gly Asp Ile Val Thr Val Lys
            340                 345                 350

Asn Thr Ile Gly Glu Thr Leu Ser Gly Tyr Asp Gly Leu Gly Asp Trp
        355                 360                 365

Asn Ile Pro Trp Ser Glu Trp Ser Lys Gly Asn Ala Asp Gln Thr Ser
    370                 375                 380

Ala Trp
385
```

<210> 2515
<211> 497
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(474)
<223> RXA01969

<400> 2515

```
aaa tgc cag cgt cgt ggt tta agc cag gat ccg ttg tat aaa aac cgg   48
Lys Cys Gln Arg Arg Gly Leu Ser Gln Asp Pro Leu Tyr Lys Asn Arg
  1               5                  10                  15

aat tcc ttg ttg acc acg cag aag tgg ttt agt cct cgt cag caa gaa   96
Asn Ser Leu Leu Thr Thr Gln Lys Trp Phe Ser Pro Arg Gln Gln Glu
             20                  25                  30

agc ttg gag cag ttg tgg gcg tat gac aaa gcc tac ggg gcg tta aag   144
```

```
Ser Leu Glu Gln Leu Trp Ala Tyr Asp Lys Ala Tyr Gly Ala Leu Lys
         35                  40                  45

ctt gcg tgg ctt gcg tat cag gcg att att gat tgt tat cag atg ggt   192
Leu Ala Trp Leu Ala Tyr Gln Ala Ile Ile Asp Cys Tyr Gln Met Gly
     50                  55                  60

aat aag cgt gaa gcg aag aag aaa atg cgg acc att att gat cag ctt   240
Asn Lys Arg Glu Ala Lys Lys Lys Met Arg Thr Ile Ile Asp Gln Leu
 65                  70                  75                  80

cgg gtg ttg aag ggg ccg aat aag gaa ctc gcg cag ttg ggt cgt agt   288
Arg Val Leu Lys Gly Pro Asn Lys Glu Leu Ala Gln Leu Gly Arg Ser
                 85                  90                  95

ttg ttt aaa cga ctt ggt gat gtg ttg gcg tat ttc gat gtt ggt gtc   336
Leu Phe Lys Arg Leu Gly Asp Val Leu Ala Tyr Phe Asp Val Gly Val
            100                 105                 110

tcc aac ggt ccg gtc gaa gcg atc aac gga cgg ttg gag cat ttg cgt   384
Ser Asn Gly Pro Val Glu Ala Ile Asn Gly Arg Leu Glu His Leu Arg
        115                 120                 125

ggg att gct cta ggt ttc cgt aat ttg aac cac tac att ctg cgg tgc   432
Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn His Tyr Ile Leu Arg Cys
    130                 135                 140

ctt atc cat tca ggg cag ttg gtc cat aag atc aat gca ctc           474
Leu Ile His Ser Gly Gln Leu Val His Lys Ile Asn Ala Leu
145                 150                 155

taaaacagga agagccactt aag                                        497


<210> 2516
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 2516
Lys Cys Gln Arg Arg Gly Leu Ser Gln Asp Pro Leu Tyr Lys Asn Arg
  1               5                  10                  15

Asn Ser Leu Leu Thr Thr Gln Lys Trp Phe Ser Pro Arg Gln Gln Glu
             20                  25                  30

Ser Leu Glu Gln Leu Trp Ala Tyr Asp Lys Ala Tyr Gly Ala Leu Lys
         35                  40                  45

Leu Ala Trp Leu Ala Tyr Gln Ala Ile Ile Asp Cys Tyr Gln Met Gly
     50                  55                  60

Asn Lys Arg Glu Ala Lys Lys Lys Met Arg Thr Ile Ile Asp Gln Leu
 65                  70                  75                  80

Arg Val Leu Lys Gly Pro Asn Lys Glu Leu Ala Gln Leu Gly Arg Ser
                 85                  90                  95

Leu Phe Lys Arg Leu Gly Asp Val Leu Ala Tyr Phe Asp Val Gly Val
            100                 105                 110
```

```
Ser Asn Gly Pro Val Glu Ala Ile Asn Gly Arg Leu Glu His Leu Arg
        115                 120                 125

Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn His Tyr Ile Leu Arg Cys
    130                 135                 140

Leu Ile His Ser Gly Gln Leu Val His Lys Ile Asn Ala Leu
145                 150                 155


<210> 2517
<211> 605
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(582)
<223> RXA01973

<400> 2517
tcc gcg atg tct aaa tcg cag gat gat cga aaa att gca gag ctt gaa   48
Ser Ala Met Ser Lys Ser Gln Asp Asp Arg Lys Ile Ala Glu Leu Glu
  1               5                  10                  15

gca cag ttt cat agt ctt ggt ctt aac aac act gaa cta gtt acc ctt   96
Ala Gln Phe His Ser Leu Gly Leu Asn Asn Thr Glu Leu Val Thr Leu
             20                  25                  30

gat gat gca gcg tcg cta ttg ggt gtg ccg gca ggt att cat cag att   144
Asp Asp Ala Ala Ser Leu Leu Gly Val Pro Ala Gly Ile His Gln Ile
         35                  40                  45

gag gcc gag gtg atg ttg gtg aat ttc ggt gat ggt gca gat ggc atg   192
Glu Ala Glu Val Met Leu Val Asn Phe Gly Asp Gly Ala Asp Gly Met
     50                  55                  60

ggc ggt gac acg acg aag ttt ttg cat tat cag cca gat gag tcg cag   240
Gly Gly Asp Thr Thr Lys Phe Leu His Tyr Gln Pro Asp Glu Ser Gln
 65                  70                  75                  80

cct tac gtc tgg gtg atg aag cgg gtg tat tcc ttt gag gcg atg aaa   288
Pro Tyr Val Trp Val Met Lys Arg Val Tyr Ser Phe Glu Ala Met Lys
                 85                  90                  95

aag ctc atg gtc ggg ttg ttt att ggc ttg tgc ata ctc atc gtg ggt   336
Lys Leu Met Val Gly Leu Phe Ile Gly Leu Cys Ile Leu Ile Val Gly
            100                 105                 110

ggg cca gct tta ggg ctt atg ctc ggt ggt ttt atc ggt gtg ctt att   384
Gly Pro Ala Leu Gly Leu Met Leu Gly Gly Phe Ile Gly Val Leu Ile
        115                 120                 125

ggt cta tgt cta ggt act tcc gca gcc atg att gtt ggc cct ttt ggg   432
Gly Leu Cys Leu Gly Thr Ser Ala Ala Met Ile Val Gly Pro Phe Gly
    130                 135                 140

ctt atg cgg atg aag gcg tat cca cca tgt atg gac agt cca tgg gtg   480
Leu Met Arg Met Lys Ala Tyr Pro Pro Cys Met Asp Ser Pro Trp Val
145                 150                 155                 160
```

```
tat atg tca caa gag cag tgg cgc acc gct atg ggt gcg gca cag cag   528
Tyr Met Ser Gln Glu Gln Trp Arg Thr Ala Met Gly Ala Ala Gln Gln
                165                 170                 175

acc gag gtg tct ttt gtt gag cac tgg gac aat att tac ggg gat aat   576
Thr Glu Val Ser Phe Val Glu His Trp Asp Asn Ile Tyr Gly Asp Asn
            180                 185                 190

ctg cat taacaaatta gttaataaag tgt                                 605
Leu His
```

<210> 2518
<211> 194
<212> PRT
<213> Corynebacterium glutamicum

<400> 2518

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Ser Ala Met Ser Lys Ser Gln Asp Asp Arg Lys Ile Ala Glu Leu Glu
  1               5                  10                  15

Ala Gln Phe His Ser Leu Gly Leu Asn Asn Thr Glu Leu Val Thr Leu
             20                  25                  30

Asp Asp Ala Ala Ser Leu Leu Gly Val Pro Ala Gly Ile His Gln Ile
         35                  40                  45

Glu Ala Glu Val Met Leu Val Asn Phe Gly Asp Gly Ala Asp Gly Met
     50                  55                  60

Gly Gly Asp Thr Thr Lys Phe Leu His Tyr Gln Pro Asp Glu Ser Gln
 65                  70                  75                  80

Pro Tyr Val Trp Val Met Lys Arg Val Tyr Ser Phe Glu Ala Met Lys
                 85                  90                  95

Lys Leu Met Val Gly Leu Phe Ile Gly Leu Cys Ile Leu Ile Val Gly
            100                 105                 110

Gly Pro Ala Leu Gly Leu Met Leu Gly Gly Phe Ile Gly Val Leu Ile
        115                 120                 125

Gly Leu Cys Leu Gly Thr Ser Ala Ala Met Ile Val Gly Pro Phe Gly
    130                 135                 140

Leu Met Arg Met Lys Ala Tyr Pro Pro Cys Met Asp Ser Pro Trp Val
145                 150                 155                 160

Tyr Met Ser Gln Glu Gln Trp Arg Thr Ala Met Gly Ala Ala Gln Gln
                165                 170                 175

Thr Glu Val Ser Phe Val Glu His Trp Asp Asn Ile Tyr Gly Asp Asn
            180                 185                 190

Leu His
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<210> 2519
<211> 1552

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1552)
<223> RXA01974

<400> 2519
acaatattta cggggataat ctgcattaac aaattagtta ataaagtgta gtatttaatt 60

aattattaaa ttcaattaac ttttttgtaa aggtgggaag atg acc cag gtt gtg 115
Met Thr Gln Val Val
1 5

gcg ggt acg ttg gtg gga gag tcg att aat cgt gag att gat gaa gac 163
Ala Gly Thr Leu Val Gly Glu Ser Ile Asn Arg Glu Ile Asp Glu Asp
10 15 20

aag tac cct tat ttg agc tcg tat gca gcg cct gtt gct gta ccg gtg 211
Lys Tyr Pro Tyr Leu Ser Ser Tyr Ala Ala Pro Val Ala Val Pro Val
25 30 35

cgt gag att att ggg cgc gaa gaa gaa gtc aat aag att atg gcc gcg 259
Arg Glu Ile Ile Gly Arg Glu Glu Glu Val Asn Lys Ile Met Ala Ala
40 45 50

ctg atg cgt cca gag att tct aat gtc atg ctt gtg ggt cct gct ggt 307
Leu Met Arg Pro Glu Ile Ser Asn Val Met Leu Val Gly Pro Ala Gly
55 60 65

tcg ggt aaa act acg ttg gta cag caa gca ctg gtg aaa gat cca gag 355
Ser Gly Lys Thr Thr Leu Val Gln Gln Ala Leu Val Lys Asp Pro Glu
70 75 80 85

cgt aac tac atc gag gtc gat gta gcg aaa atg gtt gcg gat ttg agc 403
Arg Asn Tyr Ile Glu Val Asp Val Ala Lys Met Val Ala Asp Leu Ser
90 95 100

acc ccg gcg caa atg gct gcg cgt att aaa ggt gtg ttt gag gac gcc 451
Thr Pro Ala Gln Met Ala Ala Arg Ile Lys Gly Val Phe Glu Asp Ala
105 110 115

att gcc tat cgc aag cac gaa ggt cat gaa ttg gtg ctg ttc gtt gat 499
Ile Ala Tyr Arg Lys His Glu Gly His Glu Leu Val Leu Phe Val Asp
120 125 130

gag ttt cac caa att gtg cag ctg tct aat gct gcg gta gag gca atc 547
Glu Phe His Gln Ile Val Gln Leu Ser Asn Ala Ala Val Glu Ala Ile
135 140 145

aag ccg att ttg gcg atg tct ggt gtc ctt ggt gtg cgc gtt atc gct 595
Lys Pro Ile Leu Ala Met Ser Gly Val Leu Gly Val Arg Val Ile Ala
150 155 160 165

gcg aca act ctc gaa gaa ttt cac gaa cac atc agg ccg aac caa gca 643
Ala Thr Thr Leu Glu Glu Phe His Glu His Ile Arg Pro Asn Gln Ala
170 175 180

ttg acg gag cgt ttg cag gaa att cga cta acg ccg acc gat cag aag 691
Leu Thr Glu Arg Leu Gln Glu Ile Arg Leu Thr Pro Thr Asp Gln Lys

```
            185                 190                 195

acc act gtg gcg att ttg cgt ggt atg gca gat cgt tat ggc gta agt   739
Thr Thr Val Ala Ile Leu Arg Gly Met Ala Asp Arg Tyr Gly Val Ser
        200                 205                 210

gat cag ttc tat gac gac cac gtt ttt gag cag att tac tcc acc act   787
Asp Gln Phe Tyr Asp Asp His Val Phe Glu Gln Ile Tyr Ser Thr Thr
    215                 220                 225

gag cgt ttt atg ccg agt tct gtc cag cct cgt aaa tcc att cgt gtc   835
Glu Arg Phe Met Pro Ser Ser Val Gln Pro Arg Lys Ser Ile Arg Val
230                 235                 240                 245

ctt gat gcg atg gtt ggt tgg cat cga ctt tcc ggc aag ccg atg gat   883
Leu Asp Ala Met Val Gly Trp His Arg Leu Ser Gly Lys Pro Met Asp
                250                 255                 260

atg gat ctg ctc ggt gat gtg ctc cac gat gct att ggt gtc gat att   931
Met Asp Leu Leu Gly Asp Val Leu His Asp Ala Ile Gly Val Asp Ile
            265                 270                 275

gca ttc aag gtc gat ggt acg agc att aaa gac aag ctt gat gag aag   979
Ala Phe Lys Val Asp Gly Thr Ser Ile Lys Asp Lys Leu Asp Glu Lys
        280                 285                 290

gta atg gcg caa agt ctt gcc acc act gtg gta gca cgt cgt ttg cag   1027
Val Met Ala Gln Ser Leu Ala Thr Thr Val Val Ala Arg Arg Leu Gln
    295                 300                 305

ctg gtg gtg gcg gat ctt cat gat aaa tca cgg cca ctg tcg aac ttc   1075
Leu Val Val Ala Asp Leu His Asp Lys Ser Arg Pro Leu Ser Asn Phe
310                 315                 320                 325

ttg ttc acc ggg cct act ggt gtc ggt aaa aca gag ctg gtc aag caa   1123
Leu Phe Thr Gly Pro Thr Gly Val Gly Lys Thr Glu Leu Val Lys Gln
                330                 335                 340

cta gca cgg gtg ctc ttt ggt gat gac act ggg cga ttg att cgt ttt   1171
Leu Ala Arg Val Leu Phe Gly Asp Asp Thr Gly Arg Leu Ile Arg Phe
            345                 350                 355

gac atg tca gag ttc gcc tta gaa tca agt ctt gac ctt ttc agg tct   1219
Asp Met Ser Glu Phe Ala Leu Glu Ser Ser Leu Asp Leu Phe Arg Ser
        360                 365                 370

gag ctc act cgt cgt gtc gct gac cag ggt aac gct att gtc ctg ctc   1267
Glu Leu Thr Arg Arg Val Ala Asp Gln Gly Asn Ala Ile Val Leu Leu
    375                 380                 385

gat gag gtt gag aaa gct gat cga gct att gcg cgg ttg tta ctg cag   1315
Asp Glu Val Glu Lys Ala Asp Arg Ala Ile Ala Arg Leu Leu Leu Gln
390                 395                 400                 405

gta ctt gat gat ggc cga cta tct gac gat tac aac cgt gag gtg agt   1363
Val Leu Asp Asp Gly Arg Leu Ser Asp Asp Tyr Asn Arg Glu Val Ser
                410                 415                 420

ttt ctt aat acc tat atc gtc atg aca act aac gct ggt tct gag att   1411
Phe Leu Asn Thr Tyr Ile Val Met Thr Thr Asn Ala Gly Ser Glu Ile
            425                 430                 435
```

```
ttc gag aca att tcg aac tat gcc act gat gac acg ggc gat ggt cgg   1459
Phe Glu Thr Ile Ser Asn Tyr Ala Thr Asp Asp Thr Gly Asp Gly Arg
        440                 445                 450

gcg atc aaa gac ttt gtg aaa aac att cac acg tcg atc aag aat aag   1507
Ala Ile Lys Asp Phe Val Lys Asn Ile His Thr Ser Ile Lys Asn Lys
    455                 460                 465

ggt ttt cca cct gag ctt ctt ggt cgt gta gat gaa att gtg cct       1552
Gly Phe Pro Pro Glu Leu Leu Gly Arg Val Asp Glu Ile Val Pro
470                 475                 480
```

<210> 2520
<211> 484
<212> PRT
<213> Corynebacterium glutamicum

<400> 2520

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Met Thr Gln Val Val Ala Gly Thr Leu Val Gly Glu Ser Ile Asn Arg
  1               5                  10                  15

Glu Ile Asp Glu Asp Lys Tyr Pro Tyr Leu Ser Ser Tyr Ala Ala Pro
             20                  25                  30

Val Ala Val Pro Val Arg Glu Ile Ile Gly Arg Glu Glu Glu Val Asn
         35                  40                  45

Lys Ile Met Ala Ala Leu Met Arg Pro Glu Ile Ser Asn Val Met Leu
     50                  55                  60

Val Gly Pro Ala Gly Ser Gly Lys Thr Thr Leu Val Gln Gln Ala Leu
 65                  70                  75                  80

Val Lys Asp Pro Glu Arg Asn Tyr Ile Glu Val Asp Val Ala Lys Met
                 85                  90                  95

Val Ala Asp Leu Ser Thr Pro Ala Gln Met Ala Ala Arg Ile Lys Gly
            100                 105                 110

Val Phe Glu Asp Ala Ile Ala Tyr Arg Lys His Glu Gly His Glu Leu
        115                 120                 125

Val Leu Phe Val Asp Glu Phe His Gln Ile Val Gln Leu Ser Asn Ala
    130                 135                 140

Ala Val Glu Ala Ile Lys Pro Ile Leu Ala Met Ser Gly Val Leu Gly
145                 150                 155                 160

Val Arg Val Ile Ala Ala Thr Thr Leu Glu Glu Phe His Glu His Ile
                165                 170                 175

Arg Pro Asn Gln Ala Leu Thr Glu Arg Leu Gln Glu Ile Arg Leu Thr
            180                 185                 190

Pro Thr Asp Gln Lys Thr Thr Val Ala Ile Leu Arg Gly Met Ala Asp
        195                 200                 205

Arg Tyr Gly Val Ser Asp Gln Phe Tyr Asp Asp His Val Phe Glu Gln
    210                 215                 220
```

```
Ile Tyr Ser Thr Thr Glu Arg Phe Met Pro Ser Ser Val Gln Pro Arg
225                 230                 235                 240

Lys Ser Ile Arg Val Leu Asp Ala Met Val Gly Trp His Arg Leu Ser
                245                 250                 255

Gly Lys Pro Met Asp Met Asp Leu Leu Gly Asp Val Leu His Asp Ala
            260                 265                 270

Ile Gly Val Asp Ile Ala Phe Lys Val Asp Gly Thr Ser Ile Lys Asp
        275                 280                 285

Lys Leu Asp Glu Lys Val Met Ala Gln Ser Leu Ala Thr Thr Val Val
    290                 295                 300

Ala Arg Arg Leu Gln Leu Val Val Ala Asp Leu His Asp Lys Ser Arg
305                 310                 315                 320

Pro Leu Ser Asn Phe Leu Phe Thr Gly Pro Thr Gly Val Gly Lys Thr
                325                 330                 335

Glu Leu Val Lys Gln Leu Ala Arg Val Leu Phe Gly Asp Asp Thr Gly
            340                 345                 350

Arg Leu Ile Arg Phe Asp Met Ser Glu Phe Ala Leu Glu Ser Ser Leu
        355                 360                 365

Asp Leu Phe Arg Ser Glu Leu Thr Arg Arg Val Ala Asp Gln Gly Asn
    370                 375                 380

Ala Ile Val Leu Leu Asp Glu Val Glu Lys Ala Asp Arg Ala Ile Ala
385                 390                 395                 400

Arg Leu Leu Leu Gln Val Leu Asp Asp Gly Arg Leu Ser Asp Asp Tyr
                405                 410                 415

Asn Arg Glu Val Ser Phe Leu Asn Thr Tyr Ile Val Met Thr Thr Asn
            420                 425                 430

Ala Gly Ser Glu Ile Phe Glu Thr Ile Ser Asn Tyr Ala Thr Asp Asp
        435                 440                 445

Thr Gly Asp Gly Arg Ala Ile Lys Asp Phe Val Lys Asn Ile His Thr
    450                 455                 460

Ser Ile Lys Asn Lys Gly Phe Pro Pro Glu Leu Leu Gly Arg Val Asp
465                 470                 475                 480

Glu Ile Val Pro
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<210> 2521
<211> 1644
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1621)

<223> RXA01976

<400> 2521

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gtgattccgg gcgtcttcgc ttagagtaaa ttaaaccgta aaaataaact caattaagtt 60

agtatattaa ttacttgatt taattgaagg ggtttatagt atg acg caa aca ctt   115
                                              Met Thr Gln Thr Leu
                                                1               5

gct ggc gag cgc aga atc gtc acc acg gca gag ctt aaa gcg atg ctg   163
Ala Gly Glu Arg Arg Ile Val Thr Thr Ala Glu Leu Lys Ala Met Leu
                10                  15                  20

gca cga ggg gat aag gtg ttt ctg cct ggt gtc gca gcg cgg gcg cca   211
Ala Arg Gly Asp Lys Val Phe Leu Pro Gly Val Ala Ala Arg Ala Pro
            25                  30                  35

gag atc ctc gac aac ttc gat cca gca gat cgg gca cgt ctc gac gtg   259
Glu Ile Leu Asp Asn Phe Asp Pro Ala Asp Arg Ala Arg Leu Asp Val
        40                  45                  50

ccc gca gca gac aat gaa atc gtc tct gta gaa ttc tcc cgc cgc gat   307
Pro Ala Ala Asp Asn Glu Ile Val Ser Val Glu Phe Ser Arg Arg Asp
    55                  60                  65

acc gtg caa tgc atc agc att gcc gac cgt gac cat ctc tac atc act   355
Thr Val Gln Cys Ile Ser Ile Ala Asp Arg Asp His Leu Tyr Ile Thr
70                  75                  80                  85

gac gat atg atc ccg acc cac aac acg tcc aac att atc ttc ttg aaa   403
Asp Asp Met Ile Pro Thr His Asn Thr Ser Asn Ile Ile Phe Leu Lys
                90                  95                 100

tcc aca gac gaa aca atg att aag acg ttg gtg gat tgg tca ggt gag   451
Ser Thr Asp Glu Thr Met Ile Lys Thr Leu Val Asp Trp Ser Gly Glu
            105                 110                 115

cga cat gtt gta cgc aga aat tca aag acc gta acc cgt gac ttg gca   499
Arg His Val Val Arg Arg Asn Ser Lys Thr Val Thr Arg Asp Leu Ala
        120                 125                 130

cag tta gtt atg cgc acc gag ggt aaa gtg tcg tac acg tct gca act   547
Gln Leu Val Met Arg Thr Glu Gly Lys Val Ser Tyr Thr Ser Ala Thr
    135                 140                 145

gaa aaa gag ccg gtg gtg tct tat aat gac cta aat act ctg cca tcg   595
Glu Lys Glu Pro Val Val Ser Tyr Asn Asp Leu Asn Thr Leu Pro Ser
150                 155                 160                 165

cag aac gcc atc gtc ttc cgt gcg ggt cag tat ccg gtg tgg tca cgc   643
Gln Asn Ala Ile Val Phe Arg Ala Gly Gln Tyr Pro Val Trp Ser Arg
                170                 175                 180

aat gaa acg att tgg ccg atg tcg ttc atg ttg ttt gct aac cag att   691
Asn Glu Thr Ile Trp Pro Met Ser Phe Met Leu Phe Ala Asn Gln Ile
            185                 190                 195

atc caa ccg ggt cgc gaa tac tcg ttg cag act att cca aca ctg tcg   739
Ile Gln Pro Gly Arg Glu Tyr Ser Leu Gln Thr Ile Pro Thr Leu Ser
        200                 205                 210
```

```
agc gct aat gaa ttc gat gtg aat caa aat gca ccg gac ttt atg gcg   787
Ser Ala Asn Glu Phe Asp Val Asn Gln Asn Ala Pro Asp Phe Met Ala
    215                 220                 225

atg ctg gaa aag cgc atg gcg cag tcg att cgt act cag cgt gcc gtc   835
Met Leu Glu Lys Arg Met Ala Gln Ser Ile Arg Thr Gln Arg Ala Val
230                 235                 240                 245

gat att tat aaa aag gcg act ggg ctc gat gac tct gat att gca cgc   883
Asp Ile Tyr Lys Lys Ala Thr Gly Leu Asp Asp Ser Asp Ile Ala Arg
                250                 255                 260

ctg gat atg gat gtg tat tca gca gaa atc atg gac atc gtg gac acg   931
Leu Asp Met Asp Val Tyr Ser Ala Glu Ile Met Asp Ile Val Asp Thr
            265                 270                 275

atg atc gcg aaa gat gag tac gat gac acg ccg gat tat gac gag ggg   979
Met Ile Ala Lys Asp Glu Tyr Asp Asp Thr Pro Asp Tyr Asp Glu Gly
        280                 285                 290

gat gag tct gtc atg aat gct cgt gat ttc atg gag tct gaa tat gac   1027
Asp Glu Ser Val Met Asn Ala Arg Asp Phe Met Glu Ser Glu Tyr Asp
    295                 300                 305

gtt ttt gat gat gag ttc gaa gac agt gct cag ggc ttc ccc gtg gct   1075
Val Phe Asp Asp Glu Phe Glu Asp Ser Ala Gln Gly Phe Pro Val Ala
310                 315                 320                 325

act ggt acg aag gtg aaa aag aaa tct ctg tct gaa gaa gca gag gtc   1123
Thr Gly Thr Lys Val Lys Lys Lys Ser Leu Ser Glu Glu Ala Glu Val
                330                 335                 340

aat gat gaa ttc att cac gat cag gag aat gca gaa cat aag ctc gct   1171
Asn Asp Glu Phe Ile His Asp Gln Glu Asn Ala Glu His Lys Leu Ala
            345                 350                 355

gac atg cgg ttg aag cgt tat gcc gaa ggc aag gtg tca cga gat atg   1219
Asp Met Arg Leu Lys Arg Tyr Ala Glu Gly Lys Val Ser Arg Asp Met
        360                 365                 370

ctg gct gat caa ttc ggc cac atc ctg cag gac tca ctc gaa gat gag   1267
Leu Ala Asp Gln Phe Gly His Ile Leu Gln Asp Ser Leu Glu Asp Glu
    375                 380                 385

ctc act gca gcc tat gat gag agc ctg cac gct ttt gct caa gat ccg   1315
Leu Thr Ala Ala Tyr Asp Glu Ser Leu His Ala Phe Ala Gln Asp Pro
390                 395                 400                 405

aat ttc cgg gtg act gct aac aac ggc ttg gtt aat gct gtc gat ggc   1363
Asn Phe Arg Val Thr Ala Asn Asn Gly Leu Val Asn Ala Val Asp Gly
                410                 415                 420

act gtg ttg att gag gcg ttg tcg cag gaa gat att gca ctt atg cgc   1411
Thr Val Leu Ile Glu Ala Leu Ser Gln Glu Asp Ile Ala Leu Met Arg
            425                 430                 435

gcg caa gca gga gtg gag cag tcg cgt gtc tac tct gag ggt gaa gaa   1459
Ala Gln Ala Gly Val Glu Gln Ser Arg Val Tyr Ser Glu Gly Glu Glu
        440                 445                 450

gct cta tct ggc aca gag gat gat ccg ctg tct gct atg ggt aaa tat   1507
```

```
Ala Leu Ser Gly Thr Glu Asp Asp Pro Leu Ser Ala Met Gly Lys Tyr
    455                 460                 465

aag acc acc cga gca ttc cgc atc atg ctg gtg gag ctt ccg cat tgg   1555
Lys Thr Thr Arg Ala Phe Arg Ile Met Leu Val Glu Leu Pro His Trp
470                 475                 480                 485

cgt gat ctc gcc cag ggt cac ttt gat aaa gaa gtc gcg cga gcc ttt   1603
Arg Asp Leu Ala Gln Gly His Phe Asp Lys Glu Val Ala Arg Ala Phe
                490                 495                 500

agg cgt att gaa gat gct taagtgtcgt gagcgataaa aaa                 1644
Arg Arg Ile Glu Asp Ala
            505


<210> 2522
<211> 507
<212> PRT
<213> Corynebacterium glutamicum

<400> 2522
Met Thr Gln Thr Leu Ala Gly Glu Arg Arg Ile Val Thr Thr Ala Glu
  1               5                  10                  15

Leu Lys Ala Met Leu Ala Arg Gly Asp Lys Val Phe Leu Pro Gly Val
             20                  25                  30

Ala Ala Arg Ala Pro Glu Ile Leu Asp Asn Phe Asp Pro Ala Asp Arg
         35                  40                  45

Ala Arg Leu Asp Val Pro Ala Ala Asp Asn Glu Ile Val Ser Val Glu
     50                  55                  60

Phe Ser Arg Arg Asp Thr Val Gln Cys Ile Ser Ile Ala Asp Arg Asp
 65                  70                  75                  80

His Leu Tyr Ile Thr Asp Asp Met Ile Pro Thr His Asn Thr Ser Asn
                 85                  90                  95

Ile Ile Phe Leu Lys Ser Thr Asp Glu Thr Met Ile Lys Thr Leu Val
            100                 105                 110

Asp Trp Ser Gly Glu Arg His Val Val Arg Arg Asn Ser Lys Thr Val
        115                 120                 125

Thr Arg Asp Leu Ala Gln Leu Val Met Arg Thr Glu Gly Lys Val Ser
    130                 135                 140

Tyr Thr Ser Ala Thr Glu Lys Glu Pro Val Val Ser Tyr Asn Asp Leu
145                 150                 155                 160

Asn Thr Leu Pro Ser Gln Asn Ala Ile Val Phe Arg Ala Gly Gln Tyr
                165                 170                 175

Pro Val Trp Ser Arg Asn Glu Thr Ile Trp Pro Met Ser Phe Met Leu
            180                 185                 190

Phe Ala Asn Gln Ile Ile Gln Pro Gly Arg Glu Tyr Ser Leu Gln Thr
        195                 200                 205
```

```
Ile Pro Thr Leu Ser Ser Ala Asn Glu Phe Asp Val Asn Gln Asn Ala
    210                 215                 220

Pro Asp Phe Met Ala Met Leu Glu Lys Arg Met Ala Gln Ser Ile Arg
225                 230                 235                 240

Thr Gln Arg Ala Val Asp Ile Tyr Lys Lys Ala Thr Gly Leu Asp Asp
                245                 250                 255

Ser Asp Ile Ala Arg Leu Asp Met Asp Val Tyr Ser Ala Glu Ile Met
            260                 265                 270

Asp Ile Val Asp Thr Met Ile Ala Lys Asp Glu Tyr Asp Asp Thr Pro
        275                 280                 285

Asp Tyr Asp Glu Gly Asp Glu Ser Val Met Asn Ala Arg Asp Phe Met
    290                 295                 300

Glu Ser Glu Tyr Asp Val Phe Asp Asp Glu Phe Glu Asp Ser Ala Gln
305                 310                 315                 320

Gly Phe Pro Val Ala Thr Gly Thr Lys Val Lys Lys Lys Ser Leu Ser
                325                 330                 335

Glu Glu Ala Glu Val Asn Asp Glu Phe Ile His Asp Gln Glu Asn Ala
            340                 345                 350

Glu His Lys Leu Ala Asp Met Arg Leu Lys Arg Tyr Ala Glu Gly Lys
        355                 360                 365

Val Ser Arg Asp Met Leu Ala Asp Gln Phe Gly His Ile Leu Gln Asp
    370                 375                 380

Ser Leu Glu Asp Glu Leu Thr Ala Ala Tyr Asp Glu Ser Leu His Ala
385                 390                 395                 400

Phe Ala Gln Asp Pro Asn Phe Arg Val Thr Ala Asn Asn Gly Leu Val
                405                 410                 415

Asn Ala Val Asp Gly Thr Val Leu Ile Glu Ala Leu Ser Gln Glu Asp
            420                 425                 430

Ile Ala Leu Met Arg Ala Gln Ala Gly Val Glu Gln Ser Arg Val Tyr
        435                 440                 445

Ser Glu Gly Glu Glu Ala Leu Ser Gly Thr Glu Asp Asp Pro Leu Ser
    450                 455                 460

Ala Met Gly Lys Tyr Lys Thr Thr Arg Ala Phe Arg Ile Met Leu Val
465                 470                 475                 480

Glu Leu Pro His Trp Arg Asp Leu Ala Gln Gly His Phe Asp Lys Glu
                485                 490                 495

Val Ala Arg Ala Phe Arg Arg Ile Glu Asp Ala
            500                 505
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<210> 2523
<211> 699
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(676)
<223> RXA01977

<400> 2523
aagtccagtg actaatacca atagaattga agaccactac ctcaagggcg gacgtggcag 60

gggcacagac gatcctagca atatgcaaat tgcaggaagt atg ttg cgc aca tta 115
Met Leu Arg Thr Leu
1 5

ttc gtc cgc aag att aga gcg ctg ctg ctg gtt ttg atg att gcg cca 163
Phe Val Arg Lys Ile Arg Ala Leu Leu Leu Val Leu Met Ile Ala Pro
10 15 20

act cca ttg gtc gaa ggg cta act tcg act gca atg att gta tcc gta 211
Thr Pro Leu Val Glu Gly Leu Thr Ser Thr Ala Met Ile Val Ser Val
25 30 35

gta atc ctg gcg atc tac atg gcg ata aca atg tat aga gta gtg cac 259
Val Ile Leu Ala Ile Tyr Met Ala Ile Thr Met Tyr Arg Val Val His
40 45 50

ggt cgc cat gag ttc gcg cat atc gca cgt cgc atg gcg ctt tac gtc 307
Gly Arg His Glu Phe Ala His Ile Ala Arg Arg Met Ala Leu Tyr Val
55 60 65

aac aag act tct tct agg ttc agt gtt gtt att gct tat gta gta tta 355
Asn Lys Thr Ser Ser Arg Phe Ser Val Val Ile Ala Tyr Val Val Leu
70 75 80 85

att gct att tat gcg cta cta att ccc gga ctt gtc tac tct gtt aca 403
Ile Ala Ile Tyr Ala Leu Leu Ile Pro Gly Leu Val Tyr Ser Val Thr
90 95 100

ttt gga ttc atc gtc cca agc aca cct aat acg ttt agt gat gca cct 451
Phe Gly Phe Ile Val Pro Ser Thr Pro Asn Thr Phe Ser Asp Ala Pro
105 110 115

gca tgg att atg tgc gta tcg ctg ctg ctc att gca gtc gcc agt ttc 499
Ala Trp Ile Met Cys Val Ser Leu Leu Leu Ile Ala Val Ala Ser Phe
120 125 130

atc aca tca atc atg gat gac ttt att gat ggc ata ctc act gat ttt 547
Ile Thr Ser Ile Met Asp Asp Phe Ile Asp Gly Ile Leu Thr Asp Phe
135 140 145

tat gac gaa gat aat gct gat agc ccc gat agt cct gcc gag gat ata 595
Tyr Asp Glu Asp Asn Ala Asp Ser Pro Asp Ser Pro Ala Glu Asp Ile
150 155 160 165

gcc acc cgt cct gtc gag agc gca aca aca agt gct ctt gct gga ttt 643
Ala Thr Arg Pro Val Glu Ser Ala Thr Thr Ser Ala Leu Ala Gly Phe
170 175 180

gct gtt ggt tat att tgt ggg cgc ttt aat cgc taacacttaa aacacttctc 696
Ala Val Gly Tyr Ile Cys Gly Arg Phe Asn Arg
185 190

aac 699

<210> 2524
<211> 192
<212> PRT
<213> Corynebacterium glutamicum

<400> 2524
Met Leu Arg Thr Leu Phe Val Arg Lys Ile Arg Ala Leu Leu Leu Val
1 5 10 15

Leu Met Ile Ala Pro Thr Pro Leu Val Glu Gly Leu Thr Ser Thr Ala
20 25 30

Met Ile Val Ser Val Val Ile Leu Ala Ile Tyr Met Ala Ile Thr Met
35 40 45

Tyr Arg Val Val His Gly Arg His Glu Phe Ala His Ile Ala Arg Arg
50 55 60

Met Ala Leu Tyr Val Asn Lys Thr Ser Ser Arg Phe Ser Val Val Ile
65 70 75 80

Ala Tyr Val Val Leu Ile Ala Ile Tyr Ala Leu Leu Ile Pro Gly Leu
85 90 95

Val Tyr Ser Val Thr Phe Gly Phe Ile Val Pro Ser Thr Pro Asn Thr
100 105 110

Phe Ser Asp Ala Pro Ala Trp Ile Met Cys Val Ser Leu Leu Leu Ile
115 120 125

Ala Val Ala Ser Phe Ile Thr Ser Ile Met Asp Asp Phe Ile Asp Gly
130 135 140

Ile Leu Thr Asp Phe Tyr Asp Glu Asp Asn Ala Asp Ser Pro Asp Ser
145 150 155 160

Pro Ala Glu Asp Ile Ala Thr Arg Pro Val Glu Ser Ala Thr Thr Ser
165 170 175

Ala Leu Ala Gly Phe Ala Val Gly Tyr Ile Cys Gly Arg Phe Asn Arg
180 185 190

<210> 2525
<211> 1281
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1258)
<223> RXA01982

<400> 2525

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tgccgccgac catgagatga tcaagcgctt tttcaccctg caccttcgct aagactctac 60

cttcacccaa ctcatcatct actgaaagaa ggcttctgct atg gct acc acc agc   115
                                            Met Ala Thr Thr Ser
                                              1               5

ctc ccc acg acg att aca ccg gat tcc gag gag acc gta gaa aag cgt   163
Leu Pro Thr Thr Ile Thr Pro Asp Ser Glu Glu Thr Val Glu Lys Arg
                 10                  15                  20

cac tcc ctg acc ccg atc ctg gat tca ctt ccc tgc gag tca gtt ccc   211
His Ser Leu Thr Pro Ile Leu Asp Ser Leu Pro Cys Glu Ser Val Pro
             25                  30                  35

tat gct ctg gct gca ggt gag gga caa caa cac cag ctt ggc ccc tac   259
Tyr Ala Leu Ala Ala Gly Glu Gly Gln Gln His Gln Leu Gly Pro Tyr
         40                  45                  50

cat ctc aca gtt atg tcc cgt ccc gaa gac aac ggt gga ata ttt tcg   307
His Leu Thr Val Met Ser Arg Pro Glu Asp Asn Gly Gly Ile Phe Ser
     55                  60                  65

ctg gct cgt gtg agc gca ggc aag act ccc gcc acc cgg ttc ttc tct   355
Leu Ala Arg Val Ser Ala Gly Lys Thr Pro Ala Thr Arg Phe Phe Ser
 70                  75                  80                  85

gtc gca gga ccg acg ttc ctc tac atg atg gag ggg cgg ttg act ctc   403
Val Ala Gly Pro Thr Phe Leu Tyr Met Met Glu Gly Arg Leu Thr Leu
                 90                  95                 100

tgg ttc gct gat gga cgt caa gag atc atc gct ggc ggc agt gcc acc   451
Trp Phe Ala Asp Gly Arg Gln Glu Ile Ile Ala Gly Gly Ser Ala Thr
             105                 110                 115

att cct acg aat acg ccc tgg tcc ttc gcc tgt gag ggc cta gta aat   499
Ile Pro Thr Asn Thr Pro Trp Ser Phe Ala Cys Glu Gly Leu Val Asn
         120                 125                 130

tca gct cta gtg tac tac tca tcc tcg aat gca ttc cta cac gcg gca   547
Ser Ala Leu Val Tyr Tyr Ser Ser Ser Asn Ala Phe Leu His Ala Ala
     135                 140                 145

gag aaa ctt ggc acg tcc tcg ttc tcc cac acc ttc cgc gtc agt ggc   595
Glu Lys Leu Gly Thr Ser Ser Phe Ser His Thr Phe Arg Val Ser Gly
150                 155                 160                 165

gag gtc aca ggg att ccc tac gag gaa ctg gag gat tgc gga ttc aca   643
Glu Val Thr Gly Ile Pro Tyr Glu Glu Leu Glu Asp Cys Gly Phe Thr
                 170                 175                 180

ttc tat gag cgg gac cac ctt gcc gag ctc ggg ccg cat ttc gat cgc   691
Phe Tyr Glu Arg Asp His Leu Ala Glu Leu Gly Pro His Phe Asp Arg
             185                 190                 195

ctc cca gaa gat atg aag gcg ttt gcc ctg aac gat ggt gag ggg gac   739
Leu Pro Glu Asp Met Lys Ala Phe Ala Leu Asn Asp Gly Glu Gly Asp
         200                 205                 210

cgg ctt gag cag ttc gag cag atc aac agc ttc gtc tgc cgt ccg aga   787
Arg Leu Glu Gln Phe Glu Gln Ile Asn Ser Phe Val Cys Arg Pro Arg
     215                 220                 225
```

```
cac acc gga aat cag ttc ctc gct atg cag acc aag ggt gcc aag acg   835
His Thr Gly Asn Gln Phe Leu Ala Met Gln Thr Lys Gly Ala Lys Thr
230                 235                 240                 245

cct tat ata cct cgt cat ttc cac cgc ctt cac acc gaa aac ttc atc   883
Pro Tyr Ile Pro Arg His Phe His Arg Leu His Thr Glu Asn Phe Ile
                250                 255                 260

tgt ctg gac ggg cgc gtc aaa ctg cac gtc aac ggt caa gag atc atc   931
Cys Leu Asp Gly Arg Val Lys Leu His Val Asn Gly Gln Glu Ile Ile
            265                 270                 275

ctc tcc cgt ggg gat tac gtt cat gcc cca gcc gga acc atc cac tct   979
Leu Ser Arg Gly Asp Tyr Val His Ala Pro Ala Gly Thr Ile His Ser
        280                 285                 290

ttc gcc ttc gca ggg cac aat acc cag atg ctg gga gtg ctc acc aca   1027
Phe Ala Phe Ala Gly His Asn Thr Gln Met Leu Gly Val Leu Thr Thr
    295                 300                 305

gag gta ttc gag aag ttc ttt gac tac ata aac act ccg act aat gct   1075
Glu Val Phe Glu Lys Phe Phe Asp Tyr Ile Asn Thr Pro Thr Asn Ala
310                 315                 320                 325

cga gtt cag ctg gag gac ggg ggg aag cca ttt ttt cct gct gaa gca   1123
Arg Val Gln Leu Glu Asp Gly Gly Lys Pro Phe Phe Pro Ala Glu Ala
                330                 335                 340

ttc gcg aaa gtc caa gct gaa ctc gat gtc gtg gtg gtc ggc ccc cca   1171
Phe Ala Lys Val Gln Ala Glu Leu Asp Val Val Val Val Gly Pro Pro
            345                 350                 355

cga att agt acc ctg gat gtt gtt aca aac tcg cgt ttc gaa cca att   1219
Arg Ile Ser Thr Leu Asp Val Val Thr Asn Ser Arg Phe Glu Pro Ile
        360                 365                 370

aac aga act atc acc tat cgt gcg ctg gac gct aac caa tagtgagtga   1268
Asn Arg Thr Ile Thr Tyr Arg Ala Leu Asp Ala Asn Gln
    375                 380                 385

gccgaaatcc ctg                                                  1281
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<210> 2526
<211> 386
<212> PRT
<213> Corynebacterium glutamicum

<400> 2526

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Met Ala Thr Thr Ser Leu Pro Thr Thr Ile Thr Pro Asp Ser Glu Glu
  1               5                  10                  15

Thr Val Glu Lys Arg His Ser Leu Thr Pro Ile Leu Asp Ser Leu Pro
             20                  25                  30

Cys Glu Ser Val Pro Tyr Ala Leu Ala Ala Gly Glu Gly Gln Gln His
         35                  40                  45

Gln Leu Gly Pro Tyr His Leu Thr Val Met Ser Arg Pro Glu Asp Asn
     50                  55                  60
```

```
Gly Gly Ile Phe Ser Leu Ala Arg Val Ser Ala Gly Lys Thr Pro Ala
 65                  70                  75                  80

Thr Arg Phe Phe Ser Val Ala Gly Pro Thr Phe Leu Tyr Met Met Glu
                85                  90                  95

Gly Arg Leu Thr Leu Trp Phe Ala Asp Gly Arg Gln Glu Ile Ile Ala
            100                 105                 110

Gly Gly Ser Ala Thr Ile Pro Thr Asn Thr Pro Trp Ser Phe Ala Cys
        115                 120                 125

Glu Gly Leu Val Asn Ser Ala Leu Val Tyr Tyr Ser Ser Ser Asn Ala
    130                 135                 140

Phe Leu His Ala Ala Glu Lys Leu Gly Thr Ser Ser Phe Ser His Thr
145                 150                 155                 160

Phe Arg Val Ser Gly Glu Val Thr Gly Ile Pro Tyr Glu Glu Leu Glu
                165                 170                 175

Asp Cys Gly Phe Thr Phe Tyr Glu Arg Asp His Leu Ala Glu Leu Gly
            180                 185                 190

Pro His Phe Asp Arg Leu Pro Glu Asp Met Lys Ala Phe Ala Leu Asn
        195                 200                 205

Asp Gly Glu Gly Asp Arg Leu Glu Gln Phe Glu Gln Ile Asn Ser Phe
    210                 215                 220

Val Cys Arg Pro Arg His Thr Gly Asn Gln Phe Leu Ala Met Gln Thr
225                 230                 235                 240

Lys Gly Ala Lys Thr Pro Tyr Ile Pro Arg His Phe His Arg Leu His
                245                 250                 255

Thr Glu Asn Phe Ile Cys Leu Asp Gly Arg Val Lys Leu His Val Asn
            260                 265                 270

Gly Gln Glu Ile Ile Leu Ser Arg Gly Asp Tyr Val His Ala Pro Ala
        275                 280                 285

Gly Thr Ile His Ser Phe Ala Phe Ala Gly His Asn Thr Gln Met Leu
    290                 295                 300

Gly Val Leu Thr Thr Glu Val Phe Glu Lys Phe Phe Asp Tyr Ile Asn
305                 310                 315                 320

Thr Pro Thr Asn Ala Arg Val Gln Leu Glu Asp Gly Gly Lys Pro Phe
                325                 330                 335

Phe Pro Ala Glu Ala Phe Ala Lys Val Gln Ala Glu Leu Asp Val Val
            340                 345                 350

Val Val Gly Pro Pro Arg Ile Ser Thr Leu Asp Val Val Thr Asn Ser
        355                 360                 365

Arg Phe Glu Pro Ile Asn Arg Thr Ile Thr Tyr Arg Ala Leu Asp Ala
    370                 375                 380
```

Asn Gln
385

<210> 2527
<211> 1022
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(999)
<223> RXA01990

<400> 2527

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aca tct gat cat gtg gca cag ttt ggt atg gca act gcg tct gct gcg   48
Thr Ser Asp His Val Ala Gln Phe Gly Met Ala Thr Ala Ser Ala Ala
  1               5                  10                  15

acg ttg ccg gac agt att gtg acc agt gtt tct tat acg ttg aac ggg   96
Thr Leu Pro Asp Ser Ile Val Thr Ser Val Ser Tyr Thr Leu Asn Gly
             20                  25                  30

ctg tca ttt tct gac ccg gtt gag ctg ggt atc agt gac aac gac aag   144
Leu Ser Phe Ser Asp Pro Val Glu Leu Gly Ile Ser Asp Asn Asp Lys
         35                  40                  45

cgt gaa gag ctt cta gga gac atc acc aag ggt gaa ctg cga ttg cag   192
Arg Glu Glu Leu Leu Gly Asp Ile Thr Lys Gly Glu Leu Arg Leu Gln
     50                  55                  60

atg gag ttt tcg atc ccg gat tca gca act gcc gag gat gag tac gtc   240
Met Glu Phe Ser Ile Pro Asp Ser Ala Thr Ala Glu Asp Glu Tyr Val
 65                  70                  75                  80

ttt aat ctc acc ggc gat gga ctt cgg ttt ttc aat tca aac gat cgc   288
Phe Asn Leu Thr Gly Asp Gly Leu Arg Phe Phe Asn Ser Asn Asp Arg
                 85                  90                  95

acc gtc cct gta cgc aat gat gca ggt att cgt gtc gca gat ctt ttg   336
Thr Val Pro Val Arg Asn Asp Ala Gly Ile Arg Val Ala Asp Leu Leu
            100                 105                 110

gtg agc aac ggt ggt acg cgc ggt acg ttg aca aac ttt agt tcg gat   384
Val Ser Asn Gly Gly Thr Arg Gly Thr Leu Thr Asn Phe Ser Ser Asp
        115                 120                 125

gct ggc act act tct cgc acc gca gct ctt gat atg gaa ctg tac ggg   432
Ala Gly Thr Thr Ser Arg Thr Ala Ala Leu Asp Met Glu Leu Tyr Gly
    130                 135                 140

tgg gtg agt agc gcc cag cag acg ggt gag cga cca att caa gac tgg   480
Trp Val Ser Ser Ala Gln Gln Thr Gly Glu Arg Pro Ile Gln Asp Trp
145                 150                 155                 160

act gtg ggt aag act gag ggt cag gtt gag aac aag gta gtc cgc tac   528
Thr Val Gly Lys Thr Glu Gly Gln Val Glu Asn Lys Val Val Arg Tyr
                165                 170                 175

ggc gtt gct gga cac ccg tgg att atc agt act gtc cag cac acg tgg   576
Gly Val Ala Gly His Pro Trp Ile Ile Ser Thr Val Gln His Thr Trp
```

```
            180                 185                 190

gtt aag tct acg cag acc gtg tcg cat ttc cga agt gaa caa gac tgg   624
Val Lys Ser Thr Gln Thr Val Ser His Phe Arg Ser Glu Gln Asp Trp
        195                 200                 205

aag att aat caa cca cca gct gtt gat atg ggc gca tta gca tac gca   672
Lys Ile Asn Gln Pro Pro Ala Val Asp Met Gly Ala Leu Ala Tyr Ala
    210                 215                 220

gct cca ctt ggc gtc gtg gtc ggg cac gcc aat gtt gtc att agc aat   720
Ala Pro Leu Gly Val Val Val Gly His Ala Asn Val Val Ile Ser Asn
225                 230                 235                 240

aac aac ggt gct gga ttc cgg ggt gcg ctt gtc aat acc aca ccc acc   768
Asn Asn Gly Ala Gly Phe Arg Gly Ala Leu Val Asn Thr Thr Pro Thr
                245                 250                 255

aca cgc gac gtg ata ctt aat ttc aca gcc gca gac gga gcc act tta   816
Thr Arg Asp Val Ile Leu Asn Phe Thr Ala Ala Asp Gly Ala Thr Leu
            260                 265                 270

cgc gaa cgt tcc gga ggt gga ttt gag gat ttc gac gtt ttc tcg gaa   864
Arg Glu Arg Ser Gly Gly Gly Phe Glu Asp Phe Asp Val Phe Ser Glu
        275                 280                 285

gtt cct cgg gta gag gaa aca tcg acg agg atc agc tat tct tac aaa   912
Val Pro Arg Val Glu Glu Thr Ser Thr Arg Ile Ser Tyr Ser Tyr Lys
    290                 295                 300

aat tca ttt gaa tat gac gaa ttt gtt gcc gca ttt ccc gag tac cga   960
Asn Ser Phe Glu Tyr Asp Glu Phe Val Ala Ala Phe Pro Glu Tyr Arg
305                 310                 315                 320

cgt agc tgc gtg gga acc aac cgt tgt gta ttc agc gga taagaccaca   1009
Arg Ser Cys Val Gly Thr Asn Arg Cys Val Phe Ser Gly
                325                 330

gcaacagcga cgt                                                  1022
```

<210> 2528
<211> 333
<212> PRT
<213> Corynebacterium glutamicum

<400> 2528

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Thr Ser Asp His Val Ala Gln Phe Gly Met Ala Thr Ala Ser Ala Ala
  1               5                  10                  15

Thr Leu Pro Asp Ser Ile Val Thr Ser Val Ser Tyr Thr Leu Asn Gly
            20                  25                  30

Leu Ser Phe Ser Asp Pro Val Glu Leu Gly Ile Ser Asp Asn Asp Lys
        35                  40                  45

Arg Glu Glu Leu Leu Gly Asp Ile Thr Lys Gly Glu Leu Arg Leu Gln
    50                  55                  60

Met Glu Phe Ser Ile Pro Asp Ser Ala Thr Ala Glu Asp Glu Tyr Val
65                  70                  75                  80
```

```
Phe Asn Leu Thr Gly Asp Gly Leu Arg Phe Phe Asn Ser Asn Asp Arg
                 85                  90                  95

Thr Val Pro Val Arg Asn Asp Ala Gly Ile Arg Val Ala Asp Leu Leu
            100                 105                 110

Val Ser Asn Gly Gly Thr Arg Gly Thr Leu Thr Asn Phe Ser Ser Asp
        115                 120                 125

Ala Gly Thr Thr Ser Arg Thr Ala Ala Leu Asp Met Glu Leu Tyr Gly
    130                 135                 140

Trp Val Ser Ser Ala Gln Gln Thr Gly Glu Arg Pro Ile Gln Asp Trp
145                 150                 155                 160

Thr Val Gly Lys Thr Glu Gly Gln Val Glu Asn Lys Val Val Arg Tyr
                165                 170                 175

Gly Val Ala Gly His Pro Trp Ile Ile Ser Thr Val Gln His Thr Trp
            180                 185                 190

Val Lys Ser Thr Gln Thr Val Ser His Phe Arg Ser Glu Gln Asp Trp
        195                 200                 205

Lys Ile Asn Gln Pro Pro Ala Val Asp Met Gly Ala Leu Ala Tyr Ala
    210                 215                 220

Ala Pro Leu Gly Val Val Val Gly His Ala Asn Val Val Ile Ser Asn
225                 230                 235                 240

Asn Asn Gly Ala Gly Phe Arg Gly Ala Leu Val Asn Thr Thr Pro Thr
                245                 250                 255

Thr Arg Asp Val Ile Leu Asn Phe Thr Ala Ala Asp Gly Ala Thr Leu
            260                 265                 270

Arg Glu Arg Ser Gly Gly Gly Phe Glu Asp Phe Asp Val Phe Ser Glu
        275                 280                 285

Val Pro Arg Val Glu Glu Thr Ser Thr Arg Ile Ser Tyr Ser Tyr Lys
    290                 295                 300

Asn Ser Phe Glu Tyr Asp Glu Phe Val Ala Ala Phe Pro Glu Tyr Arg
305                 310                 315                 320

Arg Ser Cys Val Gly Thr Asn Arg Cys Val Phe Ser Gly
                325                 330
```

<210> 2529
<211> 573
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(550)
<223> RXA01992

<400> 2529

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atagatcaat gctggcataa actaaaggca caacagccga ttcacttatt tttaggcgaa 60

tgcttgaagt cgaagtaagt gaggggggaga ggatccgtta gtg tac tgc cca ttt   115
                                            Val Tyr Cys Pro Phe
                                              1               5

tgc caa cat gat cat tca aaa gtc att gac tcc cgc gtc att gac gcc   163
Cys Gln His Asp His Ser Lys Val Ile Asp Ser Arg Val Ile Asp Ala
                 10                  15                  20

gga agc gcc att cgc agg cgc cgc gag tgc agc aaa tgc gaa ggc cgt   211
Gly Ser Ala Ile Arg Arg Arg Arg Glu Cys Ser Lys Cys Glu Gly Arg
             25                  30                  35

ttc acc acc atc gaa aaa gct gtt ctc ctc gtt gtt aaa aga aac ggc   259
Phe Thr Thr Ile Glu Lys Ala Val Leu Leu Val Val Lys Arg Asn Gly
         40                  45                  50

gtc act gaa ccg ttc agt cga gaa aaa gta gtc acc ggt gtc cgt cgt   307
Val Thr Glu Pro Phe Ser Arg Glu Lys Val Val Thr Gly Val Arg Arg
     55                  60                  65

gca tgc caa ggc cgc gac gta tca gat gac gcg ttg aaa cgc cta gct   355
Ala Cys Gln Gly Arg Asp Val Ser Asp Asp Ala Leu Lys Arg Leu Ala
 70                  75                  80                  85

cag caa gtg gaa gaa aca gtc cgc agc aac gga agc tct caa gta cgc   403
Gln Gln Val Glu Glu Thr Val Arg Ser Asn Gly Ser Ser Gln Val Arg
                 90                  95                 100

gct aac gat att ggt tta gcc att ctc gat cca ctg aga gaa ctc gac   451
Ala Asn Asp Ile Gly Leu Ala Ile Leu Asp Pro Leu Arg Glu Leu Asp
             105                 110                 115

gag gta gcg tac cta cgc ttt gcc tct gtg tat aag tct ttt gac agt   499
Glu Val Ala Tyr Leu Arg Phe Ala Ser Val Tyr Lys Ser Phe Asp Ser
         120                 125                 130

gct gac gac ttt gaa aaa gaa atc cgc ctc atg cgc aga cgc gga agg   547
Ala Asp Asp Phe Glu Lys Glu Ile Arg Leu Met Arg Arg Arg Gly Arg
     135                 140                 145

gac tagcagacac aaagtcttaa cta                                    573
Asp
150
```

<210> 2530
<211> 150
<212> PRT
<213> Corynebacterium glutamicum

<400> 2530

```
Val Tyr Cys Pro Phe Cys Gln His Asp His Ser Lys Val Ile Asp Ser
  1               5                  10                  15

Arg Val Ile Asp Ala Gly Ser Ala Ile Arg Arg Arg Arg Glu Cys Ser
             20                  25                  30

Lys Cys Glu Gly Arg Phe Thr Thr Ile Glu Lys Ala Val Leu Leu Val
         35                  40                  45
```

```
Val Lys Arg Asn Gly Val Thr Glu Pro Phe Ser Arg Glu Lys Val Val
     50                  55                  60

Thr Gly Val Arg Arg Ala Cys Gln Gly Arg Asp Val Ser Asp Asp Ala
 65                  70                  75                  80

Leu Lys Arg Leu Ala Gln Gln Val Glu Glu Thr Val Arg Ser Asn Gly
                 85                  90                  95

Ser Ser Gln Val Arg Ala Asn Asp Ile Gly Leu Ala Ile Leu Asp Pro
            100                 105                 110

Leu Arg Glu Leu Asp Glu Val Ala Tyr Leu Arg Phe Ala Ser Val Tyr
        115                 120                 125

Lys Ser Phe Asp Ser Ala Asp Asp Phe Glu Lys Glu Ile Arg Leu Met
    130                 135                 140

Arg Arg Arg Gly Arg Asp
145                 150
```

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<210> 2531
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(571)
<223> RXA01999

<400> 2531
gggtatgtag ttagagacga cagacacaga aatcttcagc ctcgcgaacc gagtgatagc 60

atacttgacc atatcgaatt ctctaccagc tcgaggcatc atg act ctc ccc acc   115
                                              Met Thr Leu Pro Thr
                                                1               5

cct aca cat tcc acc aaa ggc agt tca ggc cgc atg aaa cga atg gcc   163
Pro Thr His Ser Thr Lys Gly Ser Ser Gly Arg Met Lys Arg Met Ala
                10                  15                  20

ctt atc ggc tcc tcg ctc att att tcc atg gga ctt att act gcg tgc   211
Leu Ile Gly Ser Ser Leu Ile Ile Ser Met Gly Leu Ile Thr Ala Cys
            25                  30                  35

ggt tcg gcc gct gca gaa ccc gaa gcc cct gca cca aca gtt acc gaa   259
Gly Ser Ala Ala Ala Glu Pro Glu Ala Pro Ala Pro Thr Val Thr Glu
        40                  45                  50

act gta aca gcc acg gtg aca acc aca gct aaa gcc agc acg atc acc   307
Thr Val Thr Ala Thr Val Thr Thr Thr Ala Lys Ala Ser Thr Ile Thr
    55                  60                  65

tcg aca gtg acg gaa act acc tcc gcg gaa gat ctt gcc caa gaa att   355
Ser Thr Val Thr Glu Thr Thr Ser Ala Glu Asp Leu Ala Gln Glu Ile
70                  75                  80                  85

gtg aag cca gcg gcc gtg gag gaa tat tca gag cct cag gta aat acg   403
```

```
Val Lys Pro Ala Ala Val Glu Glu Tyr Ser Glu Pro Gln Val Asn Thr
                  90                  95                  100

cca cag cag ttt gcg gcc atc ccg gaa cct gca ccg gcg gtt gca cca   451
Pro Gln Gln Phe Ala Ala Ile Pro Glu Pro Ala Pro Ala Val Ala Pro
            105                 110                 115

gct caa acg tat tac gcc aac tgc gcg gca gtt cgt gcg gcg ggt gca   499
Ala Gln Thr Tyr Tyr Ala Asn Cys Ala Ala Val Arg Ala Ala Gly Ala
        120                 125                 130

gct ccc ctt tat gcg gga tca cct gga tat agt tcc aag ctt gat cgc   547
Ala Pro Leu Tyr Ala Gly Ser Pro Gly Tyr Ser Ser Lys Leu Asp Arg
    135                 140                 145

gat ggc gac gga att gcc tgc gaa taaataggaa tagttaaaaa cac         594
Asp Gly Asp Gly Ile Ala Cys Glu
150                 155
```

<210> 2532
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

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<400> 2532
Met Thr Leu Pro Thr Pro Thr His Ser Thr Lys Gly Ser Ser Gly Arg
  1               5                  10                  15

Met Lys Arg Met Ala Leu Ile Gly Ser Ser Leu Ile Ile Ser Met Gly
             20                  25                  30

Leu Ile Thr Ala Cys Gly Ser Ala Ala Ala Glu Pro Glu Ala Pro Ala
         35                  40                  45

Pro Thr Val Thr Glu Thr Val Thr Ala Thr Val Thr Thr Thr Ala Lys
     50                  55                  60

Ala Ser Thr Ile Thr Ser Thr Val Thr Glu Thr Thr Ser Ala Glu Asp
 65                  70                  75                  80

Leu Ala Gln Glu Ile Val Lys Pro Ala Ala Val Glu Glu Tyr Ser Glu
                 85                  90                  95

Pro Gln Val Asn Thr Pro Gln Gln Phe Ala Ala Ile Pro Glu Pro Ala
            100                 105                 110

Pro Ala Val Ala Pro Ala Gln Thr Tyr Tyr Ala Asn Cys Ala Ala Val
        115                 120                 125

Arg Ala Ala Gly Ala Ala Pro Leu Tyr Ala Gly Ser Pro Gly Tyr Ser
    130                 135                 140

Ser Lys Leu Asp Arg Asp Gly Asp Gly Ile Ala Cys Glu
145                 150                 155
```

<210> 2533
<211> 572
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(549)
<223> RXA02001

<400> 2533

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acc cgc gac ccc atc gtc gca gcc gtc gga att gtc caa gcg ttt caa   48
Thr Arg Asp Pro Ile Val Ala Ala Val Gly Ile Val Gln Ala Phe Gln
  1               5                  10                  15

acg ata gtc agc cgg aat cac aat ccg gtc gag gac ctt gtc gtg tcg   96
Thr Ile Val Ser Arg Asn His Asn Pro Val Glu Asp Leu Val Val Ser
            20                  25                  30

gtc acg caa atc cac acc ggc agc gcc gat aat atc atc ccc gaa acc   144
Val Thr Gln Ile His Thr Gly Ser Ala Asp Asn Ile Ile Pro Glu Thr
        35                  40                  45

gcc tat atc aac ggc act gtc cgc acc ttc aac aaa gac gtg cag gcc   192
Ala Tyr Ile Asn Gly Thr Val Arg Thr Phe Asn Lys Asp Val Gln Ala
    50                  55                  60

atg gtc atc acg cgg atg gaa gaa atc gtc gcg ggc caa gct gca gcc   240
Met Val Ile Thr Arg Met Glu Glu Ile Val Ala Gly Gln Ala Ala Ala
65                  70                  75                  80

tat ggg gtc gag gcg acg ctg acc tac aac cgc aac tat ccc gcc acc   288
Tyr Gly Val Glu Ala Thr Leu Thr Tyr Asn Arg Asn Tyr Pro Ala Thr
                85                  90                  95

att aac gac gcc gcc aaa gcc gcc atc gct gcc gaa gtc gcg ggc gag   336
Ile Asn Asp Ala Ala Lys Ala Ala Ile Ala Ala Glu Val Ala Gly Glu
            100                 105                 110

gtc ggc ctc ggg gtc aac ccg aac ggc tcg cgc ggg atg ggg gcc gag   384
Val Gly Leu Gly Val Asn Pro Asn Gly Ser Arg Gly Met Gly Ala Glu
        115                 120                 125

gat ttc tcg tat ttc ctc gaa aag cgc ccg ggt gcc tac ctg ttc gtc   432
Asp Phe Ser Tyr Phe Leu Glu Lys Arg Pro Gly Ala Tyr Leu Phe Val
    130                 135                 140

ggt aat ggc gac agc gcg ggc ctt cac aac ccc gcc tat aat ttc aac   480
Gly Asn Gly Asp Ser Ala Gly Leu His Asn Pro Ala Tyr Asn Phe Asn
145                 150                 155                 160

gac gag gcc gcg ccc tac ggc gca tcg ttc ttg gcc cgc atg gca gaa   528
Asp Glu Ala Ala Pro Tyr Gly Ala Ser Phe Leu Ala Arg Met Ala Glu
                165                 170                 175

cgc ccc ttg ccg tta aag ggc tgatccatgg cgctcgaaga tgc             572
Arg Pro Leu Pro Leu Lys Gly
            180
```

<210> 2534
<211> 183
<212> PRT
<213> Corynebacterium glutamicum

<400> 2534
Thr Arg Asp Pro Ile Val Ala Ala Val Gly Ile Val Gln Ala Phe Gln
1 5 10 15

Thr Ile Val Ser Arg Asn His Asn Pro Val Glu Asp Leu Val Val Ser
20 25 30

Val Thr Gln Ile His Thr Gly Ser Ala Asp Asn Ile Ile Pro Glu Thr
35 40 45

Ala Tyr Ile Asn Gly Thr Val Arg Thr Phe Asn Lys Asp Val Gln Ala
50 55 60

Met Val Ile Thr Arg Met Glu Glu Ile Val Ala Gly Gln Ala Ala Ala
65 70 75 80

Tyr Gly Val Glu Ala Thr Leu Thr Tyr Asn Arg Asn Tyr Pro Ala Thr
85 90 95

Ile Asn Asp Ala Ala Lys Ala Ala Ile Ala Ala Glu Val Ala Gly Glu
100 105 110

Val Gly Leu Gly Val Asn Pro Asn Gly Ser Arg Gly Met Gly Ala Glu
115 120 125

Asp Phe Ser Tyr Phe Leu Glu Lys Arg Pro Gly Ala Tyr Leu Phe Val
130 135 140

Gly Asn Gly Asp Ser Ala Gly Leu His Asn Pro Ala Tyr Asn Phe Asn
145 150 155 160

Asp Glu Ala Ala Pro Tyr Gly Ala Ser Phe Leu Ala Arg Met Ala Glu
165 170 175

Arg Pro Leu Pro Leu Lys Gly
180

<210> 2535
<211> 230
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(207)
<223> RXA02004

<400> 2535
cgc gtc ggc cgt ctg atg cgt cag aac ggc att ctc atc atc cgc agc 48
Arg Val Gly Arg Leu Met Arg Gln Asn Gly Ile Leu Ile Ile Arg Ser
1 5 10 15

cgg aag ttc aag cgc acg acc ggc agc gat cat acc ttc aac atc gca 96
Arg Lys Phe Lys Arg Thr Thr Gly Ser Asp His Thr Phe Asn Ile Ala
20 25 30

ccg aac ttt ctg cag cag gac ttt atg gcg agc agg ccg aac cag aag 144
Pro Asn Phe Leu Gln Gln Asp Phe Met Ala Ser Arg Pro Asn Gln Lys
35 40 45

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tgg gcg ggc gac atc acc tat gtc tgg acg cgc gag ggc ctg ggt cta   192
Trp Ala Gly Asp Ile Thr Tyr Val Trp Thr Arg Glu Gly Leu Gly Leu
     50                  55                  60

tct ggc cga cat tct tgacctttat ccccgccggg tga                    230
Ser Gly Arg His Ser
 65
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<210> 2536
<211> 69
<212> PRT
<213> Corynebacterium glutamicum

<400> 2536

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Arg Val Gly Arg Leu Met Arg Gln Asn Gly Ile Leu Ile Ile Arg Ser
  1               5                  10                  15

Arg Lys Phe Lys Arg Thr Thr Gly Ser Asp His Thr Phe Asn Ile Ala
             20                  25                  30

Pro Asn Phe Leu Gln Gln Asp Phe Met Ala Ser Arg Pro Asn Gln Lys
         35                  40                  45

Trp Ala Gly Asp Ile Thr Tyr Val Trp Thr Arg Glu Gly Leu Gly Leu
     50                  55                  60

Ser Gly Arg His Ser
 65
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<210> 2537
<211> 565
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (71)..(565)
<223> RXA02006

<400> 2537

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atcatccata catgcagagc acagctttca cacatagaca tcactgcaca tttatctaat 60

gggagactca atg aca gtt gca cac aaa cga agt ctg aca tgg atc aag    109
          Met Thr Val Ala His Lys Arg Ser Leu Thr Trp Ile Lys
            1               5                  10

aga cta tct gcg act aca ttt gca gct ttt ctt ggc att cag ctt gtg   157
Arg Leu Ser Ala Thr Thr Phe Ala Ala Phe Leu Gly Ile Gln Leu Val
     15                  20                  25

acc ccc gct cac tca att gaa aac acg acg cag att cca gaa agc gaa   205
Thr Pro Ala His Ser Ile Glu Asn Thr Thr Gln Ile Pro Glu Ser Glu
 30                  35                  40                  45

ttg cac aac ctc ggg ctc aca gac gaa gaa att caa gaa ttc aat caa   253
Leu His Asn Leu Gly Leu Thr Asp Glu Glu Ile Gln Glu Phe Asn Gln
                 50                  55                  60

tat ctc att gac gag tca ctc ttt caa gag act gta gaa acc tct ccg   301
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Tyr Leu Ile Asp Glu Ser Leu Phe Gln Glu Thr Val Glu Thr Ser Pro
            65                  70                  75

atc gta gtc agc gac aat gaa gat gca gcc caa gat ccc ggt ttc ggc   349
Ile Val Val Ser Asp Asn Glu Asp Ala Ala Gln Asp Pro Gly Phe Gly
         80                  85                  90

ctt ttc acc aca aat cct gtg aaa cac aca gat gag cac att ggc gct   397
Leu Phe Thr Thr Asn Pro Val Lys His Thr Asp Glu His Ile Gly Ala
     95                  100                 105

cta tac ttc tcc gac cta cca ggt att tcc aat ctt acg tgc act gcc   445
Leu Tyr Phe Ser Asp Leu Pro Gly Ile Ser Asn Leu Thr Cys Thr Ala
110                 115                 120                 125

aac tac atc ggt gga aaa ttc tgg acc aca gca cat cat tgt gtt gaa   493
Asn Tyr Ile Gly Gly Lys Phe Trp Thr Thr Ala His His Cys Val Glu
                130                 135                 140

ggc cgc agt cgc ttc gtc ggc ttc atc gag cag tcg gac gga caa tat   541
Gly Arg Ser Arg Phe Val Gly Phe Ile Glu Gln Ser Asp Gly Gln Tyr
            145                 150                 155

gca ggc att gag cat gtt tac aca                                  565
Ala Gly Ile Glu His Val Tyr Thr
        160                 165


<210> 2538
<211> 165
<212> PRT
<213> Corynebacterium glutamicum

<400> 2538
Met Thr Val Ala His Lys Arg Ser Leu Thr Trp Ile Lys Arg Leu Ser
  1               5                  10                  15

Ala Thr Thr Phe Ala Ala Phe Leu Gly Ile Gln Leu Val Thr Pro Ala
             20                  25                  30

His Ser Ile Glu Asn Thr Thr Gln Ile Pro Glu Ser Glu Leu His Asn
         35                  40                  45

Leu Gly Leu Thr Asp Glu Glu Ile Gln Glu Phe Asn Gln Tyr Leu Ile
     50                  55                  60

Asp Glu Ser Leu Phe Gln Glu Thr Val Glu Thr Ser Pro Ile Val Val
 65                  70                  75                  80

Ser Asp Asn Glu Asp Ala Ala Gln Asp Pro Gly Phe Gly Leu Phe Thr
                 85                  90                  95

Thr Asn Pro Val Lys His Thr Asp Glu His Ile Gly Ala Leu Tyr Phe
            100                 105                 110

Ser Asp Leu Pro Gly Ile Ser Asn Leu Thr Cys Thr Ala Asn Tyr Ile
        115                 120                 125

Gly Gly Lys Phe Trp Thr Thr Ala His His Cys Val Glu Gly Arg Ser
    130                 135                 140
```

```
Arg Phe Val Gly Phe Ile Glu Gln Ser Asp Gly Gln Tyr Ala Gly Ile
145                 150                 155                 160

Glu His Val Tyr Thr
                165


<210> 2539
<211> 223
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(223)
<223> RXA02009

<400> 2539
aactgcatca ttgtcgttcc tgaacaagcg ccgtggttta agccagccat catcaaacag 60

gcttaaaaat actcaatcgt cccattcaag aaaagagcac atg acc atg tac aac   115
                                              Met Thr Met Tyr Asn
                                                1               5

gcc gca aag acc ctt gtt ccc cag att gtt gct ttc gat gac aca gca   163
Ala Ala Lys Thr Leu Val Pro Gln Ile Val Ala Phe Asp Asp Thr Ala
                10                  15                  20

atc atc gca ctc gac caa gcc gcg gaa gat gaa ttc cgc aag gct aac   211
Ile Ile Ala Leu Asp Gln Ala Ala Glu Asp Glu Phe Arg Lys Ala Asn
            25                  30                  35

tac ccc gag gtt                                                  223
Tyr Pro Glu Val
        40


<210> 2540
<211> 41
<212> PRT
<213> Corynebacterium glutamicum

<400> 2540
Met Thr Met Tyr Asn Ala Ala Lys Thr Leu Val Pro Gln Ile Val Ala
  1               5                  10                  15

Phe Asp Asp Thr Ala Ile Ile Ala Leu Asp Gln Ala Ala Glu Asp Glu
            20                  25                  30

Phe Arg Lys Ala Asn Tyr Pro Glu Val
        35                  40


<210> 2541
<211> 649
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(649)
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<223> RXA02013

<400> 2541

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atcaccgcgc tggcgacaat ttcagaaaac tcccacaaag cactgcttgg cctttatttg 60

tccggtctta aacacggcat gatggctaac atcggagaac atg acg gaa agt cct   115
                                        Met Thr Glu Ser Pro
                                          1               5

gat cta gca gtt tcc ttt tta gcc gcc ttc aat gac atc gaa gcg cac   163
Asp Leu Ala Val Ser Phe Leu Ala Ala Phe Asn Asp Ile Glu Ala His
                 10                  15                  20

ctt cga acc cag ctc cgc gct aaa cgc tcc gac agt ttc aga tgg atg   211
Leu Arg Thr Gln Leu Arg Ala Lys Arg Ser Asp Ser Phe Arg Trp Met
             25                  30                  35

gta cgt atc gcc gag aaa cag cat ctg att tcc aaa gaa caa gca gaa   259
Val Arg Ile Ala Glu Lys Gln His Leu Ile Ser Lys Glu Gln Ala Glu
         40                  45                  50

acc ctt gat gct ttt gcg gag ctg cgc aac gca att agc cac ggc caa   307
Thr Leu Asp Ala Phe Ala Glu Leu Arg Asn Ala Ile Ser His Gly Gln
     55                  60                  65

tac aac gat cta cgc ccg att gcc gat ccc cgc ccc gac acc gtg gac   355
Tyr Asn Asp Leu Arg Pro Ile Ala Asp Pro Arg Pro Asp Thr Val Asp
 70                  75                  80                  85

acc att gag aag att cgc tcc ctc ctt ctc aat cct cca att gcg tta   403
Thr Ile Glu Lys Ile Arg Ser Leu Leu Leu Asn Pro Pro Ile Ala Leu
                 90                  95                 100

aac gtc ctc ccg gag caa aag gtc cgc tcc tac tca ctt gaa gat cca   451
Asn Val Leu Pro Glu Gln Lys Val Arg Ser Tyr Ser Leu Glu Asp Pro
            105                 110                 115

gtg agt agg gcc tta gaa gtt gtg cac acc acg gag atc tcc caa ttc   499
Val Ser Arg Ala Leu Glu Val Val His Thr Thr Glu Ile Ser Gln Phe
        120                 125                 130

ccc ata tat aag gga acg gaa tac gtg gca ctg cta act acc aac aca   547
Pro Ile Tyr Lys Gly Thr Glu Tyr Val Ala Leu Leu Thr Thr Asn Thr
    135                 140                 145

atc gct cgc tgg gtt gcc tcc gat tta cat gac aat gcc cag ctg gat   595
Ile Ala Arg Trp Val Ala Ser Asp Leu His Asp Asn Ala Gln Leu Asp
150                 155                 160                 165

gca cgt tct atc aaa gag gtt ctg gat tat gca gaa tcc tct gac act   643
Ala Arg Ser Ile Lys Glu Val Leu Asp Tyr Ala Glu Ser Ser Asp Thr
                170                 175                 180

gca gtt                                                          649
Ala Val
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<210> 2542
<211> 183
<212> PRT

<213> Corynebacterium glutamicum

<400> 2542

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Met Thr Glu Ser Pro Asp Leu Ala Val Ser Phe Leu Ala Ala Phe Asn
  1               5                  10                  15

Asp Ile Glu Ala His Leu Arg Thr Gln Leu Arg Ala Lys Arg Ser Asp
             20                  25                  30

Ser Phe Arg Trp Met Val Arg Ile Ala Glu Lys Gln His Leu Ile Ser
         35                  40                  45

Lys Glu Gln Ala Glu Thr Leu Asp Ala Phe Ala Glu Leu Arg Asn Ala
     50                  55                  60

Ile Ser His Gly Gln Tyr Asn Asp Leu Arg Pro Ile Ala Asp Pro Arg
 65                  70                  75                  80

Pro Asp Thr Val Asp Thr Ile Glu Lys Ile Arg Ser Leu Leu Leu Asn
                 85                  90                  95

Pro Pro Ile Ala Leu Asn Val Leu Pro Glu Gln Lys Val Arg Ser Tyr
            100                 105                 110

Ser Leu Glu Asp Pro Val Ser Arg Ala Leu Glu Val Val His Thr Thr
        115                 120                 125

Glu Ile Ser Gln Phe Pro Ile Tyr Lys Gly Thr Glu Tyr Val Ala Leu
    130                 135                 140

Leu Thr Thr Asn Thr Ile Ala Arg Trp Val Ala Ser Asp Leu His Asp
145                 150                 155                 160

Asn Ala Gln Leu Asp Ala Arg Ser Ile Lys Glu Val Leu Asp Tyr Ala
                165                 170                 175

Glu Ser Ser Asp Thr Ala Val
            180
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<210> 2543
<211> 1071
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1048)
<223> RXA02021

<400> 2543

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ttgggtcgcc gaggagatct aatcctggtt tgagttcaga gttcacaggt ttaagcctac 60

aaaccttagt taaaacatga tggaagcggt cgattaaaaa atg agt gaa aac att   115
                                               Met Ser Glu Asn Ile
                                                 1               5

cgc gga gcc caa gca gtt gga atc gca aat atc gcc atg gac ggg acc   163
Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile Ala Met Asp Gly Thr
                10                  15                  20
```

```
atc ctg gac acg tgg tac cca gaa ccc caa att ttc aac ccg gat cag   211
Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile Phe Asn Pro Asp Gln
            25                  30                  35

tgg gct gaa cgc tac cca ttg gaa gtg ggc acc aca cgc ctc gga gca   259
Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr Thr Arg Leu Gly Ala
        40                  45                  50

aac gaa ctc acc cca cgg atg ctg cag ttg gta aaa ctg gac caa gat   307
Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val Lys Leu Asp Gln Asp
    55                  60                  65

cgc ctc gtc gaa cag gta gca gtc cgc acc gtt atc ccc gat ctg tct   355
Arg Leu Val Glu Gln Val Ala Val Arg Thr Val Ile Pro Asp Leu Ser
70                  75                  80                  85

caa cct cca gta gac gcg cac gat gtt tac ctg cgc ctc cac ctg ctt   403
Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu Arg Leu His Leu Leu
                90                  95                  100

tcc cac cgg ctg gtc cgc ccc cac gaa atg cac atg caa aac acc ttg   451
Ser His Arg Leu Val Arg Pro His Glu Met His Met Gln Asn Thr Leu
            105                 110                 115

gag ctg ctg tcc gac gtg gtg tgg aca aac aag ggc cct tgc ctt cct   499
Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys Gly Pro Cys Leu Pro
        120                 125                 130

gaa aac ttt gag tgg gtg cgt ggt gct ctg cgg tcc cgc gga ctc atc   547
Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg Ser Arg Gly Leu Ile
    135                 140                 145

cac gtc tac tgt gtg gac cgt ctt ccc cgc atg gtc gac tat gtg gtt   595
His Val Tyr Cys Val Asp Arg Leu Pro Arg Met Val Asp Tyr Val Val
150                 155                 160                 165

ccc cct gga gtc cgc atc tcc gaa gca gaa cgc gtg cgc cta ggt gca   643
Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg Val Arg Leu Gly Ala
                170                 175                 180

tac ctt gct ccg ggt acc tct gtg ctg cgt gaa ggt ttc gtg tct ttc   691
Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu Gly Phe Val Ser Phe
            185                 190                 195

aac tcc ggc acc ttg ggt gcc gca aag gtg gaa ggc cgc ctg agt tcc   739
Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu Gly Arg Leu Ser Ser
        200                 205                 210

ggt gtg gtc atc ggt gaa ggt tcc gag att gga ctg tct tct act att   787
Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly Leu Ser Ser Thr Ile
    215                 220                 225

cag tcc ccg aga gat gaa cag cgc cgc cgt ttg ccg ttg agc atc ggc   835
Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu Pro Leu Ser Ile Gly
230                 235                 240                 245

caa aac tgc aac ttt ggt gtc agc tcc gga atc atc gga gtc agt ctg   883
Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile Ile Gly Val Ser Leu
                250                 255                 260

gga gac aat tgc gac atc gga aat aac att gtc ttg gat gga gat acc   931
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```
Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val Leu Asp Gly Asp Thr
            265                 270                 275

ccc att tgg ttc gca gcc gat gag gag tta cgc act atc gac tcc atc   979
Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg Thr Ile Asp Ser Ile
        280                 285                 290

gaa ggc caa gca aat tgg tca atc aag cgt gaa tcc ggc ttc cat gag   1027
Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu Ser Gly Phe His Glu
    295                 300                 305

cca gtt gcc cgc ctc aaa gct tgacccattt tcataaccag tgc            1071
Pro Val Ala Arg Leu Lys Ala
310                 315
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<210> 2544
<211> 316
<212> PRT
<213> Corynebacterium glutamicum

<400> 2544

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Met Ser Glu Asn Ile Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile
  1               5                  10                  15

Ala Met Asp Gly Thr Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile
             20                  25                  30

Phe Asn Pro Asp Gln Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr
         35                  40                  45

Thr Arg Leu Gly Ala Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val
     50                  55                  60

Lys Leu Asp Gln Asp Arg Leu Val Glu Gln Val Ala Val Arg Thr Val
 65                  70                  75                  80

Ile Pro Asp Leu Ser Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu
                 85                  90                  95

Arg Leu His Leu Leu Ser His Arg Leu Val Arg Pro His Glu Met His
            100                 105                 110

Met Gln Asn Thr Leu Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys
        115                 120                 125

Gly Pro Cys Leu Pro Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg
    130                 135                 140

Ser Arg Gly Leu Ile His Val Tyr Cys Val Asp Arg Leu Pro Arg Met
145                 150                 155                 160

Val Asp Tyr Val Val Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg
                165                 170                 175

Val Arg Leu Gly Ala Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu
            180                 185                 190

Gly Phe Val Ser Phe Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu
        195                 200                 205
```

```
Gly Arg Leu Ser Ser Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly
    210                 215                 220

Leu Ser Ser Thr Ile Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu
225                 230                 235                 240

Pro Leu Ser Ile Gly Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile
                245                 250                 255

Ile Gly Val Ser Leu Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val
            260                 265                 270

Leu Asp Gly Asp Thr Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg
        275                 280                 285

Thr Ile Asp Ser Ile Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu
    290                 295                 300

Ser Gly Phe His Glu Pro Val Ala Arg Leu Lys Ala
305                 310                 315


<210> 2545
<211> 504
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(481)
<223> RXA02036

<400> 2545
ctaaaatgga aggcaatgga tacccgccgc atgaacctcc gccaatggaa aatcctcgtt 60

gccctcatct ctgctgcagt ggcggctctc ggagggtggt gtg cat att cct ttt   115
                                              Val His Ile Pro Phe
                                                1               5

ggg cac ctc gcc gac acc gtc tcc tgg gac tgc ggg gga ggc agc tgc   163
Gly His Leu Ala Asp Thr Val Ser Trp Asp Cys Gly Gly Gly Ser Cys
               10                  15                  20

gcc acc aac gat ttg gta tcc ctg ttc atg ccg gcc gcc ttc atg agt   211
Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro Ala Ala Phe Met Ser
            25                  30                  35

acc ctc gcc gcc tgc gta ttt ggc gcg tgg gcc ata ggt ttg atc gct   259
Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala Ile Gly Leu Ile Ala
        40                  45                  50

ccc gca cta ttc atc gcg gtg act gcc tgg gca ttt cgc tcc ggc gtg   307
Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala Phe Arg Ser Gly Val
    55                  60                  65

cag gct gcg att gcc gac ggc tac acg tcc gcg act tcc gtc ggc ttc   355
Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala Thr Ser Val Gly Phe
70                  75                  80                  85

gaa atg act gtc tcg ctc att ctt ttc atc atc gca ggt ctg tgc ttt   403
Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile Ala Gly Leu Cys Phe
```

```
                90                  95                  100

ctg ggc tgg atc ccc atg ttc atc aac aac cgc caa gtc gcg cgc aag   451
Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg Gln Val Ala Arg Lys
            105                 110                 115

gtc cgc gag agg gct gcg ggc ttg agc aat taggctctcg cttttcgacg     501
Val Arg Glu Arg Ala Ala Gly Leu Ser Asn
        120                 125

ttt                                                               504


<210> 2546
<211> 127
<212> PRT
<213> Corynebacterium glutamicum

<400> 2546
Val His Ile Pro Phe Gly His Leu Ala Asp Thr Val Ser Trp Asp Cys
  1               5                  10                  15

Gly Gly Gly Ser Cys Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro
             20                  25                  30

Ala Ala Phe Met Ser Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala
         35                  40                  45

Ile Gly Leu Ile Ala Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala
     50                  55                  60

Phe Arg Ser Gly Val Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala
 65                  70                  75                  80

Thr Ser Val Gly Phe Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile
                 85                  90                  95

Ala Gly Leu Cys Phe Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg
            100                 105                 110

Gln Val Ala Arg Lys Val Arg Glu Arg Ala Ala Gly Leu Ser Asn
        115                 120                 125


<210> 2547
<211> 551
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(528)
<223> RXA02040

<400> 2547
tac ata cct ttt gtc att tgg tcc gat ctc ggt gag gct gcc gaa ggt   48
Tyr Ile Pro Phe Val Ile Trp Ser Asp Leu Gly Glu Ala Ala Glu Gly
  1               5                  10                  15

gag aac ttt gct cgc ttc tgg tcc tgg ctg aaa tcg cgc cgg gac aaa   96
Glu Asn Phe Ala Arg Phe Trp Ser Trp Leu Lys Ser Arg Arg Asp Lys
```

```
            20                  25                  30

gct cgc cag cag gga caa acc ttc ggt gtg ttc tgc tat gcc agc aac   144
Ala Arg Gln Gln Gly Gln Thr Phe Gly Val Phe Cys Tyr Ala Ser Asn
         35                  40                  45

ggc gaa aac cac tgg atg ctc tcc act gct cgc aga ttc ttc ggc aaa   192
Gly Glu Asn His Trp Met Leu Ser Thr Ala Arg Arg Phe Phe Gly Lys
     50                  55                  60

gtc aaa ggt gtg ccc gac gag caa gaa atc cgc agc ttc att agc tct   240
Val Lys Gly Val Pro Asp Glu Gln Glu Ile Arg Ser Phe Ile Ser Ser
 65                  70                  75                  80

gac caa tgg aat gac atg ttt gct gtc gcg cgc tcc caa ctt gtt ggc   288
Asp Gln Trp Asn Asp Met Phe Ala Val Ala Arg Ser Gln Leu Val Gly
                 85                  90                  95

ccc ggt ggt tta ggt ctg aaa caa ctc gcg ccg gca gct gga ttc cat   336
Pro Gly Gly Leu Gly Leu Lys Gln Leu Ala Pro Ala Ala Gly Phe His
            100                 105                 110

tgg gag gaa gaa gac ttc gca ggt gaa gat agc ctc cac gca tat ctc   384
Trp Glu Glu Glu Asp Phe Ala Gly Glu Asp Ser Leu His Ala Tyr Leu
        115                 120                 125

att gct tcc acg gct gcc gaa cca gaa gct gag gcc gct cgt gct caa   432
Ile Ala Ser Thr Ala Ala Glu Pro Glu Ala Glu Ala Ala Arg Ala Gln
    130                 135                 140

ttg ctc agc tac aac ggc gat gat tgc agg gcc acc gca gcg gtt cgc   480
Leu Leu Ser Tyr Asn Gly Asp Asp Cys Arg Ala Thr Ala Ala Val Arg
145                 150                 155                 160

cat tgg ctt cga caa ggt gcg cgc acg gca cct gtg ctg ggg aat att   528
His Trp Leu Arg Gln Gly Ala Arg Thr Ala Pro Val Leu Gly Asn Ile
                165                 170                 175

taaaccaagg aaggattctc cag                                        551
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<210> 2548
<211> 176
<212> PRT
<213> Corynebacterium glutamicum

<400> 2548

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Tyr Ile Pro Phe Val Ile Trp Ser Asp Leu Gly Glu Ala Ala Glu Gly
  1               5                  10                  15

Glu Asn Phe Ala Arg Phe Trp Ser Trp Leu Lys Ser Arg Arg Asp Lys
             20                  25                  30

Ala Arg Gln Gln Gly Gln Thr Phe Gly Val Phe Cys Tyr Ala Ser Asn
         35                  40                  45

Gly Glu Asn His Trp Met Leu Ser Thr Ala Arg Arg Phe Phe Gly Lys
     50                  55                  60

Val Lys Gly Val Pro Asp Glu Gln Glu Ile Arg Ser Phe Ile Ser Ser
 65                  70                  75                  80
```

```
Asp Gln Trp Asn Asp Met Phe Ala Val Ala Arg Ser Gln Leu Val Gly
                 85                  90                  95

Pro Gly Gly Leu Gly Leu Lys Gln Leu Ala Pro Ala Ala Gly Phe His
            100                 105                 110

Trp Glu Glu Glu Asp Phe Ala Gly Glu Asp Ser Leu His Ala Tyr Leu
        115                 120                 125

Ile Ala Ser Thr Ala Ala Glu Pro Glu Ala Glu Ala Ala Arg Ala Gln
    130                 135                 140

Leu Leu Ser Tyr Asn Gly Asp Asp Cys Arg Ala Thr Ala Ala Val Arg
145                 150                 155                 160

His Trp Leu Arg Gln Gly Ala Arg Thr Ala Pro Val Leu Gly Asn Ile
                165                 170                 175
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Sequence Listing Free Text

<210> 2549
<211> 364
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(364)
<223> RXA02046

<400> 2549

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tccgtgccat caccaccggc gagatcactg gcatcgtgga cgcaaaacaa acagcaacag 60

aaattattaa catccgacgc aacgcttcag gagagtcctc atg aaa gag aca ctg   115
                                              Met Lys Glu Thr Leu
                                                1               5

acc acc ggt tta acc cac caa atg acc tac ata gtg cca gca aac cgc   163
Thr Thr Gly Leu Thr His Gln Met Thr Tyr Ile Val Pro Ala Asn Arg
                10                  15                  20

aca gtt ccg cat ctg ctt ccc gaa gca gca gaa ttt gaa acc atg cca   211
Thr Val Pro His Leu Leu Pro Glu Ala Ala Glu Phe Glu Thr Met Pro
            25                  30                  35

gat gtc ctg gcc act gga tat atg gtc ggc atc atc gag tgg gcc tgc   259
Asp Val Leu Ala Thr Gly Tyr Met Val Gly Ile Ile Glu Trp Ala Cys
        40                  45                  50

atg gaa ctt ctg cgt ccc cat ttg gac gac ggt gaa atc tcg ctg ggc   307
Met Glu Leu Leu Arg Pro His Leu Asp Asp Gly Glu Ile Ser Leu Gly
    55                  60                  65

act cat gtg aac ttc tcc cac gca gct cca acg gtt cct gga tcc acg   355
Thr His Val Asn Phe Ser His Ala Ala Pro Thr Val Pro Gly Ser Thr
70                  75                  80                  85

gtc acc atc                                                      364
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Val Thr Ile

<210> 2550
<211> 88
<212> PRT
<213> Corynebacterium glutamicum

<400> 2550
Met Lys Glu Thr Leu Thr Thr Gly Leu Thr His Gln Met Thr Tyr Ile
1 5 10 15

Val Pro Ala Asn Arg Thr Val Pro His Leu Leu Pro Glu Ala Ala Glu
20 25 30

Phe Glu Thr Met Pro Asp Val Leu Ala Thr Gly Tyr Met Val Gly Ile
35 40 45

Ile Glu Trp Ala Cys Met Glu Leu Leu Arg Pro His Leu Asp Asp Gly
50 55 60

Glu Ile Ser Leu Gly Thr His Val Asn Phe Ser His Ala Ala Pro Thr
65 70 75 80

Val Pro Gly Ser Thr Val Thr Ile
85

<210> 2551
<211> 621
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(598)
<223> RXA02051

<400> 2551
cgcactgatc ggtgtagtaa ctggcggtat tttgctgcta attaactcgc aaaacggtga 60

gcagacatca tcttcaactc gcacaacagt caatgactcc atg gtc atc aga gct 115
Met Val Ile Arg Ala
1 5

ctc cag cgc gaa gaa gaa atc gtc ctt ctc agc gcc gga gca ctt gga 163
Leu Gln Arg Glu Glu Glu Ile Val Leu Leu Ser Ala Gly Ala Leu Gly
10 15 20

atc cat gag aaa acc gtt gaa cgt aca att cgt gga aaa cgt att cct 211
Ile His Glu Lys Thr Val Glu Arg Thr Ile Arg Gly Lys Arg Ile Pro
25 30 35

ggc acg caa aag acc gtg cac gtc caa tac agc tac acc gga aaa ctc 259
Gly Thr Gln Lys Thr Val His Val Gln Tyr Ser Tyr Thr Gly Lys Leu
40 45 50

gga atc gat gcc tca gat gtt gaa atc aaa tcc gca ggt gac aat aag 307
Gly Ile Asp Ala Ser Asp Val Glu Ile Lys Ser Ala Gly Asp Asn Lys
55 60 65

```
ctt tcc atc act atc cct gag ttc atc ttc atc gga tac gac gat cta   355
Leu Ser Ile Thr Ile Pro Glu Phe Ile Phe Ile Gly Tyr Asp Asp Leu
 70                  75                  80                  85

aag ttt aag acc ata gcc gaa gat gac ggt tgg atc agt ttc agc act   403
Lys Phe Lys Thr Ile Ala Glu Asp Asp Gly Trp Ile Ser Phe Ser Thr
                90                  95                 100

gac gat atc gat act gca gaa gta gtt tct gag atc atg agc caa gag   451
Asp Asp Ile Asp Thr Ala Glu Val Val Ser Glu Ile Met Ser Gln Glu
            105                 110                 115

aac ttc gtc gag caa gta acc act aac cgg gaa atg ttg gaa gat caa   499
Asn Phe Val Glu Gln Val Thr Thr Asn Arg Glu Met Leu Glu Asp Gln
        120                 125                 130

gcg gtt gat ttc tac aac gac ctg ctc cac gaa ttc acc gag aaa ctc   547
Ala Val Asp Phe Tyr Asn Asp Leu Leu His Glu Phe Thr Glu Lys Leu
    135                 140                 145

gat aca gat cga tac gaa gac acc aag att gag ctc gaa ttc gag ttt   595
Asp Thr Asp Arg Tyr Glu Asp Thr Lys Ile Glu Leu Glu Phe Glu Phe
150                 155                 160                 165

gag tagatagtgc ttcgaagaca gtt                                    621
Glu
```

<210> 2552
<211> 166
<212> PRT
<213> Corynebacterium glutamicum

<400> 2552

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Met Val Ile Arg Ala Leu Gln Arg Glu Glu Glu Ile Val Leu Leu Ser
  1               5                  10                  15

Ala Gly Ala Leu Gly Ile His Glu Lys Thr Val Glu Arg Thr Ile Arg
             20                  25                  30

Gly Lys Arg Ile Pro Gly Thr Gln Lys Thr Val His Val Gln Tyr Ser
         35                  40                  45

Tyr Thr Gly Lys Leu Gly Ile Asp Ala Ser Asp Val Glu Ile Lys Ser
     50                  55                  60

Ala Gly Asp Asn Lys Leu Ser Ile Thr Ile Pro Glu Phe Ile Phe Ile
 65                  70                  75                  80

Gly Tyr Asp Asp Leu Lys Phe Lys Thr Ile Ala Glu Asp Asp Gly Trp
                 85                  90                  95

Ile Ser Phe Ser Thr Asp Asp Ile Asp Thr Ala Glu Val Val Ser Glu
            100                 105                 110

Ile Met Ser Gln Glu Asn Phe Val Glu Gln Val Thr Thr Asn Arg Glu
        115                 120                 125

Met Leu Glu Asp Gln Ala Val Asp Phe Tyr Asn Asp Leu Leu His Glu
```

```
    130                 135                 140

Phe Thr Glu Lys Leu Asp Thr Asp Arg Tyr Glu Asp Thr Lys Ile Glu
145                 150                 155                 160

Leu Glu Phe Glu Phe Glu
                165


<210> 2553
<211> 702
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(679)
<223> RXA02053

<400> 2553
aaccagccag aaactatctc caaaagctaa taaaaccctt gcactgacaa ataaggcgac 60

ctaccatgac tctgtttcca acacataaaa aggataaaaa atg tca ctt tca gtc   115
                                            Met Ser Leu Ser Val
                                              1               5


gtc gag gcg att acc aac cgc cgc gcc acc cgc aaa tac acc gat gaa   163
Val Glu Ala Ile Thr Asn Arg Arg Ala Thr Arg Lys Tyr Thr Asp Glu
                 10                  15                  20

gct cct acc cct gag ctg atc gac aaa atc gtt gac ctt gcc ctg gag   211
Ala Pro Thr Pro Glu Leu Ile Asp Lys Ile Val Asp Leu Ala Leu Glu
             25                  30                  35

gca ccc agt gcg ttc aat gcg cag caa cgt gaa att gtt gtg att act   259
Ala Pro Ser Ala Phe Asn Ala Gln Gln Arg Glu Ile Val Val Ile Thr
         40                  45                  50

gat ccc gca cag aag cag aag ctt tac gag gcc tcc cat cag aaa caa   307
Asp Pro Ala Gln Lys Gln Lys Leu Tyr Glu Ala Ser His Gln Lys Gln
     55                  60                  65

ttc ctc acc gca cct gta act ttc att gcg gtt gcc cgc gtg gaa aac   355
Phe Leu Thr Ala Pro Val Thr Phe Ile Ala Val Ala Arg Val Glu Asn
 70                  75                  80                  85

gag cct gag gat ttg gaa gag att ctt ggt acg gaa agg gct gaa cgt   403
Glu Pro Glu Asp Leu Glu Glu Ile Leu Gly Thr Glu Arg Ala Glu Arg
                 90                  95                 100

gtc gcg gga ttc atc aac ggt cgc agc att cag cag gca cgc gaa gca   451
Val Ala Gly Phe Ile Asn Gly Arg Ser Ile Gln Gln Ala Arg Glu Ala
             105                 110                 115

acg ttg agg gat gcc agc ctc gcg gcg gct ttt cta att ctg gct gcc   499
Thr Leu Arg Asp Ala Ser Leu Ala Ala Ala Phe Leu Ile Leu Ala Ala
         120                 125                 130

cag gcg gag ggt ttg agt acc agc ccg act act ggt tgg gat gag gaa   547
Gln Ala Glu Gly Leu Ser Thr Ser Pro Thr Thr Gly Trp Asp Glu Glu
     135                 140                 145
```

```
aaa gtg aag gaa gca atc ggt ctc ggc ggg cgt gag gat cgt gca atc   595
Lys Val Lys Glu Ala Ile Gly Leu Gly Gly Arg Glu Asp Arg Ala Ile
150                 155                 160                 165

gcc ctt gtt att gct acc gga ttc cct aat gaa cag ccg gag cac cct   643
Ala Leu Val Ile Ala Thr Gly Phe Pro Asn Glu Gln Pro Glu His Pro
                170                 175                 180

ggt cgt ttg cag aat agg cgc atc gac aac agc tac taactctgcc        689
Gly Arg Leu Gln Asn Arg Arg Ile Asp Asn Ser Tyr
            185                 190

agctcgcccg gac                                                   702
```

<210> 2554
<211> 193
<212> PRT
<213> Corynebacterium glutamicum

<400> 2554

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Met Ser Leu Ser Val Val Glu Ala Ile Thr Asn Arg Arg Ala Thr Arg
  1               5                  10                  15

Lys Tyr Thr Asp Glu Ala Pro Thr Pro Glu Leu Ile Asp Lys Ile Val
             20                  25                  30

Asp Leu Ala Leu Glu Ala Pro Ser Ala Phe Asn Ala Gln Gln Arg Glu
         35                  40                  45

Ile Val Val Ile Thr Asp Pro Ala Gln Lys Gln Lys Leu Tyr Glu Ala
     50                  55                  60

Ser His Gln Lys Gln Phe Leu Thr Ala Pro Val Thr Phe Ile Ala Val
 65                  70                  75                  80

Ala Arg Val Glu Asn Glu Pro Glu Asp Leu Glu Glu Ile Leu Gly Thr
                 85                  90                  95

Glu Arg Ala Glu Arg Val Ala Gly Phe Ile Asn Gly Arg Ser Ile Gln
            100                 105                 110

Gln Ala Arg Glu Ala Thr Leu Arg Asp Ala Ser Leu Ala Ala Ala Phe
        115                 120                 125

Leu Ile Leu Ala Ala Gln Ala Glu Gly Leu Ser Thr Ser Pro Thr Thr
    130                 135                 140

Gly Trp Asp Glu Glu Lys Val Lys Glu Ala Ile Gly Leu Gly Gly Arg
145                 150                 155                 160

Glu Asp Arg Ala Ile Ala Leu Val Ile Ala Thr Gly Phe Pro Asn Glu
                165                 170                 175

Gln Pro Glu His Pro Gly Arg Leu Gln Asn Arg Arg Ile Asp Asn Ser
            180                 185                 190

Tyr
```

<210> 2555
<211> 654
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(631)
<223> RXA02057

<400> 2555
aagtctttat agtcctgcac tagcctagaa gggccttatg ccgtgtgaat cacacagcat 60

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acggcccttt ttgctgccgt ggttgcctaa ggtggaaggt atg aaa cga atc tgt   115
                                             Met Lys Arg Ile Cys
                                               1               5

gcg gtc gcg atc tct tca gta ctt ttg tta agt ggc tgc tcc tcc act   163
Ala Val Ala Ile Ser Ser Val Leu Leu Leu Ser Gly Cys Ser Ser Thr
                 10                  15                  20

tcc aca acg cag ctc gag gga ttc gat gga cgc tca gcg cag gag atc   211
Ser Thr Thr Gln Leu Glu Gly Phe Asp Gly Arg Ser Ala Gln Glu Ile
             25                  30                  35

atc aca gaa ctt gat caa acc cca gtc gca gac aga gca act aac ctc   259
Ile Thr Glu Leu Asp Gln Thr Pro Val Ala Asp Arg Ala Thr Asn Leu
         40                  45                  50

atg gcc tcc att cgg gca gat gag tta att ctg tcg gat caa agc gga   307
Met Ala Ser Ile Arg Ala Asp Glu Leu Ile Leu Ser Asp Gln Ser Gly
     55                  60                  65

cag ctc agc att gac atg cct gca gat gag ttc tat atc tcc gca gcc   355
Gln Leu Ser Ile Asp Met Pro Ala Asp Glu Phe Tyr Ile Ser Ala Ala
 70                  75                  80                  85

ccg tac acc acc aca acc cac gag tgc ttc tat cac agc ctc acc aca   403
Pro Tyr Thr Thr Thr Thr His Glu Cys Phe Tyr His Ser Leu Thr Thr
                 90                  95                 100

tgt act ggt gaa ctc gcc aac acc cca gtg aaa gta acg gtg gtg gca   451
Cys Thr Gly Glu Leu Ala Asn Thr Pro Val Lys Val Thr Val Val Ala
            105                 110                 115

gat aat gga gaa acc atc ctc gaa gag gac acc atc acc tac gat aat   499
Asp Asn Gly Glu Thr Ile Leu Glu Glu Asp Thr Ile Thr Tyr Asp Asn
        120                 125                 130

gga ttt gtt ggg atg tgg ctc ccc cgc aac att gat gcc aca ctc acc   547
Gly Phe Val Gly Met Trp Leu Pro Arg Asn Ile Asp Ala Thr Leu Thr
    135                 140                 145

atc gaa cat gac ggc ctg aaa tcc acc cag ccg atc tct acg ggt gat   595
Ile Glu His Asp Gly Leu Lys Ser Thr Gln Pro Ile Ser Thr Gly Asp
150                 155                 160                 165

gac gcc ccc acg tgc atc acc acg gct gaa cta gcg tgaaaatcct        641
Asp Ala Pro Thr Cys Ile Thr Thr Ala Glu Leu Ala
                170                 175
```

ttagacaata aga 654

<210> 2556
<211> 177
<212> PRT
<213> Corynebacterium glutamicum

<400> 2556
Met Lys Arg Ile Cys Ala Val Ala Ile Ser Ser Val Leu Leu Leu Ser
1 5 10 15

Gly Cys Ser Ser Thr Ser Thr Thr Gln Leu Glu Gly Phe Asp Gly Arg
20 25 30

Ser Ala Gln Glu Ile Ile Thr Glu Leu Asp Gln Thr Pro Val Ala Asp
35 40 45

Arg Ala Thr Asn Leu Met Ala Ser Ile Arg Ala Asp Glu Leu Ile Leu
50 55 60

Ser Asp Gln Ser Gly Gln Leu Ser Ile Asp Met Pro Ala Asp Glu Phe
65 70 75 80

Tyr Ile Ser Ala Ala Pro Tyr Thr Thr Thr Thr His Glu Cys Phe Tyr
85 90 95

His Ser Leu Thr Thr Cys Thr Gly Glu Leu Ala Asn Thr Pro Val Lys
100 105 110

Val Thr Val Val Ala Asp Asn Gly Glu Thr Ile Leu Glu Glu Asp Thr
115 120 125

Ile Thr Tyr Asp Asn Gly Phe Val Gly Met Trp Leu Pro Arg Asn Ile
130 135 140

Asp Ala Thr Leu Thr Ile Glu His Asp Gly Leu Lys Ser Thr Gln Pro
145 150 155 160

Ile Ser Thr Gly Asp Asp Ala Pro Thr Cys Ile Thr Thr Ala Glu Leu
165 170 175

Ala

<210> 2557
<211> 675
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(652)
<223> RXA02058

<400> 2557
gaagcggatt ttagtccttg cgcttggtgc ctcggtagcg ggatgctcaa cgctttccca 60

agaaccttca ccacctgttc cgttgggaaa cgttgatact gtg cag att gtc tct 115

```
                                                  Val Gln Ile Val Ser
                                                    1               5

ccc aat ggg gag att gag tct ttt gtg ctg ggg aag ctg tat gag acc   163
Pro Asn Gly Glu Ile Glu Ser Phe Val Leu Gly Lys Leu Tyr Glu Thr
                10                  15                  20

gca tta gtg gaa cgt ggc aga tct gca tca gtt cag ctg att gac ggc   211
Ala Leu Val Glu Arg Gly Arg Ser Ala Ser Val Gln Leu Ile Asp Gly
            25                  30                  35

gac ttg gat gag caa cta tct atg ctg cga gat gac agc act gat ttg   259
Asp Leu Asp Glu Gln Leu Ser Met Leu Arg Asp Asp Ser Thr Asp Leu
        40                  45                  50

gtg att gct tgc tca gga caa tta ctg gaa tat tac aac cca gat tta   307
Val Ile Ala Cys Ser Gly Gln Leu Leu Glu Tyr Tyr Asn Pro Asp Leu
    55                  60                  65

gcc tcc gag ttt gcc gtc gaa tac gct aat cag aca gcc ttt gat aaa   355
Ala Ser Glu Phe Ala Val Glu Tyr Ala Asn Gln Thr Ala Phe Asp Lys
70                  75                  80                  85

aac tct ggt gaa tgg cgc gaa aaa gtc tac gat gct ctc caa gga tcg   403
Asn Ser Gly Glu Trp Arg Glu Lys Val Tyr Asp Ala Leu Gln Gly Ser
                90                  95                  100

ctg ccg gac tcc atc gtg gcc acc gat cct tcc aat gct att ggt tgt   451
Leu Pro Asp Ser Ile Val Ala Thr Asp Pro Ser Asn Ala Ile Gly Cys
            105                 110                 115

aag gac gat acg tcg ctg cct caa aac atc gtg cca att tat aga aag   499
Lys Asp Asp Thr Ser Leu Pro Gln Asn Ile Val Pro Ile Tyr Arg Lys
        120                 125                 130

ccc aat ctg gat agg gac aat cgg gac acc ctg aac ttt gtg agc ggt   547
Pro Asn Leu Asp Arg Asp Asn Arg Asp Thr Leu Asn Phe Val Ser Gly
    135                 140                 145

tct ttg ggt aca agc gat ttg gaa gca ttg gtc aag gac gcc caa aca   595
Ser Leu Gly Thr Ser Asp Leu Glu Ala Leu Val Lys Asp Ala Gln Thr
150                 155                 160                 165

aca ggc aca acc tct gaa act gcg ctg gat ttc tta ttg tct aaa gga   643
Thr Gly Thr Thr Ser Glu Thr Ala Leu Asp Phe Leu Leu Ser Lys Gly
                170                 175                 180

ttt tca cgc tagttcagcc gtggtgatgc acg                             675
Phe Ser Arg
```

<210> 2558
<211> 184
<212> PRT
<213> Corynebacterium glutamicum

<400> 2558

```
Val Gln Ile Val Ser Pro Asn Gly Glu Ile Glu Ser Phe Val Leu Gly
  1               5                  10                  15
```

```
Lys Leu Tyr Glu Thr Ala Leu Val Glu Arg Gly Arg Ser Ala Ser Val
            20                  25                  30

Gln Leu Ile Asp Gly Asp Leu Asp Glu Gln Leu Ser Met Leu Arg Asp
        35                  40                  45

Asp Ser Thr Asp Leu Val Ile Ala Cys Ser Gly Gln Leu Leu Glu Tyr
    50                  55                  60

Tyr Asn Pro Asp Leu Ala Ser Glu Phe Ala Val Glu Tyr Ala Asn Gln
65                  70                  75                  80

Thr Ala Phe Asp Lys Asn Ser Gly Glu Trp Arg Glu Lys Val Tyr Asp
                85                  90                  95

Ala Leu Gln Gly Ser Leu Pro Asp Ser Ile Val Ala Thr Asp Pro Ser
            100                 105                 110

Asn Ala Ile Gly Cys Lys Asp Asp Thr Ser Leu Pro Gln Asn Ile Val
        115                 120                 125

Pro Ile Tyr Arg Lys Pro Asn Leu Asp Arg Asp Asn Arg Asp Thr Leu
    130                 135                 140

Asn Phe Val Ser Gly Ser Leu Gly Thr Ser Asp Leu Glu Ala Leu Val
145                 150                 155                 160

Lys Asp Ala Gln Thr Thr Gly Thr Thr Ser Glu Thr Ala Leu Asp Phe
                165                 170                 175

Leu Leu Ser Lys Gly Phe Ser Arg
            180
```

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<210> 2559
<211> 702
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(679)
<223> RXA02069

<400> 2559
cgccatctgc ttggtgccgt agctgtcgat gacttgctcg accacatgct gccagaagac 60

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tggcgcgacg ccggaatccg accaggaaag gagcacaccc atg gct gat ttc aac   115
                                            Met Ala Asp Phe Asn
                                              1               5

cgc tct gaa tta gac agc cca ctt ttt gga tcc cgc aaa cga ttt aaa   163
Arg Ser Glu Leu Asp Ser Pro Leu Phe Gly Ser Arg Lys Arg Phe Lys
                10                  15                  20

ttc gac gat gac acc att ggt gcc tac gcc gaa aaa gta gcc cgg ttc   211
Phe Asp Asp Asp Thr Ile Gly Ala Tyr Ala Glu Lys Val Ala Arg Phe
            25                  30                  35

ttt ggc acg gga cag tac ctg ttt tgg caa acc att ttc gtg gtg gtg   259
Phe Gly Thr Gly Gln Tyr Leu Phe Trp Gln Thr Ile Phe Val Val Val
```

```
         40                  45                  50

tgg att ttc ctc aac atc ggt ggt tgg gcc tgg agt tgg gac ccc tac   307
Trp Ile Phe Leu Asn Ile Gly Gly Trp Ala Trp Ser Trp Asp Pro Tyr
     55                  60                  65

cct ttc atc ctg ctc aac ctg gca ttc tcc acg cag gct gct tat gct   355
Pro Phe Ile Leu Leu Asn Leu Ala Phe Ser Thr Gln Ala Ala Tyr Ala
 70                  75                  80                  85

gct ccg ctg atc ctg ttg gcg caa aac cgt caa gaa gac cgc gat aag   403
Ala Pro Leu Ile Leu Leu Ala Gln Asn Arg Gln Glu Asp Arg Asp Lys
                 90                  95                 100

cac acc att ttg gcg gat cgt cgg cgt gct gaa gag aca aaa gcc gat   451
His Thr Ile Leu Ala Asp Arg Arg Arg Ala Glu Glu Thr Lys Ala Asp
            105                 110                 115

act gaa ttc ctc gca cgg gaa ctc gca ggc gtt cgc tta gcc ttg gga   499
Thr Glu Phe Leu Ala Arg Glu Leu Ala Gly Val Arg Leu Ala Leu Gly
        120                 125                 130

gat act gtc aca cgt gac tat ttg cgc cat gag tta gaa gat ctc cgc   547
Asp Thr Val Thr Arg Asp Tyr Leu Arg His Glu Leu Glu Asp Leu Arg
    135                 140                 145

gga ctt ctt gac cgc att gaa gcc aag ctc gac gac gag gca gcg tcc   595
Gly Leu Leu Asp Arg Ile Glu Ala Lys Leu Asp Asp Glu Ala Ala Ser
150                 155                 160                 165

cgt att gca gac cgc cac gaa cag cac gga tca gga cct caa gat ttg   643
Arg Ile Ala Asp Arg His Glu Gln His Gly Ser Gly Pro Gln Asp Leu
                170                 175                 180

tct gac ccc act cag ggt gat gtt gca gac gaa ttt tagggagtat        689
Ser Asp Pro Thr Gln Gly Asp Val Ala Asp Glu Phe
            185                 190

caaaacttgg gac                                                   702


<210> 2560
<211> 193
<212> PRT
<213> Corynebacterium glutamicum

<400> 2560
Met Ala Asp Phe Asn Arg Ser Glu Leu Asp Ser Pro Leu Phe Gly Ser
  1               5                  10                  15

Arg Lys Arg Phe Lys Phe Asp Asp Asp Thr Ile Gly Ala Tyr Ala Glu
             20                  25                  30

Lys Val Ala Arg Phe Phe Gly Thr Gly Gln Tyr Leu Phe Trp Gln Thr
         35                  40                  45

Ile Phe Val Val Val Trp Ile Phe Leu Asn Ile Gly Gly Trp Ala Trp
     50                  55                  60

Ser Trp Asp Pro Tyr Pro Phe Ile Leu Leu Asn Leu Ala Phe Ser Thr
 65                  70                  75                  80
```

```
Gln Ala Ala Tyr Ala Ala Pro Leu Ile Leu Leu Ala Gln Asn Arg Gln
                 85                  90                  95

Glu Asp Arg Asp Lys His Thr Ile Leu Ala Asp Arg Arg Arg Ala Glu
            100                 105                 110

Glu Thr Lys Ala Asp Thr Glu Phe Leu Ala Arg Glu Leu Ala Gly Val
        115                 120                 125

Arg Leu Ala Leu Gly Asp Thr Val Thr Arg Asp Tyr Leu Arg His Glu
    130                 135                 140

Leu Glu Asp Leu Arg Gly Leu Leu Asp Arg Ile Glu Ala Lys Leu Asp
145                 150                 155                 160

Asp Glu Ala Ala Ser Arg Ile Ala Asp Arg His Glu Gln His Gly Ser
                165                 170                 175

Gly Pro Gln Asp Leu Ser Asp Pro Thr Gln Gly Asp Val Ala Asp Glu
            180                 185                 190

Phe
```

Generated by PCGene

<210> 2561
<211> 1221
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1198)
<223> RXA02070

<400> 2561

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agcacggatc aggacctcaa gatttgtctg accccactca gggtgatgtt gcagacgaat 60

tttagggagt atcaaaactt gggactacta tcgatacgtg atg act caa gta acc   115
                                            Met Thr Gln Val Thr
                                              1               5

gaa tcc gct gtc cgc agc gcg cta tcc cgc gta gag gat cca gag atc   163
Glu Ser Ala Val Arg Ser Ala Leu Ser Arg Val Glu Asp Pro Glu Ile
                10                  15                  20

ggt aag ccc atc aca gag ctc ggc atg gtc aaa tca gtg tcc atc gac   211
Gly Lys Pro Ile Thr Glu Leu Gly Met Val Lys Ser Val Ser Ile Asp
            25                  30                  35

ggc tct gat gtc cag gtg gag gtc tac ctg acg atc gcg gct tgc ccg   259
Gly Ser Asp Val Gln Val Glu Val Tyr Leu Thr Ile Ala Ala Cys Pro
        40                  45                  50

atg aaa acc acc att gtc acc aac act gaa gca gct ctc aaa gac atc   307
Met Lys Thr Thr Ile Val Thr Asn Thr Glu Ala Ala Leu Lys Asp Ile
    55                  60                  65

gac ggg gtt ggc caa gtt cat gtc acc acc gat gtc atg agt gat gaa   355
Asp Gly Val Gly Gln Val His Val Thr Thr Asp Val Met Ser Asp Glu
```

```
 70                  75                  80                  85

cag cgc cgt gcg ctc cgc gtc tcc ctg cgc ggt gaa act tct gag cca   403
Gln Arg Arg Ala Leu Arg Val Ser Leu Arg Gly Glu Thr Ser Glu Pro
                90                  95                 100

gtg att cca ttc gct cag cct ggt tcc act acc cgc gtt tac gct gtt   451
Val Ile Pro Phe Ala Gln Pro Gly Ser Thr Thr Arg Val Tyr Ala Val
            105                 110                 115

gct tcc ggc aaa ggt ggc gta gga aaa tcc tcc atg acg gtg aac ttg   499
Ala Ser Gly Lys Gly Gly Val Gly Lys Ser Ser Met Thr Val Asn Leu
        120                 125                 130

gct gca gcc cta gcc aag cgc ggg ctg tct gtg gga att ttg gat gcc   547
Ala Ala Ala Leu Ala Lys Arg Gly Leu Ser Val Gly Ile Leu Asp Ala
    135                 140                 145

gat att tac gga cac tca gtg ccc gga atg ctc ggc tcg gac caa cgc   595
Asp Ile Tyr Gly His Ser Val Pro Gly Met Leu Gly Ser Asp Gln Arg
150                 155                 160                 165

cca cac cag gtc gat gac atg atc atg cct ccc cag gcg cac ggc gtg   643
Pro His Gln Val Asp Asp Met Ile Met Pro Pro Gln Ala His Gly Val
                170                 175                 180

aag atg ata tcc att gct cac ttc acc gaa gga aat gct cct gtg gtg   691
Lys Met Ile Ser Ile Ala His Phe Thr Glu Gly Asn Ala Pro Val Val
            185                 190                 195

tgg cgt gga cca atg ctg cac cgt gcc atc cag caa ttc ctc act gac   739
Trp Arg Gly Pro Met Leu His Arg Ala Ile Gln Gln Phe Leu Thr Asp
        200                 205                 210

gtg ttc tgg ggc gac ctg gat att ttg ctg ctg gat ctt cct cca gga   787
Val Phe Trp Gly Asp Leu Asp Ile Leu Leu Leu Asp Leu Pro Pro Gly
    215                 220                 225

act ggt gac atc gcc atc acc gtt gcc caa ttg atc ccg aat gct gag   835
Thr Gly Asp Ile Ala Ile Thr Val Ala Gln Leu Ile Pro Asn Ala Glu
230                 235                 240                 245

ttg ctc att gtg acc act cct cag gct gcc gca gct gag gtt gcc gag   883
Leu Leu Ile Val Thr Thr Pro Gln Ala Ala Ala Ala Glu Val Ala Glu
                250                 255                 260

cga gca gga acg atc tct gtg cag acc aac cag aag gtt gct ggc gtg   931
Arg Ala Gly Thr Ile Ser Val Gln Thr Asn Gln Lys Val Ala Gly Val
            265                 270                 275

att gaa aac atg tct gcc atg gtg ctt cct gat ggc acc acc atg gat   979
Ile Glu Asn Met Ser Ala Met Val Leu Pro Asp Gly Thr Thr Met Asp
        280                 285                 290

gtt ttc ggc acc ggc ggc ggt caa aag att gct gat cgt ctt acc gct   1027
Val Phe Gly Thr Gly Gly Gly Gln Lys Ile Ala Asp Arg Leu Thr Ala
    295                 300                 305

gtg aca ggt gaa gag gtc aag gtt atc gga tct gtt cca ttg gat ccg   1075
Val Thr Gly Glu Glu Val Lys Val Ile Gly Ser Val Pro Leu Asp Pro
310                 315                 320                 325
```

```
aac ctg cgt atc ggt ggc gat gtg gga aat cct att gcg att tct gaa   1123
Asn Leu Arg Ile Gly Gly Asp Val Gly Asn Pro Ile Ala Ile Ser Glu
                330                 335                 340

cca cac tcc cca acc gct gca gcg atc aat gag atc gct gaa cac cta   1171
Pro His Ser Pro Thr Ala Ala Ala Ile Asn Glu Ile Ala Glu His Leu
            345                 350                 355

gct cac cgc aag gta tcg ccc acc aaa tgacccagaa ccacaccgca         1218
Ala His Arg Lys Val Ser Pro Thr Lys
        360                 365

aac                                                              1221
```

<210> 2562
<211> 366
<212> PRT
<213> Corynebacterium glutamicum

<400> 2562

```
Met Thr Gln Val Thr Glu Ser Ala Val Arg Ser Ala Leu Ser Arg Val
  1               5                  10                  15

Glu Asp Pro Glu Ile Gly Lys Pro Ile Thr Glu Leu Gly Met Val Lys
             20                  25                  30

Ser Val Ser Ile Asp Gly Ser Asp Val Gln Val Glu Val Tyr Leu Thr
         35                  40                  45

Ile Ala Ala Cys Pro Met Lys Thr Thr Ile Val Thr Asn Thr Glu Ala
     50                  55                  60

Ala Leu Lys Asp Ile Asp Gly Val Gly Gln Val His Val Thr Thr Asp
 65                  70                  75                  80

Val Met Ser Asp Glu Gln Arg Arg Ala Leu Arg Val Ser Leu Arg Gly
                 85                  90                  95

Glu Thr Ser Glu Pro Val Ile Pro Phe Ala Gln Pro Gly Ser Thr Thr
            100                 105                 110

Arg Val Tyr Ala Val Ala Ser Gly Lys Gly Gly Val Gly Lys Ser Ser
        115                 120                 125

Met Thr Val Asn Leu Ala Ala Ala Leu Ala Lys Arg Gly Leu Ser Val
    130                 135                 140

Gly Ile Leu Asp Ala Asp Ile Tyr Gly His Ser Val Pro Gly Met Leu
145                 150                 155                 160

Gly Ser Asp Gln Arg Pro His Gln Val Asp Asp Met Ile Met Pro Pro
                165                 170                 175

Gln Ala His Gly Val Lys Met Ile Ser Ile Ala His Phe Thr Glu Gly
            180                 185                 190

Asn Ala Pro Val Val Trp Arg Gly Pro Met Leu His Arg Ala Ile Gln
        195                 200                 205
```

```
Gln Phe Leu Thr Asp Val Phe Trp Gly Asp Leu Asp Ile Leu Leu Leu
    210                 215                 220

Asp Leu Pro Pro Gly Thr Gly Asp Ile Ala Ile Thr Val Ala Gln Leu
225                 230                 235                 240

Ile Pro Asn Ala Glu Leu Leu Ile Val Thr Thr Pro Gln Ala Ala Ala
                245                 250                 255

Ala Glu Val Ala Glu Arg Ala Gly Thr Ile Ser Val Gln Thr Asn Gln
            260                 265                 270

Lys Val Ala Gly Val Ile Glu Asn Met Ser Ala Met Val Leu Pro Asp
        275                 280                 285

Gly Thr Thr Met Asp Val Phe Gly Thr Gly Gly Gly Gln Lys Ile Ala
    290                 295                 300

Asp Arg Leu Thr Ala Val Thr Gly Glu Glu Val Lys Val Ile Gly Ser
305                 310                 315                 320

Val Pro Leu Asp Pro Asn Leu Arg Ile Gly Gly Asp Val Gly Asn Pro
                325                 330                 335

Ile Ala Ile Ser Glu Pro His Ser Pro Thr Ala Ala Ala Ile Asn Glu
            340                 345                 350

Ile Ala Glu His Leu Ala His Arg Lys Val Ser Pro Thr Lys
        355                 360                 365


<210> 2563
<211> 930
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(907)
<223> RXA02080

<400> 2563
cgtaaattcg aagcgagctt ctaattctag caagcttggt gatggagtat cctgccaaaa 60

tttgtcctgt tgcttattgt gcaggaattc ggaggcggac atg tca atc gag tgg   115
                                              Met Ser Ile Glu Trp
                                                1               5

tta caa att gtt gaa tta gga gcg atc ttt ggt gca ggt ttc ctc gca   163
Leu Gln Ile Val Glu Leu Gly Ala Ile Phe Gly Ala Gly Phe Leu Ala
                10                  15                  20

gga agc atc aat gta att gtc gga gca gga aca tta gtg tcg ttt cct   211
Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr Leu Val Ser Phe Pro
            25                  30                  35

att ctc gtg ttc ctg ggc ctt cca ccg ttg act gcc acc atc gcc aac   259
Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr Ala Thr Ile Ala Asn
        40                  45                  50

acc atc ggc atc gtt cct gga agt att tcg ggt gtg gtt gct tat aga   307
```

```
Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly Val Val Ala Tyr Arg
     55                  60                  65

cgt gaa cta cac gcc cat gta aaa acc atc aga ttt ctg ctg cca gca   355
Arg Glu Leu His Ala His Val Lys Thr Ile Arg Phe Leu Leu Pro Ala
 70                  75                  80                  85

tca atc ctc gga ggg atc acc ggc gcc tcg ctc ttg ctg cat ttc tcc   403
Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu Leu Leu His Phe Ser
                 90                  95                 100

gca gat gtt ttt aca gca gta att ccc tgg ctg att gga ttc ggc acg   451
Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu Ile Gly Phe Gly Thr
            105                 110                 115

ctg ttg gtt atc gca ggt cca tca att aag aag cat gtt ggc gct cat   499
Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys His Val Gly Ala His
        120                 125                 130

act tca ggt ggc atc tct gct ggg ttt agg caa ttg cct ttc ccg agc   547
Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln Leu Pro Phe Pro Ser
    135                 140                 145

cga acc acc ttc atc gtc tca gta tgt ggt gcc ctg ttg ctg ggc atg   595
Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala Leu Leu Leu Gly Met
150                 155                 160                 165

tat gga ggg tac ttc agc gca gct caa ggc att ctt ctc atc gca ttg   643
Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile Leu Leu Ile Ala Leu
                170                 175                 180

ctt ggc atc aca tca acg ctg cag atg cag gaa ctc aac gcc atc aaa   691
Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu Leu Asn Ala Ile Lys
            185                 190                 195

aac ctc aca gtg gcg gca gtt aat ctc atc gca gcc agt gtt ttt ata   739
Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala Ala Ser Val Phe Ile
        200                 205                 210

atc atc tcc cct gag ttg atc tcc tgg ccg acc gtt gcc tta atc gcg   787
Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr Val Ala Leu Ile Ala
    215                 220                 225

ctt ggc tca gct tta ggt gga tac atc ggc gga cgg tac gcc cgc cga   835
Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly Arg Tyr Ala Arg Arg
230                 235                 240                 245

ctt cgc ccc agt gtt ttt aga gca ttt gtg gtc atc gtc gga atc acc   883
Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val Ile Val Gly Ile Thr
                250                 255                 260

acg gtc atc gtt atg acg atc ggt taatgcagca gactagtaac ccc         930
Thr Val Ile Val Met Thr Ile Gly
            265
```

<210> 2564
<211> 269
<212> PRT
<213> Corynebacterium glutamicum

<400> 2564
Met Ser Ile Glu Trp Leu Gln Ile Val Glu Leu Gly Ala Ile Phe Gly
1 5 10 15

Ala Gly Phe Leu Ala Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr
20 25 30

Leu Val Ser Phe Pro Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr
35 40 45

Ala Thr Ile Ala Asn Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly
50 55 60

Val Val Ala Tyr Arg Arg Glu Leu His Ala His Val Lys Thr Ile Arg
65 70 75 80

Phe Leu Leu Pro Ala Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu
85 90 95

Leu Leu His Phe Ser Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu
100 105 110

Ile Gly Phe Gly Thr Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys
115 120 125

His Val Gly Ala His Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln
130 135 140

Leu Pro Phe Pro Ser Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala
145 150 155 160

Leu Leu Leu Gly Met Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile
165 170 175

Leu Leu Ile Ala Leu Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu
180 185 190

Leu Asn Ala Ile Lys Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala
195 200 205

Ala Ser Val Phe Ile Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr
210 215 220

Val Ala Leu Ile Ala Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly
225 230 235 240

Arg Tyr Ala Arg Arg Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val
245 250 255

Ile Val Gly Ile Thr Thr Val Ile Val Met Thr Ile Gly
260 265

<210> 2565
<211> 1752
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1729)

<223> RXA02081

<400> 2565

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cctggatgat gtcactgtct taaatccggt atacgcagat gatttgtggg aagatccgga 60

agctcaacat aattttgcgg tgccaccggt acaaaaacat atg acg tta agt ggc   115
                                            Met Thr Leu Ser Gly
                                              1               5

ttg gag ctt tta gag ttc gag cgt cga aca gct gcg atg gaa acc agg   163
Leu Glu Leu Leu Glu Phe Glu Arg Arg Thr Ala Ala Met Glu Thr Arg
                 10                  15                  20

ctt ggt cgg cat aat cgg gga gcg ggt ggc gca ttt cct gag gcg gtg   211
Leu Gly Arg His Asn Arg Gly Ala Gly Gly Ala Phe Pro Glu Ala Val
             25                  30                  35

gtg tct cga agc gtg gag ttg cca ctt ttt gta cag gcc cgg aat ttc   259
Val Ser Arg Ser Val Glu Leu Pro Leu Phe Val Gln Ala Arg Asn Phe
         40                  45                  50

ctc aac aat cag cag atc aga gct caa gtg cat cgc cgt att ttg gag   307
Leu Asn Asn Gln Gln Ile Arg Ala Gln Val His Arg Arg Ile Leu Glu
     55                  60                  65

cag ctt cca acc gag gga gag att gtg ctg ttg ggg cac agt ttg ggg   355
Gln Leu Pro Thr Glu Gly Glu Ile Val Leu Leu Gly His Ser Leu Gly
 70                  75                  80                  85

tcg gta att gct gca gac ctt ttg agg cga ttg ccg cca gag ctt acg   403
Ser Val Ile Ala Ala Asp Leu Leu Arg Arg Leu Pro Pro Glu Leu Thr
                 90                  95                 100

gtg aag gga ttt gtc acc atc ggt agt ccg ttg gca aat ggt caa ttc   451
Val Lys Gly Phe Val Thr Ile Gly Ser Pro Leu Ala Asn Gly Gln Phe
            105                 110                 115

aat gtg gat gat ttg ttt aag ttg ctg cgc acg ccg ttg agc aat gtg   499
Asn Val Asp Asp Leu Phe Lys Leu Leu Arg Thr Pro Leu Ser Asn Val
        120                 125                 130

tcg tgg tgg gtg aat ttt tgg agt gga tct gat cct gtt gca gca aaa   547
Ser Trp Trp Val Asn Phe Trp Ser Gly Ser Asp Pro Val Ala Ala Lys
    135                 140                 145

cgc gga gtg tcg gtg gct gtt ccg tgg gta ttg gat ttt cgt gtg aaa   595
Arg Gly Val Ser Val Ala Val Pro Trp Val Leu Asp Phe Arg Val Lys
150                 155                 160                 165

acc tca ctg gtc cca ggc cct ggg cat tct tcg cgg gaa tac tgt gcc   643
Thr Ser Leu Val Pro Gly Pro Gly His Ser Ser Arg Glu Tyr Cys Ala
                170                 175                 180

aat gat gca gtg gcg gaa gca att ggg ttt ggg ctg ttc gga tcg cgc   691
Asn Asp Ala Val Ala Glu Ala Ile Gly Phe Gly Leu Phe Gly Ser Arg
            185                 190                 195

agc aaa gaa atc gtc ctt gcg gag aaa aat ctg cag att ccg ctc aat   739
Ser Lys Glu Ile Val Leu Ala Glu Lys Asn Leu Gln Ile Pro Leu Asn
        200                 205                 210
```

```
gac gcg gag att ttt gtg ctg cag gcg ctg cgt tat tgt tac ctc att   787
Asp Ala Glu Ile Phe Val Leu Gln Ala Leu Arg Tyr Cys Tyr Leu Ile
    215                 220                 225

ttg caa cgg ctc aaa ggc gat gaa gcc tta agg tat gag tac gca ctt   835
Leu Gln Arg Leu Lys Gly Asp Glu Ala Leu Arg Tyr Glu Tyr Ala Leu
230                 235                 240                 245

cgg gag act cag gat cgc ctg att gag gag att aaa tcc aga aac gcc   883
Arg Glu Thr Gln Asp Arg Leu Ile Glu Glu Ile Lys Ser Arg Asn Ala
                250                 255                 260

gaa gag ggc cgg ccg att ccg aag gaa atc gca cgc ctg gat ttt gat   931
Glu Glu Gly Arg Pro Ile Pro Lys Glu Ile Ala Arg Leu Asp Phe Asp
            265                 270                 275

aac ggt gat cca aac gca gca gct cct gtt cca ggt ttg agc cca ttt   979
Asn Gly Asp Pro Asn Ala Ala Ala Pro Val Pro Gly Leu Ser Pro Phe
        280                 285                 290

atg ccc aaa gag cag gca att gag cgg ctt tta gag atc att gga cag   1027
Met Pro Lys Glu Gln Ala Ile Glu Arg Leu Leu Glu Ile Ile Gly Gln
    295                 300                 305

aac ctg ctg ctg cct ttt gag atc gag gtg ccg gag aaa att cag cgg   1075
Asn Leu Leu Leu Pro Phe Glu Ile Glu Val Pro Glu Lys Ile Gln Arg
310                 315                 320                 325

gaa gca ctg agg gat ttc acg gcg gaa act caa ttg ggt tcc acc gtg   1123
Glu Ala Leu Arg Asp Phe Thr Ala Glu Thr Gln Leu Gly Ser Thr Val
                330                 335                 340

ggc gct gat att ttt gat gca ttg caa atg gct gtt ggg gtg gtg tcg   1171
Gly Ala Asp Ile Phe Asp Ala Leu Gln Met Ala Val Gly Val Val Ser
            345                 350                 355

gga agc gcg aag agc aat tgg cgc aaa tgg gga gcg ttt ggt gtg ggg   1219
Gly Ser Ala Lys Ser Asn Trp Arg Lys Trp Gly Ala Phe Gly Val Gly
        360                 365                 370

gct gca gct ttg acc gct gca acg ggt ggt ttg gct ttg gcg gct gtg   1267
Ala Ala Ala Leu Thr Ala Ala Thr Gly Gly Leu Ala Leu Ala Ala Val
    375                 380                 385

ccg act gtt gct gga gta gcc act gtt gcc tcg aca ctc gca gca ttt   1315
Pro Thr Val Ala Gly Val Ala Thr Val Ala Ser Thr Leu Ala Ala Phe
390                 395                 400                 405

ggt cca ggt ggg atg atg ggc ggt ttg gtc act gca gga aca ctg ctc   1363
Gly Pro Gly Gly Met Met Gly Gly Leu Val Thr Ala Gly Thr Leu Leu
                410                 415                 420

aca gtt ggt ggc ggc agt tta acc gct ggg gtg ttg agc tcg gtg aac   1411
Thr Val Gly Gly Gly Ser Leu Thr Ala Gly Val Leu Ser Ser Val Asn
            425                 430                 435

acc acg gaa gag atc gaa gcg ctc gtt gta cag aag cta agt ttg gct   1459
Thr Thr Glu Glu Ile Glu Ala Leu Val Val Gln Lys Leu Ser Leu Ala
        440                 445                 450

att ttg tgg cag cgc cat gag ata gat aga act cat gag gtg tgg gaa   1507
```

```
Ile Leu Trp Gln Arg His Glu Ile Asp Arg Thr His Glu Val Trp Glu
    455                 460                 465

gaa ttc gcg gag gca gaa cgt ctg att gtg cgg gag cac acg cgt gtg   1555
Glu Phe Ala Glu Ala Glu Arg Leu Ile Val Arg Glu His Thr Arg Val
470                 475                 480                 485

aaa aac gtg tcg gat agt tct tcg ccc att ttg aaa gct ttc gag cag   1603
Lys Asn Val Ser Asp Ser Ser Ser Pro Ile Leu Lys Ala Phe Glu Gln
                490                 495                 500

cag cgt tcg act att gag cgg gcg ttg aag tat ttg agc gat cat ggg   1651
Gln Arg Ser Thr Ile Glu Arg Ala Leu Lys Tyr Leu Ser Asp His Gly
            505                 510                 515

atg gaa cct ggc tgg ttt gaa gaa ctg gaa cca cca gcc cca aca ccg   1699
Met Glu Pro Gly Trp Phe Glu Glu Leu Glu Pro Pro Ala Pro Thr Pro
        520                 525                 530

ttt cta aaa ctg cgg gct aag aaa act gat taggagaaac acaatggaga     1749
Phe Leu Lys Leu Arg Ala Lys Lys Thr Asp
    535                 540

aag                                                               1752


<210> 2566
<211> 543
<212> PRT
<213> Corynebacterium glutamicum

<400> 2566
Met Thr Leu Ser Gly Leu Glu Leu Leu Glu Phe Glu Arg Arg Thr Ala
  1               5                  10                  15

Ala Met Glu Thr Arg Leu Gly Arg His Asn Arg Gly Ala Gly Gly Ala
             20                  25                  30

Phe Pro Glu Ala Val Val Ser Arg Ser Val Glu Leu Pro Leu Phe Val
         35                  40                  45

Gln Ala Arg Asn Phe Leu Asn Asn Gln Gln Ile Arg Ala Gln Val His
     50                  55                  60

Arg Arg Ile Leu Glu Gln Leu Pro Thr Glu Gly Glu Ile Val Leu Leu
 65                  70                  75                  80

Gly His Ser Leu Gly Ser Val Ile Ala Ala Asp Leu Leu Arg Arg Leu
                 85                  90                  95

Pro Pro Glu Leu Thr Val Lys Gly Phe Val Thr Ile Gly Ser Pro Leu
            100                 105                 110

Ala Asn Gly Gln Phe Asn Val Asp Asp Leu Phe Lys Leu Leu Arg Thr
        115                 120                 125

Pro Leu Ser Asn Val Ser Trp Trp Val Asn Phe Trp Ser Gly Ser Asp
    130                 135                 140

Pro Val Ala Ala Lys Arg Gly Val Ser Val Ala Val Pro Trp Val Leu
145                 150                 155                 160
```

```
Asp Phe Arg Val Lys Thr Ser Leu Val Pro Gly Pro Gly His Ser Ser
                165                 170                 175

Arg Glu Tyr Cys Ala Asn Asp Ala Val Ala Glu Ala Ile Gly Phe Gly
            180                 185                 190

Leu Phe Gly Ser Arg Ser Lys Glu Ile Val Leu Ala Glu Lys Asn Leu
        195                 200                 205

Gln Ile Pro Leu Asn Asp Ala Glu Ile Phe Val Leu Gln Ala Leu Arg
    210                 215                 220

Tyr Cys Tyr Leu Ile Leu Gln Arg Leu Lys Gly Asp Glu Ala Leu Arg
225                 230                 235                 240

Tyr Glu Tyr Ala Leu Arg Glu Thr Gln Asp Arg Leu Ile Glu Glu Ile
                245                 250                 255

Lys Ser Arg Asn Ala Glu Glu Gly Arg Pro Ile Pro Lys Glu Ile Ala
            260                 265                 270

Arg Leu Asp Phe Asp Asn Gly Asp Pro Asn Ala Ala Ala Pro Val Pro
        275                 280                 285

Gly Leu Ser Pro Phe Met Pro Lys Glu Gln Ala Ile Glu Arg Leu Leu
    290                 295                 300

Glu Ile Ile Gly Gln Asn Leu Leu Leu Pro Phe Glu Ile Glu Val Pro
305                 310                 315                 320

Glu Lys Ile Gln Arg Glu Ala Leu Arg Asp Phe Thr Ala Glu Thr Gln
                325                 330                 335

Leu Gly Ser Thr Val Gly Ala Asp Ile Phe Asp Ala Leu Gln Met Ala
            340                 345                 350

Val Gly Val Val Ser Gly Ser Ala Lys Ser Asn Trp Arg Lys Trp Gly
        355                 360                 365

Ala Phe Gly Val Gly Ala Ala Ala Leu Thr Ala Ala Thr Gly Gly Leu
    370                 375                 380

Ala Leu Ala Ala Val Pro Thr Val Ala Gly Val Ala Thr Val Ala Ser
385                 390                 395                 400

Thr Leu Ala Ala Phe Gly Pro Gly Gly Met Met Gly Gly Leu Val Thr
                405                 410                 415

Ala Gly Thr Leu Leu Thr Val Gly Gly Gly Ser Leu Thr Ala Gly Val
            420                 425                 430

Leu Ser Ser Val Asn Thr Thr Glu Glu Ile Glu Ala Leu Val Val Gln
        435                 440                 445

Lys Leu Ser Leu Ala Ile Leu Trp Gln Arg His Glu Ile Asp Arg Thr
    450                 455                 460

His Glu Val Trp Glu Glu Phe Ala Glu Ala Glu Arg Leu Ile Val Arg
465                 470                 475                 480
```

```
Glu His Thr Arg Val Lys Asn Val Ser Asp Ser Ser Ser Pro Ile Leu
                485                 490                 495

Lys Ala Phe Glu Gln Gln Arg Ser Thr Ile Glu Arg Ala Leu Lys Tyr
            500                 505                 510

Leu Ser Asp His Gly Met Glu Pro Gly Trp Phe Glu Glu Leu Glu Pro
        515                 520                 525

Pro Ala Pro Thr Pro Phe Leu Lys Leu Arg Ala Lys Lys Thr Asp
    530                 535                 540


<210> 2567
<211> 468
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(445)
<223> RXA02084

<400> 2567
cgttgatggt tgggtggtgg gtcacagttt agaaaaagtg acttcaaatc acgtcgaaaa 60

gaaattgaaa gtacttaaga aacatgtcac gctaggagac gtg ata atc att gca   115
                                            Val Ile Ile Ile Ala
                                              1               5

agc gtt gtt ttc ctc ctc gtt ggc gca atg ttg gcg aat gct gcc gct   163
Ser Val Val Phe Leu Leu Val Gly Ala Met Leu Ala Asn Ala Ala Ala
                10                  15                  20

gcg ctc ttt agt gcc agc gag cca ttc gga cga att tcc tac ctc att   211
Ala Leu Phe Ser Ala Ser Glu Pro Phe Gly Arg Ile Ser Tyr Leu Ile
            25                  30                  35

ggc cta cct aac gaa gac gac ttc gtg ccg tac tca cta cgg ttc gtg   259
Gly Leu Pro Asn Glu Asp Asp Phe Val Pro Tyr Ser Leu Arg Phe Val
        40                  45                  50

gcc ttt ttc cca ctg atg ctc tcc gca tcg atg gca gca tcc ttc ttc   307
Ala Phe Phe Pro Leu Met Leu Ser Ala Ser Met Ala Ala Ser Phe Phe
    55                  60                  65

ggg gtg tgg gca gta cta atc att cct ttc ggt tac ttc cca tca ctg   355
Gly Val Trp Ala Val Leu Ile Ile Pro Phe Gly Tyr Phe Pro Ser Leu
70                  75                  80                  85

atg atg gtt cat aag cac aac aag cag gta cag cga acc tgg gat tcc   403
Met Met Val His Lys His Asn Lys Gln Val Gln Arg Thr Trp Asp Ser
                90                  95                  100

gtc acc gtt gct gac ttc tac gag gat tcc acc cct ctg gtc           445
Val Thr Val Ala Asp Phe Tyr Glu Asp Ser Thr Pro Leu Val
            105                 110                 115

taatttcgat ttctaaatgt cat                                        468
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<210> 2568
<211> 115
<212> PRT
<213> Corynebacterium glutamicum

<400> 2568

```
Val Ile Ile Ile Ala Ser Val Val Phe Leu Leu Val Gly Ala Met Leu
  1               5                  10                  15

Ala Asn Ala Ala Ala Ala Leu Phe Ser Ala Ser Glu Pro Phe Gly Arg
             20                  25                  30

Ile Ser Tyr Leu Ile Gly Leu Pro Asn Glu Asp Asp Phe Val Pro Tyr
         35                  40                  45

Ser Leu Arg Phe Val Ala Phe Phe Pro Leu Met Leu Ser Ala Ser Met
     50                  55                  60

Ala Ala Ser Phe Phe Gly Val Trp Ala Val Leu Ile Ile Pro Phe Gly
 65                  70                  75                  80

Tyr Phe Pro Ser Leu Met Met Val His Lys His Asn Lys Gln Val Gln
                 85                  90                  95

Arg Thr Trp Asp Ser Val Thr Val Ala Asp Phe Tyr Glu Asp Ser Thr
            100                 105                 110

Pro Leu Val
        115
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<210> 2569
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(571)
<223> RXA02089

<400> 2569

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ctagctgacc agtattaata ccaataatag aacatattat cgaacaatgt cgcttgggtg 60

ctctacactt cccactatga tcaaacaccg aaaccgccta atg tct tcc atc tac   115
                                              Met Ser Ser Ile Tyr
                                                1               5

tcc gca act cgc tac gcc gcc cac ttc aaa agc gtc ttc ccc acc gcc   163
Ser Ala Thr Arg Tyr Ala Ala His Phe Lys Ser Val Phe Pro Thr Ala
                10                  15                  20

ctg gat gac att caa tcc atg atg cgc cac cct cga tca ctg gcc aga   211
Leu Asp Asp Ile Gln Ser Met Met Arg His Pro Arg Ser Leu Ala Arg
            25                  30                  35

gcc ata ccc acg tgg cgc ccg ccg agc atc ccg cta ccg tca ctt ccc   259
Ala Ile Pro Thr Trp Arg Pro Pro Ser Ile Pro Leu Pro Ser Leu Pro
        40                  45                  50

ggc gaa gat ccc ctc acc ctc acc ttg tca cgt cac cgc gca ggc ccc   307
```

```
Gly Glu Asp Pro Leu Thr Leu Thr Leu Ser Arg His Arg Ala Gly Pro
     55                  60                  65

gcc gcc cgc caa atc atc cgc gag ttc ggt gag caa cgt gaa ccc gcc   355
Ala Ala Arg Gln Ile Ile Arg Glu Phe Gly Glu Gln Arg Glu Pro Ala
 70                  75                  80                  85

tat ctc atc acc atc cgc atc acc agc cca gag ggc ttc aaa gta tcc   403
Tyr Leu Ile Thr Ile Arg Ile Thr Ser Pro Glu Gly Phe Lys Val Ser
                 90                  95                 100

acc cgc ctc gcc gaa ggc tgg atc cgc gca att ctc agc acc gcg cac   451
Thr Arg Leu Ala Glu Gly Trp Ile Arg Ala Ile Leu Ser Thr Ala His
            105                 110                 115

agc ggc act gtc cac cag ctc acc gat gag ccg gca ccg acg ttt tgc   499
Ser Gly Thr Val His Gln Leu Thr Asp Glu Pro Ala Pro Thr Phe Cys
        120                 125                 130

tgg ctt gtc gac gcc cac ttt gat ccg gtg cgt tcc cct tcc ttc ctt   547
Trp Leu Val Asp Ala His Phe Asp Pro Val Arg Ser Pro Ser Phe Leu
    135                 140                 145

ttc gaa tat tcc aaa agt gca gcc tagaaaatga cgaaaccctg gat         594
Phe Glu Tyr Ser Lys Ser Ala Ala
150                 155


<210> 2570
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 2570
Met Ser Ser Ile Tyr Ser Ala Thr Arg Tyr Ala Ala His Phe Lys Ser
  1               5                  10                  15

Val Phe Pro Thr Ala Leu Asp Asp Ile Gln Ser Met Met Arg His Pro
             20                  25                  30

Arg Ser Leu Ala Arg Ala Ile Pro Thr Trp Arg Pro Pro Ser Ile Pro
         35                  40                  45

Leu Pro Ser Leu Pro Gly Glu Asp Pro Leu Thr Leu Thr Leu Ser Arg
     50                  55                  60

His Arg Ala Gly Pro Ala Ala Arg Gln Ile Ile Arg Glu Phe Gly Glu
 65                  70                  75                  80

Gln Arg Glu Pro Ala Tyr Leu Ile Thr Ile Arg Ile Thr Ser Pro Glu
                 85                  90                  95

Gly Phe Lys Val Ser Thr Arg Leu Ala Glu Gly Trp Ile Arg Ala Ile
            100                 105                 110

Leu Ser Thr Ala His Ser Gly Thr Val His Gln Leu Thr Asp Glu Pro
        115                 120                 125

Ala Pro Thr Phe Cys Trp Leu Val Asp Ala His Phe Asp Pro Val Arg
    130                 135                 140
```

```
Ser Pro Ser Phe Leu Phe Glu Tyr Ser Lys Ser Ala Ala
145                 150                 155


<210> 2571
<211> 924
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(901)
<223> RXA02090

<400> 2571
aggtgaaagg ctaggcgcgg attcgttgtg gacgctaggc ttgtcggcag tgtctttggg 60

ggacgtcccc agcacaaacc agatggaagg tcatcagaac atg agc ttt ttt gag   115
                                            Met Ser Phe Phe Glu
                                              1               5

gac atc gcg gct gga ctt gat agt gac ggt atc gag tcc cgc gta aac   163
Asp Ile Ala Ala Gly Leu Asp Ser Asp Gly Ile Glu Ser Arg Val Asn
                 10                  15                  20

ggc gac aca atg ttc gtt ccg atc acc tct gac ttg gaa atc cag ttc   211
Gly Asp Thr Met Phe Val Pro Ile Thr Ser Asp Leu Glu Ile Gln Phe
             25                  30                  35

gtg gag atc gat tcc ctc cta cct gca gca aac gtt tat atc gct gca   259
Val Glu Ile Asp Ser Leu Leu Pro Ala Ala Asn Val Tyr Ile Ala Ala
         40                  45                  50

gcc aat gtt gat gaa gac gat gat gag ttc gag gca gtt ctc gtt tcg   307
Ala Asn Val Asp Glu Asp Asp Asp Glu Phe Glu Ala Val Leu Val Ser
     55                  60                  65

gtg gtg ttc tct gtt gag gat gct gtc gct gct gtc gca aag cat gtt   355
Val Val Phe Ser Val Glu Asp Ala Val Ala Ala Val Ala Lys His Val
 70                  75                  80                  85

gct act gat cag gtg gtg act gtg ctg cgt gat cta ctt gaa gga act   403
Ala Thr Asp Gln Val Val Thr Val Leu Arg Asp Leu Leu Glu Gly Thr
                 90                  95                 100

gat gaa cgc atc cag gat ttg gag ttt ttc cag gat gca gtg aat gca   451
Asp Glu Arg Ile Gln Asp Leu Glu Phe Phe Gln Asp Ala Val Asn Ala
            105                 110                 115

aat ttg gtt cgt gcg gaa gtc ggc cag aat tct gag ctt cag gtt ttg   499
Asn Leu Val Arg Ala Glu Val Gly Gln Asn Ser Glu Leu Gln Val Leu
        120                 125                 130

gtc gag gtt gaa gac ggc gtc cca acc gca acg gtc aat ttc atc gcg   547
Val Glu Val Glu Asp Gly Val Pro Thr Ala Thr Val Asn Phe Ile Ala
    135                 140                 145

atc ggt gag tcc ttt gaa gat ctg att gat cag gcc att gaa gaa ttg   595
Ile Gly Glu Ser Phe Glu Asp Leu Ile Asp Gln Ala Ile Glu Glu Leu
150                 155                 160                 165
```

```
tgg gaa tcc gac ggc gac gca gtt cta tcg gat gaa gat cgc caa cgc   643
Trp Glu Ser Asp Gly Asp Ala Val Leu Ser Asp Glu Asp Arg Gln Arg
                170                 175                 180

atg ttc gct gat ttg acc tcc gag ttg gaa ttt gtc act gat gaa gtc   691
Met Phe Ala Asp Leu Thr Ser Glu Leu Glu Phe Val Thr Asp Glu Val
            185                 190                 195

ctc gac ttg ggt acc ttc act gat ttt gat cga ctt ttc gat atc ctt   739
Leu Asp Leu Gly Thr Phe Thr Asp Phe Asp Arg Leu Phe Asp Ile Leu
        200                 205                 210

tcc ctc gcc gat gac cag gct gag gat tgg gaa gca cag ctc gtt cct   787
Ser Leu Ala Asp Asp Gln Ala Glu Asp Trp Glu Ala Gln Leu Val Pro
    215                 220                 225

ttt gag gac gag gaa ttt gat gag ccg gat gtt tat gac ctt ttc gtc   835
Phe Glu Asp Glu Glu Phe Asp Glu Pro Asp Val Tyr Asp Leu Phe Val
230                 235                 240                 245

gat gac tct gaa gaa gat gac gac gac ctc gat gat gac gag gac gat   883
Asp Asp Ser Glu Glu Asp Asp Asp Asp Leu Asp Asp Asp Glu Asp Asp
                250                 255                 260

gag gat gat gac gaa gac tagattttag cctttgtcgc ggt                924
Glu Asp Asp Asp Glu Asp
            265
```

<210> 2572
<211> 267
<212> PRT
<213> Corynebacterium glutamicum

<400> 2572

```
Met Ser Phe Phe Glu Asp Ile Ala Ala Gly Leu Asp Ser Asp Gly Ile
  1               5                  10                  15

Glu Ser Arg Val Asn Gly Asp Thr Met Phe Val Pro Ile Thr Ser Asp
             20                  25                  30

Leu Glu Ile Gln Phe Val Glu Ile Asp Ser Leu Leu Pro Ala Ala Asn
         35                  40                  45

Val Tyr Ile Ala Ala Ala Asn Val Asp Glu Asp Asp Asp Glu Phe Glu
     50                  55                  60

Ala Val Leu Val Ser Val Val Phe Ser Val Glu Asp Ala Val Ala Ala
 65                  70                  75                  80

Val Ala Lys His Val Ala Thr Asp Gln Val Val Thr Val Leu Arg Asp
                 85                  90                  95

Leu Leu Glu Gly Thr Asp Glu Arg Ile Gln Asp Leu Glu Phe Phe Gln
            100                 105                 110

Asp Ala Val Asn Ala Asn Leu Val Arg Ala Glu Val Gly Gln Asn Ser
        115                 120                 125

Glu Leu Gln Val Leu Val Glu Val Glu Asp Gly Val Pro Thr Ala Thr
    130                 135                 140
```

```
Val Asn Phe Ile Ala Ile Gly Glu Ser Phe Glu Asp Leu Ile Asp Gln
145                 150                 155                 160

Ala Ile Glu Glu Leu Trp Glu Ser Asp Gly Asp Ala Val Leu Ser Asp
                165                 170                 175

Glu Asp Arg Gln Arg Met Phe Ala Asp Leu Thr Ser Glu Leu Glu Phe
            180                 185                 190

Val Thr Asp Glu Val Leu Asp Leu Gly Thr Phe Thr Asp Phe Asp Arg
        195                 200                 205

Leu Phe Asp Ile Leu Ser Leu Ala Asp Asp Gln Ala Glu Asp Trp Glu
    210                 215                 220

Ala Gln Leu Val Pro Phe Glu Asp Glu Glu Phe Asp Glu Pro Asp Val
225                 230                 235                 240

Tyr Asp Leu Phe Val Asp Asp Ser Glu Glu Asp Asp Asp Asp Leu Asp
                245                 250                 255

Asp Asp Glu Asp Asp Glu Asp Asp Asp Glu Asp
            260                 265


<210> 2573
<211> 774
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(751)
<223> RXA02091

<400> 2573
agatctagcc aacgaacttg atttcatcga gccggaagag acagaagaag agcagcaatt 60

gaagtggctt agccttatgc agtttttttgg aagtagataa atg agc atc tgg aaa   115
                                            Met Ser Ile Trp Lys
                                              1               5

cgt ctg tta gtg cag tac ccg cgc ttc gcc gac acc ctc aca gcc ggc   163
Arg Leu Leu Val Gln Tyr Pro Arg Phe Ala Asp Thr Leu Thr Ala Gly
                  10                  15                  20

caa ccc atc acg ctc gag gaa tta gca acc ccg gaa gtg atc ttg gaa   211
Gln Pro Ile Thr Leu Glu Glu Leu Ala Thr Pro Glu Val Ile Leu Glu
              25                  30                  35

gct gtt gcc aaa ggc caa gaa att ttc ggc att gag cag cca aaa cat   259
Ala Val Ala Lys Gly Gln Glu Ile Phe Gly Ile Glu Gln Pro Lys His
          40                  45                  50

gca gca caa ctc tgg ttt cac tcc ctg tgc acc gca att gtc ggc ccc   307
Ala Ala Gln Leu Trp Phe His Ser Leu Cys Thr Ala Ile Val Gly Pro
      55                  60                  65

gcc gtc acc gcc atg gtg gaa ttc gat gtc atc ccc agc ctc gac ata   355
Ala Val Thr Ala Met Val Glu Phe Asp Val Ile Pro Ser Leu Asp Ile
```

```
 70                  75                  80                  85

cgt cga ggt cag ctg cat aac atc gac ggt tac tgg ttc ggc ttc agg   403
Arg Arg Gly Gln Leu His Asn Ile Asp Gly Tyr Trp Phe Gly Phe Arg
                 90                  95                 100

ccg gag gag atg ctt gtc gac gcc tcc ctc cac ctg tcg ggc acc caa   451
Pro Glu Glu Met Leu Val Asp Ala Ser Leu His Leu Ser Gly Thr Gln
            105                 110                 115

ttc ggc gag agt atc cgc gtg gtg att gat gca tta tgc gct gcc acg   499
Phe Gly Glu Ser Ile Arg Val Val Ile Asp Ala Leu Cys Ala Ala Thr
        120                 125                 130

gat ctg cga ccg gca ccc ctg tgg gcg gtt gcc tca gat gcg ttg gga   547
Asp Leu Arg Pro Ala Pro Leu Trp Ala Val Ala Ser Asp Ala Leu Gly
    135                 140                 145

atc gca gct agc ggc gca ggt gtc gag gcc ttt gaa gaa gaa cat gcc   595
Ile Ala Ala Ser Gly Ala Gly Val Glu Ala Phe Glu Glu Glu His Ala
150                 155                 160                 165

cgc gag gtg gcg gaa gcc ctc att gaa gga atg aat agt gtg aac tca   643
Arg Glu Val Ala Glu Ala Leu Ile Glu Gly Met Asn Ser Val Asn Ser
                170                 175                 180

gtt cca tcg ccg cgg ttt aac gac gac gat tat ttc att cga gct gga   691
Val Pro Ser Pro Arg Phe Asn Asp Asp Asp Tyr Phe Ile Arg Ala Gly
            185                 190                 195

tgc tgc atg att ttc cac tca cca cga gct gat ttt tgc acg tcg tgc   739
Cys Cys Met Ile Phe His Ser Pro Arg Ala Asp Phe Cys Thr Ser Cys
        200                 205                 210

cca cag aag agg tgaaaggcta ggcgcggatt cgt                        774
Pro Gln Lys Arg
    215
```

Sequence Listing - 2574 - 2574 - 2574 - 2574

<210> 2574
<211> 217
<212> PRT
<213> Corynebacterium glutamicum

<400> 2574

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Met Ser Ile Trp Lys Arg Leu Leu Val Gln Tyr Pro Arg Phe Ala Asp
  1               5                  10                  15

Thr Leu Thr Ala Gly Gln Pro Ile Thr Leu Glu Glu Leu Ala Thr Pro
             20                  25                  30

Glu Val Ile Leu Glu Ala Val Ala Lys Gly Gln Glu Ile Phe Gly Ile
         35                  40                  45

Glu Gln Pro Lys His Ala Ala Gln Leu Trp Phe His Ser Leu Cys Thr
     50                  55                  60

Ala Ile Val Gly Pro Ala Val Thr Ala Met Val Glu Phe Asp Val Ile
 65                  70                  75                  80

Pro Ser Leu Asp Ile Arg Arg Gly Gln Leu His Asn Ile Asp Gly Tyr
```

```
                85                  90                  95

Trp Phe Gly Phe Arg Pro Glu Glu Met Leu Val Asp Ala Ser Leu His
            100                 105                 110

Leu Ser Gly Thr Gln Phe Gly Glu Ser Ile Arg Val Val Ile Asp Ala
        115                 120                 125

Leu Cys Ala Ala Thr Asp Leu Arg Pro Ala Pro Leu Trp Ala Val Ala
    130                 135                 140

Ser Asp Ala Leu Gly Ile Ala Ala Ser Gly Ala Gly Val Glu Ala Phe
145                 150                 155                 160

Glu Glu Glu His Ala Arg Glu Val Ala Glu Ala Leu Ile Glu Gly Met
                165                 170                 175

Asn Ser Val Asn Ser Val Pro Ser Pro Arg Phe Asn Asp Asp Asp Tyr
            180                 185                 190

Phe Ile Arg Ala Gly Cys Cys Met Ile Phe His Ser Pro Arg Ala Asp
        195                 200                 205

Phe Cys Thr Ser Cys Pro Gln Lys Arg
    210                 215


<210> 2575
<211> 3495
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(3472)
<223> RXA02097

<400> 2575
ttggctacag atgtttcagc gcttgcagtg gggtagtgtg tttaaacatc acaattagtt 60

ctagaggaaa acgcattttt tgcgcgggga gagtgtatac atg ccg gct ggc atc   115
                                              Met Pro Ala Gly Ile
                                                1               5

gca gac atg aca gat tca ttg ctc gga tgg gca tca caa act gag ctg   163
Ala Asp Met Thr Asp Ser Leu Leu Gly Trp Ala Ser Gln Thr Glu Leu
                10                  15                  20

gat ctg aac cag cgt ctt gca ggg gta gag tac ttt cca caa att cag   211
Asp Leu Asn Gln Arg Leu Ala Gly Val Glu Tyr Phe Pro Gln Ile Gln
            25                  30                  35

ctg cga cac gat gag ctc gag cgc att cat cgg ttt tac ggc acc ttt   259
Leu Arg His Asp Glu Leu Glu Arg Ile His Arg Phe Tyr Gly Thr Phe
        40                  45                  50

ttg tcc cgc cag gta ggc gcg ggc gca agc ctt ggg gat ctt ttt gaa   307
Leu Ser Arg Gln Val Gly Ala Gly Ala Ser Leu Gly Asp Leu Phe Glu
    55                  60                  65

atg acc cca tgc ctg aca gtc acc acc ttg gtg tct cgg gcg tca cgg   355
```

```
Met Thr Pro Cys Leu Thr Val Thr Thr Leu Val Ser Arg Ala Ser Arg
 70                  75                  80                  85

atc agc gat cca gca gat ttc ttc ggt gaa tac atc gga gga ctg gga   403
Ile Ser Asp Pro Ala Asp Phe Phe Gly Glu Tyr Ile Gly Gly Leu Gly
                 90                  95                 100

ctt agc gca gaa cac gca gca gtt gtt gaa ggg ttg acc gaa aag ctc   451
Leu Ser Ala Glu His Ala Ala Val Val Glu Gly Leu Thr Glu Lys Leu
            105                 110                 115

ttc gca cag gct ggc ctg ctc gtt cct gag gga att gca tct cca ttg   499
Phe Ala Gln Ala Gly Leu Leu Val Pro Glu Gly Ile Ala Ser Pro Leu
        120                 125                 130

gag ttg tta tcc atc cac gca ggc att agt aac cac gaa gtg gcc gca   547
Glu Leu Leu Ser Ile His Ala Gly Ile Ser Asn His Glu Val Ala Ala
    135                 140                 145

gtg ctg acc gaa gtg gaa aac ggc acc acc gaa tat cca ttc atg ttc   595
Val Leu Thr Glu Val Glu Asn Gly Thr Thr Glu Tyr Pro Phe Met Phe
150                 155                 160                 165

gac gct gtc ctg cgc cta acc cct gag tgg gca cag acc ctt atc ggc   643
Asp Ala Val Leu Arg Leu Thr Pro Glu Trp Ala Gln Thr Leu Ile Gly
                170                 175                 180

gga gtt caa gaa ctc att gaa ttt gcc acc acc cac cga act tct tgg   691
Gly Val Gln Glu Leu Ile Glu Phe Ala Thr Thr His Arg Thr Ser Trp
            185                 190                 195

tca gac cgc cag cgc gaa tcc tca ctg cca gcc atg atc gat gag atc   739
Ser Asp Arg Gln Arg Glu Ser Ser Leu Pro Ala Met Ile Asp Glu Ile
        200                 205                 210

gtt gtg gcg gaa ctt cgg gaa cgc cca gtt ggt act gcc gac cgt gaa   787
Val Val Ala Glu Leu Arg Glu Arg Pro Val Gly Thr Ala Asp Arg Glu
    215                 220                 225

aac tcc gtt ggt gtg gca ctt cgt gag ctt cgc cca cgc ctc atc ctg   835
Asn Ser Val Gly Val Ala Leu Arg Glu Leu Arg Pro Arg Leu Ile Leu
230                 235                 240                 245

gat gca gaa cgc cgc aaa gtc tgc ctg cgt cta cct gaa cag cgc gtc   883
Asp Ala Glu Arg Arg Lys Val Cys Leu Arg Leu Pro Glu Gln Arg Val
                250                 255                 260

agc gac gat gaa atc aac tgg cga gtc agc cta gaa ggc acc acc cgg   931
Ser Asp Asp Glu Ile Asn Trp Arg Val Ser Leu Glu Gly Thr Thr Arg
            265                 270                 275

att ttc tcc acc cgc cga gca tgg ggc gat act tct gga tac tcc gaa   979
Ile Phe Ser Thr Arg Arg Ala Trp Gly Asp Thr Ser Gly Tyr Ser Glu
        280                 285                 290

gcc ctc gac atc act gtc gag cgt caa atc cgc gaa acc acc gtc acc   1027
Ala Leu Asp Ile Thr Val Glu Arg Gln Ile Arg Glu Thr Thr Val Thr
    295                 300                 305

gac acc tca aac caa atc acc tgg gtt gtc cca gtc gtg gac ttc aac   1075
Asp Thr Ser Asn Gln Ile Thr Trp Val Val Pro Val Val Asp Phe Asn
```

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310                 315                 320                 325

gac cca gtg ctg gtg ttt tcc gcg cgc ggt gaa aac ctc acc gac aag   1123
Asp Pro Val Leu Val Phe Ser Ala Arg Gly Glu Asn Leu Thr Asp Lys
                330                 335                 340

gtc tcc ctg cac cat caa gag att tac gtt ctc gcg cca gcg gaa gca   1171
Val Ser Leu His His Gln Glu Ile Tyr Val Leu Ala Pro Ala Glu Ala
            345                 350                 355

aaa ctc gaa gac atg gtc act ggc cag cca gta cca gtt att gag caa   1219
Lys Leu Glu Asp Met Val Thr Gly Gln Pro Val Pro Val Ile Glu Gln
        360                 365                 370

ttc ctc gta gag ggc tgg aac tca tgg gtg tgc tcc cgc gtg gac gcc   1267
Phe Leu Val Glu Gly Trp Asn Ser Trp Val Cys Ser Arg Val Asp Ala
    375                 380                 385

cgt ggc ctg tcc tct ctg aag gtc aac aaa gaa gtc cga tgc att gac   1315
Arg Gly Leu Ser Ser Leu Lys Val Asn Lys Glu Val Arg Cys Ile Asp
390                 395                 400                 405

cca cgt cga cgc gtt gcc ttc cac cac cca gcc gaa ttg gtc cct cac   1363
Pro Arg Arg Arg Val Ala Phe His His Pro Ala Glu Leu Val Pro His
                410                 415                 420

gta cga tcc att tcc gga ctc ccc gta cac gcg cag tcc ctg atc gcc   1411
Val Arg Ser Ile Ser Gly Leu Pro Val His Ala Gln Ser Leu Ile Ala
            425                 430                 435

gag ttc cca cca acc ctg agc gga caa gac gaa acc tgg atg ctc tcc   1459
Glu Phe Pro Pro Thr Leu Ser Gly Gln Asp Glu Thr Trp Met Leu Ser
        440                 445                 450

atc tcg gct ttc gca ggt gta ggc gct gct ggt gaa gaa atc gcc gag   1507
Ile Ser Ala Phe Ala Gly Val Gly Ala Ala Gly Glu Glu Ile Ala Glu
    455                 460                 465

cca gag cct ttg gaa gtc cct gcc gac ggt ggc ctt ttc gcc atc ttc   1555
Pro Glu Pro Leu Glu Val Pro Ala Asp Gly Gly Leu Phe Ala Ile Phe
470                 475                 480                 485

gac cca gaa ata tac gac gcc cca tgg gtg ggt gaa tac ctg gtc cga   1603
Asp Pro Glu Ile Tyr Asp Ala Pro Trp Val Gly Glu Tyr Leu Val Arg
                490                 495                 500

ctc cgc ggc cca cgc aat gaa tcc ttc cga ccc gaa ttc gcc atc gtc   1651
Leu Arg Gly Pro Arg Asn Glu Ser Phe Arg Pro Glu Phe Ala Ile Val
            505                 510                 515

gaa gac atg acc acc gaa ttc gaa gtc gcc tca ggt gca tca ttt cga   1699
Glu Asp Met Thr Thr Glu Phe Glu Val Ala Ser Gly Ala Ser Phe Arg
        520                 525                 530

atc cca acc acc act ggt ctc agc gaa gcc agc cta cgc gtg cgt tcc   1747
Ile Pro Thr Thr Thr Gly Leu Ser Glu Ala Ser Leu Arg Val Arg Ser
    535                 540                 545

ggt gaa aag cac ttc acc gca gag cca cgc ctg gtc acc gtt gaa gca   1795
Gly Glu Lys His Phe Thr Ala Glu Pro Arg Leu Val Thr Val Glu Ala
550                 555                 560                 565
```

```
acc gac ccc aac gca tca ttc gtg gtc acc acc gat gaa ggc gat caa   1843
Thr Asp Pro Asn Ala Ser Phe Val Val Thr Thr Asp Glu Gly Asp Gln
                570                 575                 580

atg cca ttg cga ttt gtg cca cca caa atc gcc atc gaa ctt cca ctg   1891
Met Pro Leu Arg Phe Val Pro Pro Gln Ile Ala Ile Glu Leu Pro Leu
            585                 590                 595

acc acc gag cca cca acc tgg cgc gtc acc cgt act gtc tgt gga cca   1939
Thr Thr Glu Pro Pro Thr Trp Arg Val Thr Arg Thr Val Cys Gly Pro
        600                 605                 610

cgc gac ctc gac ggt gca ggc gaa ctc cgc atc cgc acc ggt gtc gat   1987
Arg Asp Leu Asp Gly Ala Gly Glu Leu Arg Ile Arg Thr Gly Val Asp
    615                 620                 625

gtc ggc gat cca aag gtc agt gtg cgc aac cac cac ggt tca cca ctg   2035
Val Gly Asp Pro Lys Val Ser Val Arg Asn His His Gly Ser Pro Leu
630                 635                 640                 645

cga acc gtg aaa atg gtc acc cct gac aac ggc cgt acc tgg att gcc   2083
Arg Thr Val Lys Met Val Thr Pro Asp Asn Gly Arg Thr Trp Ile Ala
                650                 655                 660

agc atg aag gaa atc gca gcc agt acc ttt gtg atg cca cgc gga tcc   2131
Ser Met Lys Glu Ile Ala Ala Ser Thr Phe Val Met Pro Arg Gly Ser
            665                 670                 675

atc gaa ttt gag tgg act gac cgc aag gtt gac cgt cgc gtt tcc gtg   2179
Ile Glu Phe Glu Trp Thr Asp Arg Lys Val Asp Arg Arg Val Ser Val
        680                 685                 690

acg att gct gtc att gac aaa act gag aac ttt act ggc atc acc atc   2227
Thr Ile Ala Val Ile Asp Lys Thr Glu Asn Phe Thr Gly Ile Thr Ile
    695                 700                 705

gaa gat gga aag ctc gta ttc gaa gaa ctc gca gcc ggt cgc caa ctc   2275
Glu Asp Gly Lys Leu Val Phe Glu Glu Leu Ala Ala Gly Arg Gln Leu
710                 715                 720                 725

gct gca tgg gtg tgg cca caa acc gca ccg tgg gta agc gca gtg gaa   2323
Ala Ala Trp Val Trp Pro Gln Thr Ala Pro Trp Val Ser Ala Val Glu
                730                 735                 740

ctt gct gtc acc gga cca gag ctg gaa ctc cct gaa gtt ctc gtc ggc   2371
Leu Ala Val Thr Gly Pro Glu Leu Glu Leu Pro Glu Val Leu Val Gly
            745                 750                 755

gca ggc aac ctg att gtt caa ctc cac acc gct gac cca ttc act acc   2419
Ala Gly Asn Leu Ile Val Gln Leu His Thr Ala Asp Pro Phe Thr Thr
        760                 765                 770

tcc gtg acc cca ctg tca cca gga aaa gct gcg gtc acc gtt gag caa   2467
Ser Val Thr Pro Leu Ser Pro Gly Lys Ala Ala Val Thr Val Glu Gln
    775                 780                 785

gaa ggc tac tac tca gca caa acc gaa gaa tat gca cag ctt tca gca   2515
Glu Gly Tyr Tyr Ser Ala Gln Thr Glu Glu Tyr Ala Gln Leu Ser Ala
790                 795                 800                 805
```

```
ttc ttc ggt ggg gaa gta gaa gaa cca cca atc agt gac gct gtg gtc   2563
Phe Phe Gly Gly Glu Val Glu Glu Pro Pro Ile Ser Asp Ala Val Val
                810                 815                 820

ccc gca ctt tgg gat gtt tcc cat atc tgg acc gaa cag gga aac acc   2611
Pro Ala Leu Trp Asp Val Ser His Ile Trp Thr Glu Gln Gly Asn Thr
            825                 830                 835

gag cat ctt cca gta gtc cat gcc gcc ctg cgc tcc tca cca gcc gca   2659
Glu His Leu Pro Val Val His Ala Ala Leu Arg Ser Ser Pro Ala Ala
        840                 845                 850

gca ctg aag ggt ctg tcc gct tcg ctg gtt ccc gca cag gca cta cct   2707
Ala Leu Lys Gly Leu Ser Ala Ser Leu Val Pro Ala Gln Ala Leu Pro
    855                 860                 865

gga aaa gtc att tcc tcc gga ctg gca gcc tca ccg ttc acc acg gaa   2755
Gly Lys Val Ile Ser Ser Gly Leu Ala Ala Ser Pro Phe Thr Thr Glu
870                 875                 880                 885

tca cca gca aca gaa gtg cac cgc acc gca tgg atc gga acc ctg caa   2803
Ser Pro Ala Thr Glu Val His Arg Thr Ala Trp Ile Gly Thr Leu Gln
                890                 895                 900

ctc ctg ggt gca ctg cca agc gca ttc aag gaa gcc gaa gag ctt ggc   2851
Leu Leu Gly Ala Leu Pro Ser Ala Phe Lys Glu Ala Glu Glu Leu Gly
            905                 910                 915

aac cgc aca cca ctg ctg cca atc ctc gga caa ctt gag gaa gtc gcc   2899
Asn Arg Thr Pro Leu Leu Pro Ile Leu Gly Gln Leu Glu Glu Val Ala
        920                 925                 930

ggc aag aac atc ctg tcc acc ctt gca act ggc cgt gac tcc act ttg   2947
Gly Lys Asn Ile Leu Ser Thr Leu Ala Thr Gly Arg Asp Ser Thr Leu
    935                 940                 945

gac acc gca tgc atc gac caa tcc acc gtt gcg att gcc ggc atg aac   2995
Asp Thr Ala Cys Ile Asp Gln Ser Thr Val Ala Ile Ala Gly Met Asn
950                 955                 960                 965

gaa acc cag caa aaa gcc ctg ctg gac atg ttc ttc agc aac gcc gac   3043
Glu Thr Gln Gln Lys Ala Leu Leu Asp Met Phe Phe Ser Asn Ala Asp
                970                 975                 980

atc gtt cct gga cca cta atg gaa gac aac acc cgc ctc atg gca gtg   3091
Ile Val Pro Gly Pro Leu Met Glu Asp Asn Thr Arg Leu Met Ala Val
            985                 990                 995

ttc gaa acc ttc aag aag cgc gat gca ctc cgt gag gtt ctc cag act   3139
Phe Glu Thr Phe Lys Lys Arg Asp Ala Leu Arg Glu Val Leu Gln Thr
        1000                1005                1010

gaa ggc ttg att aag acc gct gta gaa ctt ctt cgt gcc atg cgt gga   3187
Glu Gly Leu Ile Lys Thr Ala Val Glu Leu Leu Arg Ala Met Arg Gly
    1015                1020                1025

acc cag cgt cag ctg tat tcc tcc gca cgt att cga ttc gac aag ctc   3235
Thr Gln Arg Gln Leu Tyr Ser Ser Ala Arg Ile Arg Phe Asp Lys Leu
1030                1035                1040                1045

gat ggt gtc aac act gac aac cca gaa aac atg tgg gca ctc acc cca   3283
```

```
Asp Gly Val Asn Thr Asp Asn Pro Glu Asn Met Trp Ala Leu Thr Pro
                1050                1055                1060

gtt gtg tca ctg gtg ttc gcg ttg tca tcc cgt ttg cat gca cac gaa   3331
Val Val Ser Leu Val Phe Ala Leu Ser Ser Arg Leu His Ala His Glu
            1065                1070                1075

ttg atc ggc aag acc cga act ctc gat cgt gca tct gcc ggt tgg ggt   3379
Leu Ile Gly Lys Thr Arg Thr Leu Asp Arg Ala Ser Ala Gly Trp Gly
        1080                1085                1090

cga atc gct gat ctg gtg cca gac ctt gtc acc ggt gac ttg atc tcc   3427
Arg Ile Ala Asp Leu Val Pro Asp Leu Val Thr Gly Asp Leu Ile Ser
    1095                1100                1105

gcg gag gca atg gtt ttg gga gct cga aac cca gga ctc gtc gat       3472
Ala Glu Ala Met Val Leu Gly Ala Arg Asn Pro Gly Leu Val Asp
1110                1115                1120

tagtccctga tttcatcgga ggg                                        3495


<210> 2576
<211> 1124
<212> PRT
<213> Corynebacterium glutamicum

<400> 2576
Met Pro Ala Gly Ile Ala Asp Met Thr Asp Ser Leu Leu Gly Trp Ala
  1               5                  10                  15

Ser Gln Thr Glu Leu Asp Leu Asn Gln Arg Leu Ala Gly Val Glu Tyr
             20                  25                  30

Phe Pro Gln Ile Gln Leu Arg His Asp Glu Leu Glu Arg Ile His Arg
         35                  40                  45

Phe Tyr Gly Thr Phe Leu Ser Arg Gln Val Gly Ala Gly Ala Ser Leu
     50                  55                  60

Gly Asp Leu Phe Glu Met Thr Pro Cys Leu Thr Val Thr Thr Leu Val
 65                  70                  75                  80

Ser Arg Ala Ser Arg Ile Ser Asp Pro Ala Asp Phe Phe Gly Glu Tyr
                 85                  90                  95

Ile Gly Gly Leu Gly Leu Ser Ala Glu His Ala Ala Val Val Glu Gly
            100                 105                 110

Leu Thr Glu Lys Leu Phe Ala Gln Ala Gly Leu Leu Val Pro Glu Gly
        115                 120                 125

Ile Ala Ser Pro Leu Glu Leu Leu Ser Ile His Ala Gly Ile Ser Asn
    130                 135                 140

His Glu Val Ala Ala Val Leu Thr Glu Val Glu Asn Gly Thr Thr Glu
145                 150                 155                 160

Tyr Pro Phe Met Phe Asp Ala Val Leu Arg Leu Thr Pro Glu Trp Ala
                165                 170                 175
```

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Gln Thr Leu Ile Gly Gly Val Gln Glu Leu Ile Glu Phe Ala Thr Thr
            180                 185                 190

His Arg Thr Ser Trp Ser Asp Arg Gln Arg Glu Ser Ser Leu Pro Ala
        195                 200                 205

Met Ile Asp Glu Ile Val Val Ala Glu Leu Arg Glu Arg Pro Val Gly
    210                 215                 220

Thr Ala Asp Arg Glu Asn Ser Val Gly Val Ala Leu Arg Glu Leu Arg
225                 230                 235                 240

Pro Arg Leu Ile Leu Asp Ala Glu Arg Arg Lys Val Cys Leu Arg Leu
                245                 250                 255

Pro Glu Gln Arg Val Ser Asp Asp Glu Ile Asn Trp Arg Val Ser Leu
            260                 265                 270

Glu Gly Thr Thr Arg Ile Phe Ser Thr Arg Arg Ala Trp Gly Asp Thr
        275                 280                 285

Ser Gly Tyr Ser Glu Ala Leu Asp Ile Thr Val Glu Arg Gln Ile Arg
    290                 295                 300

Glu Thr Thr Val Thr Asp Thr Ser Asn Gln Ile Thr Trp Val Val Pro
305                 310                 315                 320

Val Val Asp Phe Asn Asp Pro Val Leu Val Phe Ser Ala Arg Gly Glu
                325                 330                 335

Asn Leu Thr Asp Lys Val Ser Leu His His Gln Glu Ile Tyr Val Leu
            340                 345                 350

Ala Pro Ala Glu Ala Lys Leu Glu Asp Met Val Thr Gly Gln Pro Val
        355                 360                 365

Pro Val Ile Glu Gln Phe Leu Val Glu Gly Trp Asn Ser Trp Val Cys
    370                 375                 380

Ser Arg Val Asp Ala Arg Gly Leu Ser Ser Leu Lys Val Asn Lys Glu
385                 390                 395                 400

Val Arg Cys Ile Asp Pro Arg Arg Arg Val Ala Phe His His Pro Ala
                405                 410                 415

Glu Leu Val Pro His Val Arg Ser Ile Ser Gly Leu Pro Val His Ala
            420                 425                 430

Gln Ser Leu Ile Ala Glu Phe Pro Pro Thr Leu Ser Gly Gln Asp Glu
        435                 440                 445

Thr Trp Met Leu Ser Ile Ser Ala Phe Ala Gly Val Gly Ala Ala Gly
    450                 455                 460

Glu Glu Ile Ala Glu Pro Glu Pro Leu Glu Val Pro Ala Asp Gly Gly
465                 470                 475                 480

Leu Phe Ala Ile Phe Asp Pro Glu Ile Tyr Asp Ala Pro Trp Val Gly
                485                 490                 495

Glu Tyr Leu Val Arg Leu Arg Gly Pro Arg Asn Glu Ser Phe Arg Pro
```

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            500                 505                 510

Glu Phe Ala Ile Val Glu Asp Met Thr Thr Glu Phe Glu Val Ala Ser
        515                 520                 525

Gly Ala Ser Phe Arg Ile Pro Thr Thr Thr Gly Leu Ser Glu Ala Ser
    530                 535                 540

Leu Arg Val Arg Ser Gly Glu Lys His Phe Thr Ala Glu Pro Arg Leu
545                 550                 555                 560

Val Thr Val Glu Ala Thr Asp Pro Asn Ala Ser Phe Val Val Thr Thr
                565                 570                 575

Asp Glu Gly Asp Gln Met Pro Leu Arg Phe Val Pro Pro Gln Ile Ala
            580                 585                 590

Ile Glu Leu Pro Leu Thr Thr Glu Pro Pro Thr Trp Arg Val Thr Arg
        595                 600                 605

Thr Val Cys Gly Pro Arg Asp Leu Asp Gly Ala Gly Glu Leu Arg Ile
    610                 615                 620

Arg Thr Gly Val Asp Val Gly Asp Pro Lys Val Ser Val Arg Asn His
625                 630                 635                 640

His Gly Ser Pro Leu Arg Thr Val Lys Met Val Thr Pro Asp Asn Gly
                645                 650                 655

Arg Thr Trp Ile Ala Ser Met Lys Glu Ile Ala Ala Ser Thr Phe Val
            660                 665                 670

Met Pro Arg Gly Ser Ile Glu Phe Glu Trp Thr Asp Arg Lys Val Asp
        675                 680                 685

Arg Arg Val Ser Val Thr Ile Ala Val Ile Asp Lys Thr Glu Asn Phe
    690                 695                 700

Thr Gly Ile Thr Ile Glu Asp Gly Lys Leu Val Phe Glu Glu Leu Ala
705                 710                 715                 720

Ala Gly Arg Gln Leu Ala Ala Trp Val Trp Pro Gln Thr Ala Pro Trp
                725                 730                 735

Val Ser Ala Val Glu Leu Ala Val Thr Gly Pro Glu Leu Glu Leu Pro
            740                 745                 750

Glu Val Leu Val Gly Ala Gly Asn Leu Ile Val Gln Leu His Thr Ala
        755                 760                 765

Asp Pro Phe Thr Thr Ser Val Thr Pro Leu Ser Pro Gly Lys Ala Ala
    770                 775                 780

Val Thr Val Glu Gln Glu Gly Tyr Tyr Ser Ala Gln Thr Glu Glu Tyr
785                 790                 795                 800

Ala Gln Leu Ser Ala Phe Phe Gly Gly Glu Val Glu Glu Pro Pro Ile
                805                 810                 815

Ser Asp Ala Val Val Pro Ala Leu Trp Asp Val Ser His Ile Trp Thr
            820                 825                 830
```

```
Glu Gln Gly Asn Thr Glu His Leu Pro Val Val His Ala Ala Leu Arg
        835                 840                 845

Ser Ser Pro Ala Ala Ala Leu Lys Gly Leu Ser Ala Ser Leu Val Pro
    850                 855                 860

Ala Gln Ala Leu Pro Gly Lys Val Ile Ser Ser Gly Leu Ala Ala Ser
865                 870                 875                 880

Pro Phe Thr Thr Glu Ser Pro Ala Thr Glu Val His Arg Thr Ala Trp
                885                 890                 895

Ile Gly Thr Leu Gln Leu Leu Gly Ala Leu Pro Ser Ala Phe Lys Glu
            900                 905                 910

Ala Glu Glu Leu Gly Asn Arg Thr Pro Leu Leu Pro Ile Leu Gly Gln
        915                 920                 925

Leu Glu Glu Val Ala Gly Lys Asn Ile Leu Ser Thr Leu Ala Thr Gly
    930                 935                 940

Arg Asp Ser Thr Leu Asp Thr Ala Cys Ile Asp Gln Ser Thr Val Ala
945                 950                 955                 960

Ile Ala Gly Met Asn Glu Thr Gln Gln Lys Ala Leu Leu Asp Met Phe
                965                 970                 975

Phe Ser Asn Ala Asp Ile Val Pro Gly Pro Leu Met Glu Asp Asn Thr
            980                 985                 990

Arg Leu Met Ala Val Phe Glu Thr Phe Lys Lys Arg Asp Ala Leu Arg
        995                 1000                1005

Glu Val Leu Gln Thr Glu Gly Leu Ile Lys Thr Ala Val Glu Leu Leu
    1010                1015                1020

Arg Ala Met Arg Gly Thr Gln Arg Gln Leu Tyr Ser Ser Ala Arg Ile
1025                1030                1035                1040

Arg Phe Asp Lys Leu Asp Gly Val Asn Thr Asp Asn Pro Glu Asn Met
                1045                1050                1055

Trp Ala Leu Thr Pro Val Val Ser Leu Val Phe Ala Leu Ser Ser Arg
            1060                1065                1070

Leu His Ala His Glu Leu Ile Gly Lys Thr Arg Thr Leu Asp Arg Ala
        1075                1080                1085

Ser Ala Gly Trp Gly Arg Ile Ala Asp Leu Val Pro Asp Leu Val Thr
    1090                1095                1100

Gly Asp Leu Ile Ser Ala Glu Ala Met Val Leu Gly Ala Arg Asn Pro
1105                1110                1115                1120

Gly Leu Val Asp
```

<210> 2577
<211> 1281

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1258)
<223> RXA02102

<400> 2577
cggtaaaacg tcccgctagt gcgatggaat ctgtgtcggg gactaaaaca tcaaactgaa 60

tcttcggcat aacaccacag tagacaatag ccttggtgtt atg act agc ccc cat 115
Met Thr Ser Pro His
1 5

tct ttt tct gtc acc ccc att cgc acc atg gct gac ggc acg atc aaa 163
Ser Phe Ser Val Thr Pro Ile Arg Thr Met Ala Asp Gly Thr Ile Lys
10 15 20

cag att cac cct ttc aca ggc acc gaa gtg tgg acg gtc cct ggg cgt 211
Gln Ile His Pro Phe Thr Gly Thr Glu Val Trp Thr Val Pro Gly Arg
25 30 35

gga aat cga cct ctg tca cat ccc gct tct acg atc gtc gaa cta tct 259
Gly Asn Arg Pro Leu Ser His Pro Ala Ser Thr Ile Val Glu Leu Ser
40 45 50

gca cac gat cac acc tct tac tgt gca ttt tgt tcc gac aat atg ctc 307
Ala His Asp His Thr Ser Tyr Cys Ala Phe Cys Ser Asp Asn Met Leu
55 60 65

tcc act ccg cct gag aaa tcg cgc atc atc att gat agc tcc ggc gac 355
Ser Thr Pro Pro Glu Lys Ser Arg Ile Ile Ile Asp Ser Ser Gly Asp
70 75 80 85

ttt gac atc ctt ccc gga gca ttg cct ggt gag ctt tca gaa acc act 403
Phe Asp Ile Leu Pro Gly Ala Leu Pro Gly Glu Leu Ser Glu Thr Thr
90 95 100

ccg gaa ttt cga cga gtc ccc aat ctg ttt gag att gtc tct ttt gac 451
Pro Glu Phe Arg Arg Val Pro Asn Leu Phe Glu Ile Val Ser Phe Asp
105 110 115

tac tgg cac cag aat ttt ggt ttc gat atg gat tca gaa acc gcc atg 499
Tyr Trp His Gln Asn Phe Gly Phe Asp Met Asp Ser Glu Thr Ala Met
120 125 130

cgc atg gcg caa tac ttg gcg att cca gaa ggt cgc gaa cat gtt tta 547
Arg Met Ala Gln Tyr Leu Ala Ile Pro Glu Gly Arg Glu His Val Leu
135 140 145

gcc att gtg cgc acc cga ctt tct gcc gct ggt gaa gat ccc gcg cac 595
Ala Ile Val Arg Thr Arg Leu Ser Ala Ala Gly Glu Asp Pro Ala His
150 155 160 165

atg acc gat ggc gag ttg tta gaa aaa gct ccc agc tac ttt gct ggt 643
Met Thr Asp Gly Glu Leu Leu Glu Lys Ala Pro Ser Tyr Phe Ala Gly
170 175 180

ggt cat gac gtc atc atc gga cgc cga cac ttt gtc gat gac gca acc 691
Gly His Asp Val Ile Ile Gly Arg Arg His Phe Val Asp Asp Ala Thr

```
            185                 190                 195

acc agt gat caa ttg gcc tca tct gga aca ctg acc gtt aaa gag cat   739
Thr Ser Asp Gln Leu Ala Ser Ser Gly Thr Leu Thr Val Lys Glu His
        200                 205                 210

gag gcg ttc atc cgc ctg act gtc gat ggc atc agg gat ttg tac cac   787
Glu Ala Phe Ile Arg Leu Thr Val Asp Gly Ile Arg Asp Leu Tyr His
    215                 220                 225

cgc aac cgt tac gca ccg tat gta gtg gcg ttt caa aac tgg ttg aaa   835
Arg Asn Arg Tyr Ala Pro Tyr Val Val Ala Phe Gln Asn Trp Leu Lys
230                 235                 240                 245

ccc gcc ggc gcg tct ttt gac cat ctt cat aaa cag ctc gtc gcc att   883
Pro Ala Gly Ala Ser Phe Asp His Leu His Lys Gln Leu Val Ala Ile
                250                 255                 260

gat gaa cgc ggc cga ctt att gcc gat gaa ctg cat cat cta cgt ggc   931
Asp Glu Arg Gly Arg Leu Ile Ala Asp Glu Leu His His Leu Arg Gly
            265                 270                 275

aat ccc aat atg tac aac gaa ctt gct gtt gat tac gcc gga tac cac   979
Asn Pro Asn Met Tyr Asn Glu Leu Ala Val Asp Tyr Ala Gly Tyr His
        280                 285                 290

aac ctg atc atc gcg gaa aac gat cac gcc gtg gcc ttc gca ggt ttc  1027
Asn Leu Ile Ile Ala Glu Asn Asp His Ala Val Ala Phe Ala Gly Phe
    295                 300                 305

ggt cac cgc tac ccc acc att gag att tac tct aag tcc gct att cct  1075
Gly His Arg Tyr Pro Thr Ile Glu Ile Tyr Ser Lys Ser Ala Ile Pro
310                 315                 320                 325

gaa ccc tgg ctt caa agc gac gag gaa atc caa gcg atg agc aac ctc  1123
Glu Pro Trp Leu Gln Ser Asp Glu Glu Ile Gln Ala Met Ser Asn Leu
                330                 335                 340

atc cat gca tgc cat gct gca acc ggc gca gat gta ccc tgc aat gag  1171
Ile His Ala Cys His Ala Ala Thr Gly Ala Asp Val Pro Cys Asn Glu
            345                 350                 355

gga tgg gta cac aaa cca atc gat gtt gat atg cca atg ccc tgg cat  1219
Gly Trp Val His Lys Pro Ile Asp Val Asp Met Pro Met Pro Trp His
        360                 365                 370

gtg atg atc aaa tgg cgt gtt tct acc ctg gca ggt ttt tgaaggtggc  1268
Val Met Ile Lys Trp Arg Val Ser Thr Leu Ala Gly Phe
    375                 380                 385

accaaggtgt atc                                                 1281


<210> 2578
<211> 386
<212> PRT
<213> Corynebacterium glutamicum

<400> 2578
Met Thr Ser Pro His Ser Phe Ser Val Thr Pro Ile Arg Thr Met Ala
  1               5                  10                  15
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```
Asp Gly Thr Ile Lys Gln Ile His Pro Phe Thr Gly Thr Glu Val Trp
            20                  25                  30

Thr Val Pro Gly Arg Gly Asn Arg Pro Leu Ser His Pro Ala Ser Thr
        35                  40                  45

Ile Val Glu Leu Ser Ala His Asp His Thr Ser Tyr Cys Ala Phe Cys
    50                  55                  60

Ser Asp Asn Met Leu Ser Thr Pro Pro Glu Lys Ser Arg Ile Ile Ile
65                  70                  75                  80

Asp Ser Ser Gly Asp Phe Asp Ile Leu Pro Gly Ala Leu Pro Gly Glu
                85                  90                  95

Leu Ser Glu Thr Thr Pro Glu Phe Arg Arg Val Pro Asn Leu Phe Glu
            100                 105                 110

Ile Val Ser Phe Asp Tyr Trp His Gln Asn Phe Gly Phe Asp Met Asp
        115                 120                 125

Ser Glu Thr Ala Met Arg Met Ala Gln Tyr Leu Ala Ile Pro Glu Gly
    130                 135                 140

Arg Glu His Val Leu Ala Ile Val Arg Thr Arg Leu Ser Ala Ala Gly
145                 150                 155                 160

Glu Asp Pro Ala His Met Thr Asp Gly Glu Leu Leu Glu Lys Ala Pro
                165                 170                 175

Ser Tyr Phe Ala Gly Gly His Asp Val Ile Ile Gly Arg Arg His Phe
            180                 185                 190

Val Asp Asp Ala Thr Thr Ser Asp Gln Leu Ala Ser Ser Gly Thr Leu
        195                 200                 205

Thr Val Lys Glu His Glu Ala Phe Ile Arg Leu Thr Val Asp Gly Ile
    210                 215                 220

Arg Asp Leu Tyr His Arg Asn Arg Tyr Ala Pro Tyr Val Val Ala Phe
225                 230                 235                 240

Gln Asn Trp Leu Lys Pro Ala Gly Ala Ser Phe Asp His Leu His Lys
                245                 250                 255

Gln Leu Val Ala Ile Asp Glu Arg Gly Arg Leu Ile Ala Asp Glu Leu
            260                 265                 270

His His Leu Arg Gly Asn Pro Asn Met Tyr Asn Glu Leu Ala Val Asp
        275                 280                 285

Tyr Ala Gly Tyr His Asn Leu Ile Ile Ala Glu Asn Asp His Ala Val
    290                 295                 300

Ala Phe Ala Gly Phe Gly His Arg Tyr Pro Thr Ile Glu Ile Tyr Ser
305                 310                 315                 320

Lys Ser Ala Ile Pro Glu Pro Trp Leu Gln Ser Asp Glu Glu Ile Gln
                325                 330                 335
```

```
Ala Met Ser Asn Leu Ile His Ala Cys His Ala Ala Thr Gly Ala Asp
            340                 345                 350

Val Pro Cys Asn Glu Gly Trp Val His Lys Pro Ile Asp Val Asp Met
        355                 360                 365

Pro Met Pro Trp His Val Met Ile Lys Trp Arg Val Ser Thr Leu Ala
    370                 375                 380

Gly Phe
385
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<210> 2579
<211> 519
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(496)
<223> RXA02103

<400> 2579

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gaatctgttt gatcgtgccg tcagccatgg tgcgaatggg ggtgacagaa aaagaatggg 60

ggctagtcat aacaccaagg ctattgtcta ctgtggtgtt atg ccg aag att cag   115
                                              Met Pro Lys Ile Gln
                                                1               5

ttt gat gtt tta gtc ccc gac aca gat tcc atc gca cta gcg gga cgt   163
Phe Asp Val Leu Val Pro Asp Thr Asp Ser Ile Ala Leu Ala Gly Arg
                10                  15                  20

ttt acc gta gtc gcc aac ctt ttg atc gaa aaa ggc ctc atg gat cat   211
Phe Thr Val Val Ala Asn Leu Leu Ile Glu Lys Gly Leu Met Asp His
            25                  30                  35

ggc gtt gtt gtc cat gat cca gca gcg aaa atc gca gaa gct gtg gaa   259
Gly Val Val Val His Asp Pro Ala Ala Lys Ile Ala Glu Ala Val Glu
        40                  45                  50

gag cag ctt cgc cag act tac cgc gac gag cat gaa gat gca gac ttg   307
Glu Gln Leu Arg Gln Thr Tyr Arg Asp Glu His Glu Asp Ala Asp Leu
    55                  60                  65

gaa gaa tcc tcg gtc aac cgt tac ctc att gaa gtt gat gga gtt aaa   355
Glu Glu Ser Ser Val Asn Arg Tyr Leu Ile Glu Val Asp Gly Val Lys
70                  75                  80                  85

ggc tcc gtt aac caa gtg acc atg att ttt gcc cgt ttg ctc acc ccg   403
Gly Ser Val Asn Gln Val Thr Met Ile Phe Ala Arg Leu Leu Thr Pro
                90                  95                  100

cca gca gag ttg cca aag gac gct ttc ctc ctg gag cag gaa ctt gcc   451
Pro Ala Glu Leu Pro Lys Asp Ala Phe Leu Leu Glu Gln Glu Leu Ala
            105                 110                 115

tat gaa gtt cct gca gtc tac cca tgg act gtg gag atc ctt cgc       496
Tyr Glu Val Pro Ala Val Tyr Pro Trp Thr Val Glu Ile Leu Arg
        120                 125                 130
```

tagttttgag ctacgtattc ttg 519

<210> 2580
<211> 132
<212> PRT
<213> Corynebacterium glutamicum

<400> 2580
Met Pro Lys Ile Gln Phe Asp Val Leu Val Pro Asp Thr Asp Ser Ile
1 5 10 15

Ala Leu Ala Gly Arg Phe Thr Val Val Ala Asn Leu Leu Ile Glu Lys
20 25 30

Gly Leu Met Asp His Gly Val Val Val His Asp Pro Ala Ala Lys Ile
35 40 45

Ala Glu Ala Val Glu Glu Gln Leu Arg Gln Thr Tyr Arg Asp Glu His
50 55 60

Glu Asp Ala Asp Leu Glu Glu Ser Ser Val Asn Arg Tyr Leu Ile Glu
65 70 75 80

Val Asp Gly Val Lys Gly Ser Val Asn Gln Val Thr Met Ile Phe Ala
85 90 95

Arg Leu Leu Thr Pro Pro Ala Glu Leu Pro Lys Asp Ala Phe Leu Leu
100 105 110

Glu Gln Glu Leu Ala Tyr Glu Val Pro Ala Val Tyr Pro Trp Thr Val
115 120 125

Glu Ile Leu Arg
130

<210> 2581
<211> 1044
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1021)
<223> RXA02109

<400> 2581
gactctaagg gaagtgtttc gcttcaaccc gtacaggtct aatatgtcgg gagtcttgtt 60

ttaagctctt atataacctg tataggaaag cgaaaacctc atg ctt gca gtg cta 115
Met Leu Ala Val Leu
1 5

ttc ggg gtg gtg gcc ggt gcc atc atg cct ttc caa act tcg gtg aat 163
Phe Gly Val Val Ala Gly Ala Ile Met Pro Phe Gln Thr Ser Val Asn
10 15 20

aat aga ttg cgt cag tcc gtg gga gca cca ctg ctg gcg tct ttt att 211
Asn Arg Leu Arg Gln Ser Val Gly Ala Pro Leu Leu Ala Ser Phe Ile

```
                25                  30                  35

tcc ttt ttg gta gga act ttt tca ctc ctg gtt gca acg tgg atc acc   259
Ser Phe Leu Val Gly Thr Phe Ser Leu Leu Val Ala Thr Trp Ile Thr
         40                  45                  50

agt ggg cac ccg tat cct gct cta gga aat aca act ggc caa ccg tgg   307
Ser Gly His Pro Tyr Pro Ala Leu Gly Asn Thr Thr Gly Gln Pro Trp
     55                  60                  65

tgg att ttc acc ggt ggc atg ttg ggt gtt gtg ctg ctg acg gga aac   355
Trp Ile Phe Thr Gly Gly Met Leu Gly Val Val Leu Leu Thr Gly Asn
 70                  75                  80                  85

att ttg ctg ttt ccc cga gtc ggc agc gtg cag acc gtt att ttg ccc   403
Ile Leu Leu Phe Pro Arg Val Gly Ser Val Gln Thr Val Ile Leu Pro
                90                  95                 100

atc tcc gga cag atc atc atg ggc cta att atc gat aca act ggc ctg   451
Ile Ser Gly Gln Ile Ile Met Gly Leu Ile Ile Asp Thr Thr Gly Leu
            105                 110                 115

gca cat tcg cct caa gca ccg tta acc ctg ttc aga gta ttg ggt gct   499
Ala His Ser Pro Gln Ala Pro Leu Thr Leu Phe Arg Val Leu Gly Ala
        120                 125                 130

gct gcg gta ctt gtt gga tcg ctg gcc gca gtg gga gtg ttc tct aag   547
Ala Ala Val Leu Val Gly Ser Leu Ala Ala Val Gly Val Phe Ser Lys
    135                 140                 145

aaa aac atc gga cag acc caa tcc caa ggt gcc tcc att tgg ttg tgg   595
Lys Asn Ile Gly Gln Thr Gln Ser Gln Gly Ala Ser Ile Trp Leu Trp
150                 155                 160                 165

cgc ctc ttc gga gtg gtg atg ggc atg tgc caa gca acc cag gtt gca   643
Arg Leu Phe Gly Val Val Met Gly Met Cys Gln Ala Thr Gln Val Ala
                170                 175                 180

gtc aat ggt tac ttg gga act gtc cta gga tcc ccc att gag tca gca   691
Val Asn Gly Tyr Leu Gly Thr Val Leu Gly Ser Pro Ile Glu Ser Ala
            185                 190                 195

ctg gtg tct ttc gct gtt ggc acc acc gcg ctg ttt att ctg ctg ttg   739
Leu Val Ser Phe Ala Val Gly Thr Thr Ala Leu Phe Ile Leu Leu Leu
        200                 205                 210

gtc acc cga acc aag tgg cgt gga atc aac ggc gct ggg aag aaa aac   787
Val Thr Arg Thr Lys Trp Arg Gly Ile Asn Gly Ala Gly Lys Lys Asn
    215                 220                 225

cca tgg tgg atg tgg atc ggt ggc gtc atc ggc gcg act gtt att ttc   835
Pro Trp Trp Met Trp Ile Gly Gly Val Ile Gly Ala Thr Val Ile Phe
230                 235                 240                 245

agt act gct tac ctg gga ccg atc att ggc act ggt gtt acc gtg gtg   883
Ser Thr Ala Tyr Leu Gly Pro Ile Ile Gly Thr Gly Val Thr Val Val
                250                 255                 260

gtt atg ttg ctg ggc atg atg ttg gcc agc ctg atg atc gac gct ttt   931
Val Met Leu Leu Gly Met Met Leu Ala Ser Leu Met Ile Asp Ala Phe
            265                 270                 275
```

```
gga atc ctt ggc agc ccg cgc cgc cac att cac atc gcg cag ctt ctc   979
Gly Ile Leu Gly Ser Pro Arg Arg His Ile His Ile Ala Gln Leu Leu
        280                 285                 290

ggg ctc gtg gtg atc atc ctc ggc gta aca atg atc aga atc           1021
Gly Leu Val Val Ile Ile Leu Gly Val Thr Met Ile Arg Ile
    295                 300                 305

taaaccaaga atctaaacca aga                                        1044
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<210> 2582
<211> 307
<212> PRT
<213> Corynebacterium glutamicum

<400> 2582

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Met Leu Ala Val Leu Phe Gly Val Val Ala Gly Ala Ile Met Pro Phe
  1               5                  10                  15

Gln Thr Ser Val Asn Asn Arg Leu Arg Gln Ser Val Gly Ala Pro Leu
             20                  25                  30

Leu Ala Ser Phe Ile Ser Phe Leu Val Gly Thr Phe Ser Leu Leu Val
         35                  40                  45

Ala Thr Trp Ile Thr Ser Gly His Pro Tyr Pro Ala Leu Gly Asn Thr
     50                  55                  60

Thr Gly Gln Pro Trp Trp Ile Phe Thr Gly Gly Met Leu Gly Val Val
 65                  70                  75                  80

Leu Leu Thr Gly Asn Ile Leu Leu Phe Pro Arg Val Gly Ser Val Gln
                 85                  90                  95

Thr Val Ile Leu Pro Ile Ser Gly Gln Ile Ile Met Gly Leu Ile Ile
            100                 105                 110

Asp Thr Thr Gly Leu Ala His Ser Pro Gln Ala Pro Leu Thr Leu Phe
        115                 120                 125

Arg Val Leu Gly Ala Ala Ala Val Leu Val Gly Ser Leu Ala Ala Val
    130                 135                 140

Gly Val Phe Ser Lys Lys Asn Ile Gly Gln Thr Gln Ser Gln Gly Ala
145                 150                 155                 160

Ser Ile Trp Leu Trp Arg Leu Phe Gly Val Val Met Gly Met Cys Gln
                165                 170                 175

Ala Thr Gln Val Ala Val Asn Gly Tyr Leu Gly Thr Val Leu Gly Ser
            180                 185                 190

Pro Ile Glu Ser Ala Leu Val Ser Phe Ala Val Gly Thr Thr Ala Leu
        195                 200                 205

Phe Ile Leu Leu Leu Val Thr Arg Thr Lys Trp Arg Gly Ile Asn Gly
    210                 215                 220

Ala Gly Lys Lys Asn Pro Trp Trp Met Trp Ile Gly Gly Val Ile Gly
```

```
225                 230                 235                 240

Ala Thr Val Ile Phe Ser Thr Ala Tyr Leu Gly Pro Ile Ile Gly Thr
                245                 250                 255

Gly Val Thr Val Val Val Met Leu Leu Gly Met Met Leu Ala Ser Leu
            260                 265                 270

Met Ile Asp Ala Phe Gly Ile Leu Gly Ser Pro Arg Arg His Ile His
        275                 280                 285

Ile Ala Gln Leu Leu Gly Leu Val Val Ile Ile Leu Gly Val Thr Met
    290                 295                 300

Ile Arg Ile
305
```

<210> 2583
<211> 597
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(574)
<223> RXA02117

<400> 2583

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tgaacacaaa ctaccacgtt tattgcatca tgcaacaccc ttgctaggat ataaaatact 60

ctatgagtcc agacgttttt aaagggagcg aattaccata gtg tct aca gat cca   115
                                              Val Ser Thr Asp Pro
                                                1               5

gaa gag ttc gac caa gct gaa acc ctc gat caa ctc gcg tat gag atc   163
Glu Glu Phe Asp Gln Ala Glu Thr Leu Asp Gln Leu Ala Tyr Glu Ile
                10                  15                  20

atc ctg ctc acc cgg tat ggt gtc caa aac aca ccg acc aac aag cgc   211
Ile Leu Leu Thr Arg Tyr Gly Val Gln Asn Thr Pro Thr Asn Lys Arg
            25                  30                  35

gaa gcc atc atg gat cgc agc gcc ctc atc ttg ctc acc cgc ctt gac   259
Glu Ala Ile Met Asp Arg Ser Ala Leu Ile Leu Leu Thr Arg Leu Asp
        40                  45                  50

gct caa gga cct atg aca gtt aat gag cta gct gaa agc ttt gga ctt   307
Ala Gln Gly Pro Met Thr Val Asn Glu Leu Ala Glu Ser Phe Gly Leu
    55                  60                  65

aac gtt tct acc gtg cac cgc caa ctc aaa gca gcc att gcc aat ggc   355
Asn Val Ser Thr Val His Arg Gln Leu Lys Ala Ala Ile Ala Asn Gly
70                  75                  80                  85

tta att gaa gtc gtc gat gat caa gca tgc ccc gct aaa ctt cat cgt   403
Leu Ile Glu Val Val Asp Asp Gln Ala Cys Pro Ala Lys Leu His Arg
                90                  95                  100

cca act gag ttg ggt aaa gaa aaa ctg cag cag gag ctt ctt gcc cgc   451
Pro Thr Glu Leu Gly Lys Glu Lys Leu Gln Gln Glu Leu Leu Ala Arg
```

```
            105                 110                 115

cag cag gat ctc acc cgc att ctt cat gat tgg gat gag gaa gac att   499
Gln Gln Asp Leu Thr Arg Ile Leu His Asp Trp Asp Glu Glu Asp Ile
        120                 125                 130

aaa acg cat gcc aag cta ttg cgg aag cac aat gaa agc ttg gaa gaa   547
Lys Thr His Ala Lys Leu Leu Arg Lys His Asn Glu Ser Leu Glu Glu
    135                 140                 145

tac ctc gat atg aag tgg ccc cgc ccc taagtgccca taaacgcacc        594
Tyr Leu Asp Met Lys Trp Pro Arg Pro
150                 155

tct                                                              597


<210> 2584
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 2584
Val Ser Thr Asp Pro Glu Glu Phe Asp Gln Ala Glu Thr Leu Asp Gln
  1               5                  10                  15

Leu Ala Tyr Glu Ile Ile Leu Leu Thr Arg Tyr Gly Val Gln Asn Thr
             20                  25                  30

Pro Thr Asn Lys Arg Glu Ala Ile Met Asp Arg Ser Ala Leu Ile Leu
         35                  40                  45

Leu Thr Arg Leu Asp Ala Gln Gly Pro Met Thr Val Asn Glu Leu Ala
     50                  55                  60

Glu Ser Phe Gly Leu Asn Val Ser Thr Val His Arg Gln Leu Lys Ala
 65                  70                  75                  80

Ala Ile Ala Asn Gly Leu Ile Glu Val Val Asp Asp Gln Ala Cys Pro
                 85                  90                  95

Ala Lys Leu His Arg Pro Thr Glu Leu Gly Lys Glu Lys Leu Gln Gln
            100                 105                 110

Glu Leu Leu Ala Arg Gln Gln Asp Leu Thr Arg Ile Leu His Asp Trp
        115                 120                 125

Asp Glu Glu Asp Ile Lys Thr His Ala Lys Leu Leu Arg Lys His Asn
    130                 135                 140

Glu Ser Leu Glu Glu Tyr Leu Asp Met Lys Trp Pro Arg Pro
145                 150                 155


<210> 2585
<211> 1494
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
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<222> (101)..(1471)
<223> RXA02123

<400> 2585
ggattgagtc ttttcggcag ctgcgtgtga acccggcttc atgacatgca gcatacctgt 60

gcgaaaaatt cctgaccgcc cacttaaaaa aaggtctagg gtg tgg ggt gtg agt 115
Val Trp Gly Val Ser
1 5

ctt cca cca aat gta caa act gtc ggt gag ctg aag gcc gcc ggc cac 163
Leu Pro Pro Asn Val Gln Thr Val Gly Glu Leu Lys Ala Ala Gly His
10 15 20

atc tac cga cct ttg cgc gta gaa atc cgc gac aac ctc cta gcc aaa 211
Ile Tyr Arg Pro Leu Arg Val Glu Ile Arg Asp Asn Leu Leu Ala Lys
25 30 35

ctt cgc agc ggc gaa gat ccg tgg cca ggc ctg cac ggc ctg aac tac 259
Leu Arg Ser Gly Glu Asp Pro Trp Pro Gly Leu His Gly Leu Asn Tyr
40 45 50

acg gtc atc cgg cag ctt gaa cgc gcg ctc atc gcc ggc cac gac atc 307
Thr Val Ile Arg Gln Leu Glu Arg Ala Leu Ile Ala Gly His Asp Ile
55 60 65

gtg ctg ctc ggc gaa cgc ggc cag ggt aaa acc cgc ctg ctc cgc acg 355
Val Leu Leu Gly Glu Arg Gly Gln Gly Lys Thr Arg Leu Leu Arg Thr
70 75 80 85

tta ata acg ctt ctc gac gag tgg tcc ccg atc att ccc ggg cgc gac 403
Leu Ile Thr Leu Leu Asp Glu Trp Ser Pro Ile Ile Pro Gly Arg Asp
90 95 100

gtt cca gaa cac cct ctt gcg cca aac gta gag atc tcc gat gat cag 451
Val Pro Glu His Pro Leu Ala Pro Asn Val Glu Ile Ser Asp Asp Gln
105 110 115

ccc att gaa tgg gta cac cgc gat gcg cgc tat acc gag aaa ctt gcc 499
Pro Ile Glu Trp Val His Arg Asp Ala Arg Tyr Thr Glu Lys Leu Ala
120 125 130

acc cca gat act tcc gtg gct gat ctt atc ggt gat gtt gac cca atg 547
Thr Pro Asp Thr Ser Val Ala Asp Leu Ile Gly Asp Val Asp Pro Met
135 140 145

cgt gtt gct gaa ggc cgc agc ctc ggt gat cta gaa acc att cac tac 595
Arg Val Ala Glu Gly Arg Ser Leu Gly Asp Leu Glu Thr Ile His Tyr
150 155 160 165

ggt ctg att cct cgc gcc aac cgt ggc atc gtg gcg atc aac gag ctt 643
Gly Leu Ile Pro Arg Ala Asn Arg Gly Ile Val Ala Ile Asn Glu Leu
170 175 180

cct gac ctc gct gaa cgc atc cag gtt gcc atg ctc aac gtc atg gag 691
Pro Asp Leu Ala Glu Arg Ile Gln Val Ala Met Leu Asn Val Met Glu
185 190 195

gaa cgt gat gtg cag att cgt ggc tac aac att cgt ttg gac ttg gat 739
Glu Arg Asp Val Gln Ile Arg Gly Tyr Asn Ile Arg Leu Asp Leu Asp
200 205 210

```
gtg ctg gtt gtt gcc tca gcc aac cct gag gat tac acc aac cgt ggc   787
Val Leu Val Val Ala Ser Ala Asn Pro Glu Asp Tyr Thr Asn Arg Gly
    215                 220                 225

cga att atc act ccg ctc aaa gac cgc ttc ggt gca gaa atc cgc acc   835
Arg Ile Ile Thr Pro Leu Lys Asp Arg Phe Gly Ala Glu Ile Arg Thr
230                 235                 240                 245

cac tac cca ctt gag ttg gac gat gaa gtg gca att atc cgc cag gaa   883
His Tyr Pro Leu Glu Leu Asp Asp Glu Val Ala Ile Ile Arg Gln Glu
                250                 255                 260

gca gag ctt gtt gcg caa gtc cct gat atc ttg gtt gaa att ctt gcc   931
Ala Glu Leu Val Ala Gln Val Pro Asp Ile Leu Val Glu Ile Leu Ala
            265                 270                 275

cgc tac acc cga gcg ctt cgt gaa tcc tca tcg gtg aat cag cgt tct   979
Arg Tyr Thr Arg Ala Leu Arg Glu Ser Ser Ser Val Asn Gln Arg Ser
        280                 285                 290

ggt gtg tct gct cgt ttc tcc att gca ggt gca gaa act gtg gcc gca   1027
Gly Val Ser Ala Arg Phe Ser Ile Ala Gly Ala Glu Thr Val Ala Ala
    295                 300                 305

gca gct ctt cga cgc gca gca gtg ttc ggc gaa gat gag gcc gtt gcc   1075
Ala Ala Leu Arg Arg Ala Ala Val Phe Gly Glu Asp Glu Ala Val Ala
310                 315                 320                 325

cgc ctg gtt gat ttg gaa gca gcc gtg gaa gtc ctc ggc ggc aag att   1123
Arg Leu Val Asp Leu Glu Ala Ala Val Glu Val Leu Gly Gly Lys Ile
                330                 335                 340

gaa ttt gaa tcc ggc gaa gaa gga cgc gaa tgg gaa atc ctt gat tat   1171
Glu Phe Glu Ser Gly Glu Glu Gly Arg Glu Trp Glu Ile Leu Asp Tyr
            345                 350                 355

ctc ctg cgc acc gca acc gca gaa gcg ctg cgt tcc act ctg cgc tcg   1219
Leu Leu Arg Thr Ala Thr Ala Glu Ala Leu Arg Ser Thr Leu Arg Ser
        360                 365                 370

ctg gat ctc acc ccg ctc atc gca gca tta gac ggc agc atc acc gtt   1267
Leu Asp Leu Thr Pro Leu Ile Ala Ala Leu Asp Gly Ser Ile Thr Val
    375                 380                 385

tcc act ggc acg aac atc acc gcg tca gaa ttt ttg gct tcg ctc ccc   1315
Ser Thr Gly Thr Asn Ile Thr Ala Ser Glu Phe Leu Ala Ser Leu Pro
390                 395                 400                 405

gaa ctc ggc gaa agc acg cta tat gac gac atc gct caa gct ttt ggt   1363
Glu Leu Gly Glu Ser Thr Leu Tyr Asp Asp Ile Ala Gln Ala Phe Gly
                410                 415                 420

gcc acc aca cca agt act cgc gcg atg gcc att gag ctt gct ttg gaa   1411
Ala Thr Thr Pro Ser Thr Arg Ala Met Ala Ile Glu Leu Ala Leu Glu
            425                 430                 435

ggt ctt tac ctt tcc cga aaa att gcc aag gat tct ggc gaa ggt gaa   1459
Gly Leu Tyr Leu Ser Arg Lys Ile Ala Lys Asp Ser Gly Glu Gly Glu
        440                 445                 450
```

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acc att tac ggt taactggttt taaggagcac cac                              1494
Thr Ile Tyr Gly
    455


<210> 2586
<211> 457
<212> PRT
<213> Corynebacterium glutamicum

<400> 2586
Val Trp Gly Val Ser Leu Pro Pro Asn Val Gln Thr Val Gly Glu Leu
  1               5                  10                  15

Lys Ala Ala Gly His Ile Tyr Arg Pro Leu Arg Val Glu Ile Arg Asp
             20                  25                  30

Asn Leu Leu Ala Lys Leu Arg Ser Gly Glu Asp Pro Trp Pro Gly Leu
         35                  40                  45

His Gly Leu Asn Tyr Thr Val Ile Arg Gln Leu Glu Arg Ala Leu Ile
     50                  55                  60

Ala Gly His Asp Ile Val Leu Leu Gly Glu Arg Gly Gln Gly Lys Thr
 65                  70                  75                  80

Arg Leu Leu Arg Thr Leu Ile Thr Leu Leu Asp Glu Trp Ser Pro Ile
                 85                  90                  95

Ile Pro Gly Arg Asp Val Pro Glu His Pro Leu Ala Pro Asn Val Glu
            100                 105                 110

Ile Ser Asp Asp Gln Pro Ile Glu Trp Val His Arg Asp Ala Arg Tyr
        115                 120                 125

Thr Glu Lys Leu Ala Thr Pro Asp Thr Ser Val Ala Asp Leu Ile Gly
    130                 135                 140

Asp Val Asp Pro Met Arg Val Ala Glu Gly Arg Ser Leu Gly Asp Leu
145                 150                 155                 160

Glu Thr Ile His Tyr Gly Leu Ile Pro Arg Ala Asn Arg Gly Ile Val
                165                 170                 175

Ala Ile Asn Glu Leu Pro Asp Leu Ala Glu Arg Ile Gln Val Ala Met
            180                 185                 190

Leu Asn Val Met Glu Glu Arg Asp Val Gln Ile Arg Gly Tyr Asn Ile
        195                 200                 205

Arg Leu Asp Leu Asp Val Leu Val Val Ala Ser Ala Asn Pro Glu Asp
    210                 215                 220

Tyr Thr Asn Arg Gly Arg Ile Ile Thr Pro Leu Lys Asp Arg Phe Gly
225                 230                 235                 240

Ala Glu Ile Arg Thr His Tyr Pro Leu Glu Leu Asp Asp Glu Val Ala
                245                 250                 255

Ile Ile Arg Gln Glu Ala Glu Leu Val Ala Gln Val Pro Asp Ile Leu
            260                 265                 270
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Val Glu Ile Leu Ala Arg Tyr Thr Arg Ala Leu Arg Glu Ser Ser Ser
        275                 280                 285

Val Asn Gln Arg Ser Gly Val Ser Ala Arg Phe Ser Ile Ala Gly Ala
    290                 295                 300

Glu Thr Val Ala Ala Ala Ala Leu Arg Arg Ala Ala Val Phe Gly Glu
305                 310                 315                 320

Asp Glu Ala Val Ala Arg Leu Val Asp Leu Glu Ala Ala Val Glu Val
                325                 330                 335

Leu Gly Gly Lys Ile Glu Phe Glu Ser Gly Glu Glu Gly Arg Glu Trp
            340                 345                 350

Glu Ile Leu Asp Tyr Leu Leu Arg Thr Ala Thr Ala Glu Ala Leu Arg
        355                 360                 365

Ser Thr Leu Arg Ser Leu Asp Leu Thr Pro Leu Ile Ala Ala Leu Asp
    370                 375                 380

Gly Ser Ile Thr Val Ser Thr Gly Thr Asn Ile Thr Ala Ser Glu Phe
385                 390                 395                 400

Leu Ala Ser Leu Pro Glu Leu Gly Glu Ser Thr Leu Tyr Asp Asp Ile
                405                 410                 415

Ala Gln Ala Phe Gly Ala Thr Thr Pro Ser Thr Arg Ala Met Ala Ile
            420                 425                 430

Glu Leu Ala Leu Glu Gly Leu Tyr Leu Ser Arg Lys Ile Ala Lys Asp
        435                 440                 445

Ser Gly Glu Gly Glu Thr Ile Tyr Gly
    450                 455


<210> 2587
<211> 2079
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2056)
<223> RXA02124

<400> 2587
gcttgctttg gaaggtcttt acctttcccg aaaaattgcc aaggattctg gcgaaggtga 60

aaccatttac ggttaactgg ttttaaggag caccacagcc atg gcc act tca cat   115
                                               Met Ala Thr Ser His
                                                 1               5

tca cga ccc cgc cgc agc cgt tac gga cgc tac acc gga ggc cca gat   163
Ser Arg Pro Arg Arg Ser Arg Tyr Gly Arg Tyr Thr Gly Gly Pro Asp
                10                  15                  20

ccg ctg gca cct cca gtg gat ctc agc gat gcc ctg cgc gat att gct   211
Pro Leu Ala Pro Pro Val Asp Leu Ser Asp Ala Leu Arg Asp Ile Ala
```

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            25                  30                  35

gat gat gtc atg gct ggt tat tcc cct gag cag gca cta cgt gaa tac   259
Asp Asp Val Met Ala Gly Tyr Ser Pro Glu Gln Ala Leu Arg Glu Tyr
         40                  45                  50

ctg cgc aga ggc gcc cga gga cag gaa ggc ctc gat gat cta gcc tgg   307
Leu Arg Arg Gly Ala Arg Gly Gln Glu Gly Leu Asp Asp Leu Ala Trp
     55                  60                  65

cgt gca gcc gaa cgc cgc cga gaa tta ctt agc cga aac aac ctc ggt   355
Arg Ala Ala Glu Arg Arg Arg Glu Leu Leu Ser Arg Asn Asn Leu Gly
 70                  75                  80                  85

ggc aca ctc gct gag gtt cgc aag ctt ctc gat gaa ggc ctc aag ctg   403
Gly Thr Leu Ala Glu Val Arg Lys Leu Leu Asp Glu Gly Leu Lys Leu
                 90                  95                 100

gaa cgc gct caa ctg gcc cgc gat atc gat atg gat gac acc gat cga   451
Glu Arg Ala Gln Leu Ala Arg Asp Ile Asp Met Asp Asp Thr Asp Arg
            105                 110                 115

gca ttc cgc gaa atg cag atc agc aac ctc cct gaa tcc acc gcc gct   499
Ala Phe Arg Glu Met Gln Ile Ser Asn Leu Pro Glu Ser Thr Ala Ala
        120                 125                 130

gcc gtt tcc gag cta aat tcc tac gat tgg caa tcc caa gaa gca cgc   547
Ala Val Ser Glu Leu Asn Ser Tyr Asp Trp Gln Ser Gln Glu Ala Arg
    135                 140                 145

caa aag ttt gaa caa atc cgt gac ctg ctt ggc cgt gaa atg tta gat   595
Gln Lys Phe Glu Gln Ile Arg Asp Leu Leu Gly Arg Glu Met Leu Asp
150                 155                 160                 165

cag caa ttc tcc ggc atg aaa caa gcc atg gaa ggt gcc tcc gac gag   643
Gln Gln Phe Ser Gly Met Lys Gln Ala Met Glu Gly Ala Ser Asp Glu
                170                 175                 180

gac aaa gca gcc atc gcc gaa atg ctg cgc gat ctc aac gac ctg ctc   691
Asp Lys Ala Ala Ile Ala Glu Met Leu Arg Asp Leu Asn Asp Leu Leu
            185                 190                 195

tcc aaa cac cgc gag gga acg gac act ccc acc gat ttc gcc aat ttt   739
Ser Lys His Arg Glu Gly Thr Asp Thr Pro Thr Asp Phe Ala Asn Phe
        200                 205                 210

atg gcc aaa cac ggc gag cac ttc ccc gag cag ccg cgc gac atc aat   787
Met Ala Lys His Gly Glu His Phe Pro Glu Gln Pro Arg Asp Ile Asn
    215                 220                 225

gag ctc atc gat gcc ctc gca gcc cgt tcc gcc gca gcc agt cgc atg   835
Glu Leu Ile Asp Ala Leu Ala Ala Arg Ser Ala Ala Ala Ser Arg Met
230                 235                 240                 245

ttc aac tcc ata tca gag gaa caa cgc cgc gaa ctc atg aaa cta tct   883
Phe Asn Ser Ile Ser Glu Glu Gln Arg Arg Glu Leu Met Lys Leu Ser
                250                 255                 260

gcc caa gct ttc gga tcc cca gag ctg cag gaa ttg ctc ggt gac ctg   931
Ala Gln Ala Phe Gly Ser Pro Glu Leu Gln Glu Leu Leu Gly Asp Leu
            265                 270                 275
```

```
gct gga aac ctc caa ggt ctg cgc ccc gac ctc aac tgg gat ggc tcc   979
Ala Gly Asn Leu Gln Gly Leu Arg Pro Asp Leu Asn Trp Asp Gly Ser
        280                 285                 290

gaa caa ttc tcc ggc gac gaa ggc atg gga ctt ggt gat ggc acc ggc   1027
Glu Gln Phe Ser Gly Asp Glu Gly Met Gly Leu Gly Asp Gly Thr Gly
    295                 300                 305

gcc atg cag gac ctc gcc gaa ctc gac aac ctt gct gaa caa ctg agc   1075
Ala Met Gln Asp Leu Ala Glu Leu Asp Asn Leu Ala Glu Gln Leu Ser
310                 315                 320                 325

aac tcc cac acc gac ctc gac att gat gcg att cgc cgc caa ctc ggc   1123
Asn Ser His Thr Asp Leu Asp Ile Asp Ala Ile Arg Arg Gln Leu Gly
                330                 335                 340

gat gac gcc gct gtc tct gcc gaa act ttg gcc aaa ctg gag cgc gcg   1171
Asp Asp Ala Ala Val Ser Ala Glu Thr Leu Ala Lys Leu Glu Arg Ala
            345                 350                 355

ctc cgc gac agc ggc ctt ctt cgc cgc aac ccc gat ggc tca ttg aag   1219
Leu Arg Asp Ser Gly Leu Leu Arg Arg Asn Pro Asp Gly Ser Leu Lys
        360                 365                 370

ctc agc ccc cag gcc atg cgc cgt cta ggg aaa gcg ctt ctc gac gcc   1267
Leu Ser Pro Gln Ala Met Arg Arg Leu Gly Lys Ala Leu Leu Asp Ala
    375                 380                 385

gcc agc gaa caa tta tcg tcc cgc cca ggc tcg cga gac tcc cgg ttg   1315
Ala Ser Glu Gln Leu Ser Ser Arg Pro Gly Ser Arg Asp Ser Arg Leu
390                 395                 400                 405

gca gga gca aac ggt gaa gcg acg gga gca tcc cga cct tat gtt ttc   1363
Ala Gly Ala Asn Gly Glu Ala Thr Gly Ala Ser Arg Pro Tyr Val Phe
                410                 415                 420

gga gac acc caa cca tgg gat gtc acc cgc acc atc acc aat gct ctg   1411
Gly Asp Thr Gln Pro Trp Asp Val Thr Arg Thr Ile Thr Asn Ala Leu
            425                 430                 435

cag cga aca gcc gga aca gat acg gaa ggt ccg ctg cgc atc aac tta   1459
Gln Arg Thr Ala Gly Thr Asp Thr Glu Gly Pro Leu Arg Ile Asn Leu
        440                 445                 450

gat gat gtg gaa gtc att gaa act gaa gcc cgc acc ctc aac gcc gtg   1507
Asp Asp Val Glu Val Ile Glu Thr Glu Ala Arg Thr Leu Asn Ala Val
    455                 460                 465

gca ctg cta gta gac acc agt tat tcc atg gct gcc gaa ggc cgc tgg   1555
Ala Leu Leu Val Asp Thr Ser Tyr Ser Met Ala Ala Glu Gly Arg Trp
470                 475                 480                 485

gtg ccc atg aag caa aca gcg ctt gcc ctc cac cac ctg gta tcc acc   1603
Val Pro Met Lys Gln Thr Ala Leu Ala Leu His His Leu Val Ser Thr
                490                 495                 500

cgg ttt aga gga gat gaa cta gca cta atc act ttt ggt cga cat gcc   1651
Arg Phe Arg Gly Asp Glu Leu Ala Leu Ile Thr Phe Gly Arg His Ala
            505                 510                 515
```

```
caa aac atg gac atc gag gaa ctg act gca ctg cca ccg gtt cac gaa   1699
Gln Asn Met Asp Ile Glu Glu Leu Thr Ala Leu Pro Pro Val His Glu
        520                 525                 530

caa gga act aat ctc cac cac gca tta ctg ctg gca gaa cgg ttc ttt   1747
Gln Gly Thr Asn Leu His His Ala Leu Leu Leu Ala Glu Arg Phe Phe
    535                 540                 545

gct cgc cat ccc tcc atg aaa gca agc ctg ctc att gtc aca gat ggc   1795
Ala Arg His Pro Ser Met Lys Ala Ser Leu Leu Ile Val Thr Asp Gly
550                 555                 560                 565

gaa ccc aca gct cac ctc gaa gcc gat gga cac gcc tgg ttc aac tgg   1843
Glu Pro Thr Ala His Leu Glu Ala Asp Gly His Ala Trp Phe Asn Trp
                570                 575                 580

ccc act gac cca gaa acc atg ttc aag acc gtc acc caa cta gat aaa   1891
Pro Thr Asp Pro Glu Thr Met Phe Lys Thr Val Thr Gln Leu Asp Lys
            585                 590                 595

gta acc aag cga gga acc cac acc aca ctc ttc cga ctg gga cat gat   1939
Val Thr Lys Arg Gly Thr His Thr Thr Leu Phe Arg Leu Gly His Asp
        600                 605                 610

caa gga tta gag cac ttt ctc aac caa cta gcc gac cgt gtt ggc ggc   1987
Gln Gly Leu Glu His Phe Leu Asn Gln Leu Ala Asp Arg Val Gly Gly
    615                 620                 625

acc gtg gtg gct ccc gat ctg gac gga ctc ggc gcc gca gtc gtg ggc   2035
Thr Val Val Ala Pro Asp Leu Asp Gly Leu Gly Ala Ala Val Val Gly
630                 635                 640                 645

gag tat tta cga cac cgc tac tgagcattgg acgttttcgc ctt             2079
Glu Tyr Leu Arg His Arg Tyr
                650
```

Added during examination

<210> 2588
<211> 652
<212> PRT
<213> Corynebacterium glutamicum

<400> 2588

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Met Ala Thr Ser His Ser Arg Pro Arg Arg Ser Arg Tyr Gly Arg Tyr
  1               5                  10                  15

Thr Gly Gly Pro Asp Pro Leu Ala Pro Pro Val Asp Leu Ser Asp Ala
             20                  25                  30

Leu Arg Asp Ile Ala Asp Asp Val Met Ala Gly Tyr Ser Pro Glu Gln
         35                  40                  45

Ala Leu Arg Glu Tyr Leu Arg Arg Gly Ala Arg Gly Gln Glu Gly Leu
     50                  55                  60

Asp Asp Leu Ala Trp Arg Ala Ala Glu Arg Arg Arg Glu Leu Leu Ser
 65                  70                  75                  80

Arg Asn Asn Leu Gly Gly Thr Leu Ala Glu Val Arg Lys Leu Leu Asp
                 85                  90                  95
```

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Glu Gly Leu Lys Leu Glu Arg Ala Gln Leu Ala Arg Asp Ile Asp Met
            100                 105                 110

Asp Asp Thr Asp Arg Ala Phe Arg Glu Met Gln Ile Ser Asn Leu Pro
        115                 120                 125

Glu Ser Thr Ala Ala Ala Val Ser Glu Leu Asn Ser Tyr Asp Trp Gln
    130                 135                 140

Ser Gln Glu Ala Arg Gln Lys Phe Glu Gln Ile Arg Asp Leu Leu Gly
145                 150                 155                 160

Arg Glu Met Leu Asp Gln Gln Phe Ser Gly Met Lys Gln Ala Met Glu
                165                 170                 175

Gly Ala Ser Asp Glu Asp Lys Ala Ala Ile Ala Glu Met Leu Arg Asp
            180                 185                 190

Leu Asn Asp Leu Leu Ser Lys His Arg Glu Gly Thr Asp Thr Pro Thr
        195                 200                 205

Asp Phe Ala Asn Phe Met Ala Lys His Gly Glu His Phe Pro Glu Gln
    210                 215                 220

Pro Arg Asp Ile Asn Glu Leu Ile Asp Ala Leu Ala Ala Arg Ser Ala
225                 230                 235                 240

Ala Ala Ser Arg Met Phe Asn Ser Ile Ser Glu Glu Gln Arg Arg Glu
                245                 250                 255

Leu Met Lys Leu Ser Ala Gln Ala Phe Gly Ser Pro Glu Leu Gln Glu
            260                 265                 270

Leu Leu Gly Asp Leu Ala Gly Asn Leu Gln Gly Leu Arg Pro Asp Leu
        275                 280                 285

Asn Trp Asp Gly Ser Glu Gln Phe Ser Gly Asp Glu Gly Met Gly Leu
    290                 295                 300

Gly Asp Gly Thr Gly Ala Met Gln Asp Leu Ala Glu Leu Asp Asn Leu
305                 310                 315                 320

Ala Glu Gln Leu Ser Asn Ser His Thr Asp Leu Asp Ile Asp Ala Ile
                325                 330                 335

Arg Arg Gln Leu Gly Asp Asp Ala Ala Val Ser Ala Glu Thr Leu Ala
            340                 345                 350

Lys Leu Glu Arg Ala Leu Arg Asp Ser Gly Leu Leu Arg Arg Asn Pro
        355                 360                 365

Asp Gly Ser Leu Lys Leu Ser Pro Gln Ala Met Arg Arg Leu Gly Lys
    370                 375                 380

Ala Leu Leu Asp Ala Ala Ser Glu Gln Leu Ser Ser Arg Pro Gly Ser
385                 390                 395                 400

Arg Asp Ser Arg Leu Ala Gly Ala Asn Gly Glu Ala Thr Gly Ala Ser
                405                 410                 415

Arg Pro Tyr Val Phe Gly Asp Thr Gln Pro Trp Asp Val Thr Arg Thr
```

```
            420                 425                 430

Ile Thr Asn Ala Leu Gln Arg Thr Ala Gly Thr Asp Thr Glu Gly Pro
        435                 440                 445

Leu Arg Ile Asn Leu Asp Asp Val Glu Val Ile Glu Thr Glu Ala Arg
    450                 455                 460

Thr Leu Asn Ala Val Ala Leu Leu Val Asp Thr Ser Tyr Ser Met Ala
465                 470                 475                 480

Ala Glu Gly Arg Trp Val Pro Met Lys Gln Thr Ala Leu Ala Leu His
                485                 490                 495

His Leu Val Ser Thr Arg Phe Arg Gly Asp Glu Leu Ala Leu Ile Thr
            500                 505                 510

Phe Gly Arg His Ala Gln Asn Met Asp Ile Glu Glu Leu Thr Ala Leu
        515                 520                 525

Pro Pro Val His Glu Gln Gly Thr Asn Leu His His Ala Leu Leu Leu
    530                 535                 540

Ala Glu Arg Phe Phe Ala Arg His Pro Ser Met Lys Ala Ser Leu Leu
545                 550                 555                 560

Ile Val Thr Asp Gly Glu Pro Thr Ala His Leu Glu Ala Asp Gly His
                565                 570                 575

Ala Trp Phe Asn Trp Pro Thr Asp Pro Glu Thr Met Phe Lys Thr Val
            580                 585                 590

Thr Gln Leu Asp Lys Val Thr Lys Arg Gly Thr His Thr Thr Leu Phe
        595                 600                 605

Arg Leu Gly His Asp Gln Gly Leu Glu His Phe Leu Asn Gln Leu Ala
    610                 615                 620

Asp Arg Val Gly Gly Thr Val Val Ala Pro Asp Leu Asp Gly Leu Gly
625                 630                 635                 640

Ala Ala Val Val Gly Glu Tyr Leu Arg His Arg Tyr
                645                 650
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<210> 2589
<211> 924
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(901)
<223> RXA02125

<400> 2589
gacctaaaat tcatcacctc accgttttta aggcttagaa aaatagcagt gttgggatgt 60

gaatatccat ttatgctgct gtagtcggct atgtggacgc atg gtg gca acc tct 115
Met Val Ala Thr Ser
1 5

```
cag ttt atc gat gac agc gag gct gcc cag gcg gta cgc gca gct att   163
Gln Phe Ile Asp Asp Ser Glu Ala Ala Gln Ala Val Arg Ala Ala Ile
                10                  15                  20

gtt gca gga tac cga aac att gat act gcc cta gcg tat gga aac gag   211
Val Ala Gly Tyr Arg Asn Ile Asp Thr Ala Leu Ala Tyr Gly Asn Glu
            25                  30                  35

cgc ggc gtt ggc gaa ggc att cgc acc gct gga gtg ccc cgc gag gag   259
Arg Gly Val Gly Glu Gly Ile Arg Thr Ala Gly Val Pro Arg Glu Glu
        40                  45                  50

ctc ttt att tcc acc aag cta gct gca gaa atc aaa gat tac gat gga   307
Leu Phe Ile Ser Thr Lys Leu Ala Ala Glu Ile Lys Asp Tyr Asp Gly
    55                  60                  65

gca gtc gcc gcg att gat gag tct ttg gcg aaa att ggc ttg gat tat   355
Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys Ile Gly Leu Asp Tyr
70                  75                  80                  85

gtc gat ctg atg ctc att cac tcc cca caa cca tgg agt gat ttc cgt   403
Val Asp Leu Met Leu Ile His Ser Pro Gln Pro Trp Ser Asp Phe Arg
                90                  95                  100

ggt ggg gac tat tca gag gga aac cgt gaa gcg tgg cgc gcg ctg gaa   451
Gly Gly Asp Tyr Ser Glu Gly Asn Arg Glu Ala Trp Arg Ala Leu Glu
            105                 110                 115

gat gcc tac aaa gcc gga aag att cga tcc att ggt gtc tcg aac ttc   499
Asp Ala Tyr Lys Ala Gly Lys Ile Arg Ser Ile Gly Val Ser Asn Phe
        120                 125                 130

ctg gag gcc gat ctg gag aat atc tta gac tcc gcg acg gtt gct cct   547
Leu Glu Ala Asp Leu Glu Asn Ile Leu Asp Ser Ala Thr Val Ala Pro
    135                 140                 145

cac gtt aat cag ctt ctt gtg cat gtt gga aac acc cca agc gag tta   595
His Val Asn Gln Leu Leu Val His Val Gly Asn Thr Pro Ser Glu Leu
150                 155                 160                 165

atc agt ttc tgc gat tcc aag ggc att ctg gtc gaa gca tat tca ccc   643
Ile Ser Phe Cys Asp Ser Lys Gly Ile Leu Val Glu Ala Tyr Ser Pro
                170                 175                 180

atc gcc cac gga gag atg ctg aag aac cag cag gtc aag gcg att gct   691
Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln Val Lys Ala Ile Ala
            185                 190                 195

gac aag tac aac gtg agc att ccg cag cta tgc att cgg tac aca att   739
Asp Lys Tyr Asn Val Ser Ile Pro Gln Leu Cys Ile Arg Tyr Thr Ile
        200                 205                 210

caa ctg gga acg gtg tct ttg cca aag act gcc aac cca gat cat atg   787
Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala Asn Pro Asp His Met
    215                 220                 225

agc tcc aat gcg cag atc gac ttt gaa att tcc gag gaa gac atg gcg   835
Ser Ser Asn Ala Gln Ile Asp Phe Glu Ile Ser Glu Glu Asp Met Ala
230                 235                 240                 245
```

```
gca ctt caa gaa gtg acc gcc cgc gat tat ggc gag cac agc ggt ttt   883
Ala Leu Gln Glu Val Thr Ala Arg Asp Tyr Gly Glu His Ser Gly Phe
                250                 255                 260

cct gtg tat tcc ggc aag tagaaagatt tttatcatgg gac                924
Pro Val Tyr Ser Gly Lys
            265


<210> 2590
<211> 267
<212> PRT
<213> Corynebacterium glutamicum

<400> 2590
Met Val Ala Thr Ser Gln Phe Ile Asp Asp Ser Glu Ala Ala Gln Ala
  1               5                  10                  15

Val Arg Ala Ala Ile Val Ala Gly Tyr Arg Asn Ile Asp Thr Ala Leu
             20                  25                  30

Ala Tyr Gly Asn Glu Arg Gly Val Gly Glu Gly Ile Arg Thr Ala Gly
         35                  40                  45

Val Pro Arg Glu Glu Leu Phe Ile Ser Thr Lys Leu Ala Ala Glu Ile
     50                  55                  60

Lys Asp Tyr Asp Gly Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys
 65                  70                  75                  80

Ile Gly Leu Asp Tyr Val Asp Leu Met Leu Ile His Ser Pro Gln Pro
                 85                  90                  95

Trp Ser Asp Phe Arg Gly Gly Asp Tyr Ser Glu Gly Asn Arg Glu Ala
            100                 105                 110

Trp Arg Ala Leu Glu Asp Ala Tyr Lys Ala Gly Lys Ile Arg Ser Ile
        115                 120                 125

Gly Val Ser Asn Phe Leu Glu Ala Asp Leu Glu Asn Ile Leu Asp Ser
    130                 135                 140

Ala Thr Val Ala Pro His Val Asn Gln Leu Leu Val His Val Gly Asn
145                 150                 155                 160

Thr Pro Ser Glu Leu Ile Ser Phe Cys Asp Ser Lys Gly Ile Leu Val
                165                 170                 175

Glu Ala Tyr Ser Pro Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln
            180                 185                 190

Val Lys Ala Ile Ala Asp Lys Tyr Asn Val Ser Ile Pro Gln Leu Cys
        195                 200                 205

Ile Arg Tyr Thr Ile Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala
    210                 215                 220

Asn Pro Asp His Met Ser Ser Asn Ala Gln Ile Asp Phe Glu Ile Ser
225                 230                 235                 240

Glu Glu Asp Met Ala Ala Leu Gln Glu Val Thr Ala Arg Asp Tyr Gly
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245 250 255

Glu His Ser Gly Phe Pro Val Tyr Ser Gly Lys
260 265

<210> 2591
<211> 357
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(334)
<223> RXA02129

<400> 2591
tgttctgccg atccagcacc agctctggtg gcaggagctg agagttttgc caattaactt 60

ggcgaacaga cttgttggaa atgaatttgt caagaatggc atg aag atc atc ttc 115
Met Lys Ile Ile Phe
1 5

aaa atg gct agt aac aag ttc atc gac aac aaa aag ggg ctg gct atg 163
Lys Met Ala Ser Asn Lys Phe Ile Asp Asn Lys Lys Gly Leu Ala Met
10 15 20

cta gtt ttt gcc gaa ctt gtg atg gaa atg ctt gat cag cct gaa gaa 211
Leu Val Phe Ala Glu Leu Val Met Glu Met Leu Asp Gln Pro Glu Glu
25 30 35

caa ctt cat aat gtg cgt gga gtg gct att gag aag cgg gag ttc ctc 259
Gln Leu His Asn Val Arg Gly Val Ala Ile Glu Lys Arg Glu Phe Leu
40 45 50

aaa gct ctc acc gct gat ttc acc agc aga ctt aaa caa gct caa acc 307
Lys Ala Leu Thr Ala Asp Phe Thr Ser Arg Leu Lys Gln Ala Gln Thr
55 60 65

gat aag att ctt gtt tgg gat ttc gca tgactattat gtgggcgacc 354
Asp Lys Ile Leu Val Trp Asp Phe Ala
70 75

cgt 357

<210> 2592
<211> 78
<212> PRT
<213> Corynebacterium glutamicum

<400> 2592
Met Lys Ile Ile Phe Lys Met Ala Ser Asn Lys Phe Ile Asp Asn Lys
1 5 10 15

Lys Gly Leu Ala Met Leu Val Phe Ala Glu Leu Val Met Glu Met Leu
20 25 30

Asp Gln Pro Glu Glu Gln Leu His Asn Val Arg Gly Val Ala Ile Glu
35 40 45

```
Lys Arg Glu Phe Leu Lys Ala Leu Thr Ala Asp Phe Thr Ser Arg Leu
     50                  55                  60

Lys Gln Ala Gln Thr Asp Lys Ile Leu Val Trp Asp Phe Ala
 65                  70                  75


<210> 2593
<211> 739
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(739)
<223> RXA02132

<400> 2593
gcagcccacc gccagcgatt cctcgccgaa caaggctacg cataccgcat cctcgacgcc 60

gacgacatcc tcttcccact acccaagaaa gagctataac gtg cac aac ttc tcc   115
                                            Val His Asn Phe Ser
                                              1               5

ttc gac gtg gac gaa tcc tac gcc aag aag aac aac gaa atc ctc cgc   163
Phe Asp Val Asp Glu Ser Tyr Ala Lys Lys Asn Asn Glu Ile Leu Arg
                10                  15                  20

gac gca aag cga ctc cag atc tca gca ctg tgc ctt gga ctc atc ctc   211
Asp Ala Lys Arg Leu Gln Ile Ser Ala Leu Cys Leu Gly Leu Ile Leu
            25                  30                  35

ggc ggc gga gcc gta gcc gtc tac ctg ttt tct aac gga gca gtg tgg   259
Gly Gly Gly Ala Val Ala Val Tyr Leu Phe Ser Asn Gly Ala Val Trp
        40                  45                  50

atg tgg atg atc gcc atc gtc atg gtc ttc ctc gcc ctg ttg agc ttc   307
Met Trp Met Ile Ala Ile Val Met Val Phe Leu Ala Leu Leu Ser Phe
    55                  60                  65

atc atg att cct gtg atc ccc cgc caa atg ggc aac gca caa acg ctc   355
Ile Met Ile Pro Val Ile Pro Arg Gln Met Gly Asn Ala Gln Thr Leu
70                  75                  80                  85

tac gat gac tac gaa cta gcc ccc gcc atc atc gca gaa gta aac ccc   403
Tyr Asp Asp Tyr Glu Leu Ala Pro Ala Ile Ile Ala Glu Val Asn Pro
                90                  95                  100

cgc gat gtg gtc ctc ctg gca ctc gtc aac cgc aat gtg aac ccc gaa   451
Arg Asp Val Val Leu Leu Ala Leu Val Asn Arg Asn Val Asn Pro Glu
            105                 110                 115

gcc aaa cca gag tgg gca ttg gcc acc cgc acg atc gtt cgc gtc gga   499
Ala Lys Pro Glu Trp Ala Leu Ala Thr Arg Thr Ile Val Arg Val Gly
        120                 125                 130

gca cac gaa cgt cgc ctc ggc gaa cgt atc cca tcc gtc gca atc acc   547
Ala His Glu Arg Arg Leu Gly Glu Arg Ile Pro Ser Val Ala Ile Thr
    135                 140                 145

ggc cga cgc acc gtc aaa gac caa gac cac tgg gat gaa atc agc ccc   595
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```
Gly Arg Arg Thr Val Lys Asp Gln Asp His Trp Asp Glu Ile Ser Pro
150                 155                 160                 165

atg cca att acc tgg ggc acc acg gac aaa gac atc atc cgt gaa gcc   643
Met Pro Ile Thr Trp Gly Thr Thr Asp Lys Asp Ile Ile Arg Glu Ala
                170                 175                 180

gag aaa act atc ccc cac gaa ctc tgg gcc aaa cta gaa aag aac cgc   691
Glu Lys Thr Ile Pro His Glu Leu Trp Ala Lys Leu Glu Lys Asn Arg
            185                 190                 195

ggc aag ttg gag gac gtt aaa aag acc ccc aac aac ctg ttc aaa cta   739
Gly Lys Leu Glu Asp Val Lys Lys Thr Pro Asn Asn Leu Phe Lys Leu
        200                 205                 210


<210> 2594
<211> 213
<212> PRT
<213> Corynebacterium glutamicum

<400> 2594
Val His Asn Phe Ser Phe Asp Val Asp Glu Ser Tyr Ala Lys Lys Asn
  1               5                  10                  15

Asn Glu Ile Leu Arg Asp Ala Lys Arg Leu Gln Ile Ser Ala Leu Cys
             20                  25                  30

Leu Gly Leu Ile Leu Gly Gly Gly Ala Val Ala Val Tyr Leu Phe Ser
         35                  40                  45

Asn Gly Ala Val Trp Met Trp Met Ile Ala Ile Val Met Val Phe Leu
     50                  55                  60

Ala Leu Leu Ser Phe Ile Met Ile Pro Val Ile Pro Arg Gln Met Gly
 65                  70                  75                  80

Asn Ala Gln Thr Leu Tyr Asp Asp Tyr Glu Leu Ala Pro Ala Ile Ile
                 85                  90                  95

Ala Glu Val Asn Pro Arg Asp Val Val Leu Leu Ala Leu Val Asn Arg
            100                 105                 110

Asn Val Asn Pro Glu Ala Lys Pro Glu Trp Ala Leu Ala Thr Arg Thr
        115                 120                 125

Ile Val Arg Val Gly Ala His Glu Arg Arg Leu Gly Glu Arg Ile Pro
    130                 135                 140

Ser Val Ala Ile Thr Gly Arg Arg Thr Val Lys Asp Gln Asp His Trp
145                 150                 155                 160

Asp Glu Ile Ser Pro Met Pro Ile Thr Trp Gly Thr Thr Asp Lys Asp
                165                 170                 175

Ile Ile Arg Glu Ala Glu Lys Thr Ile Pro His Glu Leu Trp Ala Lys
            180                 185                 190

Leu Glu Lys Asn Arg Gly Lys Leu Glu Asp Val Lys Lys Thr Pro Asn
        195                 200                 205
```

```
Asn Leu Phe Lys Leu
    210


<210> 2595
<211> 921
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(898)
<223> RXA02137

<400> 2595
gcctactcac cgtccacaga tgagtaaacc cggaaaaacc cgtatttagt tattggtttt 60

acctgcgtgg gctgaaagtc ttcactttta atccttacag atg gtc gtt ctg att   115
                                            Met Val Val Leu Ile
                                              1               5

cct ttc aac gat gaa gtg tgc acc cct att ccc gat ttg gga ggt ttt   163
Pro Phe Asn Asp Glu Val Cys Thr Pro Ile Pro Asp Leu Gly Gly Phe
                10                  15                  20

cct tgt agc cta ttg agt gtg aaa ctt cct tgg gat aaa aat aag aac   211
Pro Cys Ser Leu Leu Ser Val Lys Leu Pro Trp Asp Lys Asn Lys Asn
            25                  30                  35

aac gaa ggg gct gac gct gca ggc caa gac gcc agc tcc acc cct gag   259
Asn Glu Gly Ala Asp Ala Ala Gly Gln Asp Ala Ser Ser Thr Pro Glu
        40                  45                  50

acc gct acg cct gac gct act gag cag aaa ttg cca aag ggg cac acg   307
Thr Ala Thr Pro Asp Ala Thr Glu Gln Lys Leu Pro Lys Gly His Thr
    55                  60                  65

gca ccg aag ggc cgt ccc act ccg aag cgt cgt gaa gtt gag tta gag   355
Ala Pro Lys Gly Arg Pro Thr Pro Lys Arg Arg Glu Val Glu Leu Glu
70                  75                  80                  85

cga ggt gtc gtt ggc ggc cag tct ttg gcg cct act gat act tat gcg   403
Arg Gly Val Val Gly Gly Gln Ser Leu Ala Pro Thr Asp Thr Tyr Ala
                90                  95                 100

cag cag cgc cag aag cgt aaa gaa ttt aaa gct tct atg acc aag gaa   451
Gln Gln Arg Gln Lys Arg Lys Glu Phe Lys Ala Ser Met Thr Lys Glu
            105                 110                 115

gaa ttc aag gca tac aag cag aaa gag cgc gat gcc cga gtt aag cgt   499
Glu Phe Lys Ala Tyr Lys Gln Lys Glu Arg Asp Ala Arg Val Lys Arg
        120                 125                 130

cag cgc gaa acc caa gct gca atg gat cgc ggc gaa gat gct tat ttg   547
Gln Arg Glu Thr Gln Ala Ala Met Asp Arg Gly Glu Asp Ala Tyr Leu
    135                 140                 145

atg gat cgc gat aag ggc gag gtt cgc cgt ttt gcg cgt gac tgg gtg   595
Met Asp Arg Asp Lys Gly Glu Val Arg Arg Phe Ala Arg Asp Trp Val
150                 155                 160                 165
```

```
gat tcc cgc agg ttc ttg tct aac ttt gtg atg cca gta gct att gct   643
Asp Ser Arg Arg Phe Leu Ser Asn Phe Val Met Pro Val Ala Ile Ala
                170                 175                 180

ttg ctg gtt gtc atg ctg atc ggt aac ttc aac cca tca ttc gct gcg   691
Leu Leu Val Val Met Leu Ile Gly Asn Phe Asn Pro Ser Phe Ala Ala
            185                 190                 195

act tct tcc atg gtt gcc atg gtt ttg atg ttg ggc ttc ctg att gag   739
Thr Ser Ser Met Val Ala Met Val Leu Met Leu Gly Phe Leu Ile Glu
        200                 205                 210

ggc atc acc act ggt cgt cgt gtg aac aag gct gct cgc acg agg ttc   787
Gly Ile Thr Thr Gly Arg Arg Val Asn Lys Ala Ala Arg Thr Arg Phe
    215                 220                 225

cct ggt acc acc gag act ggt ttt ggt ctg ggt tac tac gcg tat tcc   835
Pro Gly Thr Thr Glu Thr Gly Phe Gly Leu Gly Tyr Tyr Ala Tyr Ser
230                 235                 240                 245

cgc acc att cag cct cgt aag tgg cgt acc cct cgt gca cgc gtt gaa   883
Arg Thr Ile Gln Pro Arg Lys Trp Arg Thr Pro Arg Ala Arg Val Glu
                250                 255                 260

att ggt gct gaa gtc tagcgcatgc gcacgttagt tct                    921
Ile Gly Ala Glu Val
            265
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<210> 2596
<211> 266
<212> PRT
<213> Corynebacterium glutamicum

<400> 2596

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Met Val Val Leu Ile Pro Phe Asn Asp Glu Val Cys Thr Pro Ile Pro
  1               5                  10                  15

Asp Leu Gly Gly Phe Pro Cys Ser Leu Leu Ser Val Lys Leu Pro Trp
             20                  25                  30

Asp Lys Asn Lys Asn Asn Glu Gly Ala Asp Ala Ala Gly Gln Asp Ala
         35                  40                  45

Ser Ser Thr Pro Glu Thr Ala Thr Pro Asp Ala Thr Glu Gln Lys Leu
     50                  55                  60

Pro Lys Gly His Thr Ala Pro Lys Gly Arg Pro Thr Pro Lys Arg Arg
 65                  70                  75                  80

Glu Val Glu Leu Glu Arg Gly Val Val Gly Gly Gln Ser Leu Ala Pro
                 85                  90                  95

Thr Asp Thr Tyr Ala Gln Gln Arg Gln Lys Arg Lys Glu Phe Lys Ala
            100                 105                 110

Ser Met Thr Lys Glu Glu Phe Lys Ala Tyr Lys Gln Lys Glu Arg Asp
        115                 120                 125

Ala Arg Val Lys Arg Gln Arg Glu Thr Gln Ala Ala Met Asp Arg Gly
    130                 135                 140
```

```
Glu Asp Ala Tyr Leu Met Asp Arg Asp Lys Gly Glu Val Arg Arg Phe
145                 150                 155                 160

Ala Arg Asp Trp Val Asp Ser Arg Arg Phe Leu Ser Asn Phe Val Met
                165                 170                 175

Pro Val Ala Ile Ala Leu Leu Val Val Met Leu Ile Gly Asn Phe Asn
            180                 185                 190

Pro Ser Phe Ala Ala Thr Ser Ser Met Val Ala Met Val Leu Met Leu
        195                 200                 205

Gly Phe Leu Ile Glu Gly Ile Thr Thr Gly Arg Arg Val Asn Lys Ala
    210                 215                 220

Ala Arg Thr Arg Phe Pro Gly Thr Thr Glu Thr Gly Phe Gly Leu Gly
225                 230                 235                 240

Tyr Tyr Ala Tyr Ser Arg Thr Ile Gln Pro Arg Lys Trp Arg Thr Pro
                245                 250                 255

Arg Ala Arg Val Glu Ile Gly Ala Glu Val
            260                 265
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<210> 2597
<211> 531
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(508)
<223> RXA02141

<400> 2597

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gcccattcgt ttccgatcgc accgcaaccc gcgacggcga aaacactcag agcaacgctt 60

aagaaggagt ggcgaaaaaa tgaagtcttc agcaaaactc atg tac ggc ccg acc   115
                                              Met Tyr Gly Pro Thr
                                                1               5

gta ttc atg gcc gca atg gct gtc atc tac atc ttc gca aca atg cac   163
Val Phe Met Ala Ala Met Ala Val Ile Tyr Ile Phe Ala Thr Met His
                10                  15                  20

gtt agt gat ggc ggc agc gtt aaa ggt gtt gag tgg gtc ggt tct gtg   211
Val Ser Asp Gly Gly Ser Val Lys Gly Val Glu Trp Val Gly Ser Val
            25                  30                  35

gcc ctg gtc ctg tca gca ggt ctg acg ctt atg ctc ggt gtc tac ctt   259
Ala Leu Val Leu Ser Ala Gly Leu Thr Leu Met Leu Gly Val Tyr Leu
        40                  45                  50

cac ttc act gaa gtc cgc gta gat gtt ctt cca gag gac tgg gaa gag   307
His Phe Thr Glu Val Arg Val Asp Val Leu Pro Glu Asp Trp Glu Glu
    55                  60                  65

gct gag gtt gcc gac aag gca gga acc ctc ggg ttc ttc agc cca agc   355
Ala Glu Val Ala Asp Lys Ala Gly Thr Leu Gly Phe Phe Ser Pro Ser
```

```
 70                  75                  80                  85

tcc att tgg ccg gca gct atg tcc ggt gcg gtt gga ttc ctt gca ttc   403
Ser Ile Trp Pro Ala Ala Met Ser Gly Ala Val Gly Phe Leu Ala Phe
                 90                  95                 100

ggc gtt gtg tac ttc cac tac tgg atg atc gca gtt ggt ctg atg ctc   451
Gly Val Val Tyr Phe His Tyr Trp Met Ile Ala Val Gly Leu Met Leu
            105                 110                 115

ctg atc ttc acg atc acc aag ctc aac ctt cag tac ggc gtg cca aaa   499
Leu Ile Phe Thr Ile Thr Lys Leu Asn Leu Gln Tyr Gly Val Pro Lys
        120                 125                 130

gaa aag cac tagtactaaa accacatatg ctc                            531
Glu Lys His
    135
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<210> 2598
<211> 136
<212> PRT
<213> Corynebacterium glutamicum

<400> 2598

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Met Tyr Gly Pro Thr Val Phe Met Ala Ala Met Ala Val Ile Tyr Ile
  1               5                  10                  15

Phe Ala Thr Met His Val Ser Asp Gly Gly Ser Val Lys Gly Val Glu
             20                  25                  30

Trp Val Gly Ser Val Ala Leu Val Leu Ser Ala Gly Leu Thr Leu Met
         35                  40                  45

Leu Gly Val Tyr Leu His Phe Thr Glu Val Arg Val Asp Val Leu Pro
     50                  55                  60

Glu Asp Trp Glu Glu Ala Glu Val Ala Asp Lys Ala Gly Thr Leu Gly
 65                  70                  75                  80

Phe Phe Ser Pro Ser Ser Ile Trp Pro Ala Ala Met Ser Gly Ala Val
                 85                  90                  95

Gly Phe Leu Ala Phe Gly Val Val Tyr Phe His Tyr Trp Met Ile Ala
            100                 105                 110

Val Gly Leu Met Leu Leu Ile Phe Thr Ile Thr Lys Leu Asn Leu Gln
        115                 120                 125

Tyr Gly Val Pro Lys Glu Lys His
    130                 135
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<210> 2599
<211> 750
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(727)

<223> RXA02146

<400> 2599

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ggttctctcg cagagagaga aggagtgggg ataggggcct tccgctccga acccgacagc 60

taactcggtc agcaaacagg aagaatttgg agtttcatca gtg ggt aag cac cgt   115
                                             Val Gly Lys His Arg
                                               1               5

cgc aac aat tca aac gca act cgc aag gct gta gca gca tct gca gtt   163
Arg Asn Asn Ser Asn Ala Thr Arg Lys Ala Val Ala Ala Ser Ala Val
                  10                  15                  20

gcg ctt gga gca acc gca gct atc gcc tcc cca gca cag gca gct gag   211
Ala Leu Gly Ala Thr Ala Ala Ile Ala Ser Pro Ala Gln Ala Ala Glu
             25                  30                  35

gtt gtt gtt cct ggc acc gga atc agc gtt gac atc gct ggc atc gag   259
Val Val Val Pro Gly Thr Gly Ile Ser Val Asp Ile Ala Gly Ile Glu
         40                  45                  50

acc act cca ggt ctt aac aac gtt cca gga atc gat cag tgg atc cct   307
Thr Thr Pro Gly Leu Asn Asn Val Pro Gly Ile Asp Gln Trp Ile Pro
     55                  60                  65

tcc ctt agc agc cag gca gct cct act gct tac gca gcc gtc att gat   355
Ser Leu Ser Ser Gln Ala Ala Pro Thr Ala Tyr Ala Ala Val Ile Asp
 70                  75                  80                  85

gca cct gca gca cag gct gca cct gca gca agc acc ggt cag gca atc   403
Ala Pro Ala Ala Gln Ala Ala Pro Ala Ala Ser Thr Gly Gln Ala Ile
                 90                  95                 100

gtt gat gca gcg cgc acc aag att ggt tcc cca tac ggt tgg ggt gct   451
Val Asp Ala Ala Arg Thr Lys Ile Gly Ser Pro Tyr Gly Trp Gly Ala
            105                 110                 115

acc ggt cct aac gct ttc gac tgc tcc ggc ctt acc tca tgg gca tac   499
Thr Gly Pro Asn Ala Phe Asp Cys Ser Gly Leu Thr Ser Trp Ala Tyr
        120                 125                 130

agc cag gtt ggc aag tcc atc cca cgt acc tcc cag gct cag gct gca   547
Ser Gln Val Gly Lys Ser Ile Pro Arg Thr Ser Gln Ala Gln Ala Ala
    135                 140                 145

cag ggc acc cct gtt gct tac tct gac ctt cag gct ggc gac atc gtt   595
Gln Gly Thr Pro Val Ala Tyr Ser Asp Leu Gln Ala Gly Asp Ile Val
150                 155                 160                 165

gcg ttc tac tcc ggc gct acc cac gtt ggt atc tac tcc ggc cac ggc   643
Ala Phe Tyr Ser Gly Ala Thr His Val Gly Ile Tyr Ser Gly His Gly
                170                 175                 180

acc gtt atc cac gca ctg aac agc agc acc cct ctg tct gag cac tcc   691
Thr Val Ile His Ala Leu Asn Ser Ser Thr Pro Leu Ser Glu His Ser
            185                 190                 195

ttg gat tac atg cca ttc cac tct gca gtt cgt ttc taatctgcat        737
Leu Asp Tyr Met Pro Phe His Ser Ala Val Arg Phe
        200                 205
```

aaagtcttaa gct 750

<210> 2600
<211> 209
<212> PRT
<213> Corynebacterium glutamicum

<400> 2600

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Val Gly Lys His Arg Arg Asn Asn Ser Asn Ala Thr Arg Lys Ala Val
  1               5                  10                  15

Ala Ala Ser Ala Val Ala Leu Gly Ala Thr Ala Ala Ile Ala Ser Pro
             20                  25                  30

Ala Gln Ala Ala Glu Val Val Val Pro Gly Thr Gly Ile Ser Val Asp
         35                  40                  45

Ile Ala Gly Ile Glu Thr Thr Pro Gly Leu Asn Asn Val Pro Gly Ile
     50                  55                  60

Asp Gln Trp Ile Pro Ser Leu Ser Ser Gln Ala Ala Pro Thr Ala Tyr
 65                  70                  75                  80

Ala Ala Val Ile Asp Ala Pro Ala Ala Gln Ala Ala Pro Ala Ala Ser
                 85                  90                  95

Thr Gly Gln Ala Ile Val Asp Ala Ala Arg Thr Lys Ile Gly Ser Pro
            100                 105                 110

Tyr Gly Trp Gly Ala Thr Gly Pro Asn Ala Phe Asp Cys Ser Gly Leu
        115                 120                 125

Thr Ser Trp Ala Tyr Ser Gln Val Gly Lys Ser Ile Pro Arg Thr Ser
    130                 135                 140

Gln Ala Gln Ala Ala Gln Gly Thr Pro Val Ala Tyr Ser Asp Leu Gln
145                 150                 155                 160

Ala Gly Asp Ile Val Ala Phe Tyr Ser Gly Ala Thr His Val Gly Ile
                165                 170                 175

Tyr Ser Gly His Gly Thr Val Ile His Ala Leu Asn Ser Ser Thr Pro
            180                 185                 190

Leu Ser Glu His Ser Leu Asp Tyr Met Pro Phe His Ser Ala Val Arg
        195                 200                 205

Phe
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<210> 2601
<211> 525
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(502)
<223> RXA02152

<400> 2601
aagccgttaa aagttgagac tcgcgctgag aatctcacag aaaactccga agctcccgct 60

aaggtagcta ccggaatcaa atcttaggga aggaaaacat atg gct att tac cgt 115
Met Ala Ile Tyr Arg
1 5

aag ctt gcg gct tcc gct gca gca ctg gcc ctg tcc gca tca ctg gtc 163
Lys Leu Ala Ala Ser Ala Ala Ala Leu Ala Leu Ser Ala Ser Leu Val
10 15 20

gct tgt ggc gac tct gag gac acc acc gaa gaa acc tca acc acc tct 211
Ala Cys Gly Asp Ser Glu Asp Thr Thr Glu Glu Thr Ser Thr Thr Ser
25 30 35

tct tcg acc act tcc agc tcc tcc agc agc tct agc tcc agc acc gcg 259
Ser Ser Thr Thr Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Thr Ala
40 45 50

gct act tcc gag gaa tct tcc gca gtt gaa gag cca gca gtg gaa gct 307
Ala Thr Ser Glu Glu Ser Ser Ala Val Glu Glu Pro Ala Val Glu Ala
55 60 65

cct gtg gaa gag gct cca gtc gag gca cct gtt gag cag gca cct gtc 355
Pro Val Glu Glu Ala Pro Val Glu Ala Pro Val Glu Gln Ala Pro Val
70 75 80 85

gtg gag caa gct cca gtt gag cag gct ccg gca ccg gtt cag gaa gca 403
Val Glu Gln Ala Pro Val Glu Gln Ala Pro Ala Pro Val Gln Glu Ala
90 95 100

cct gca cca gtc gag cag gct cca gct cca gtt cag gaa gca cct gca 451
Pro Ala Pro Val Glu Gln Ala Pro Ala Pro Val Gln Glu Ala Pro Ala
105 110 115

gct gac gcg cca cct gca ctt cca ggt ggt ggc ggc gga cac gct ggc 499
Ala Asp Ala Pro Pro Ala Leu Pro Gly Gly Gly Gly Gly His Ala Gly
120 125 130

tac taaaaattca tgcttttacc cac 525
Tyr

<210> 2602
<211> 134
<212> PRT
<213> Corynebacterium glutamicum

<400> 2602
Met Ala Ile Tyr Arg Lys Leu Ala Ala Ser Ala Ala Ala Leu Ala Leu
1 5 10 15

Ser Ala Ser Leu Val Ala Cys Gly Asp Ser Glu Asp Thr Thr Glu Glu
20 25 30

Thr Ser Thr Thr Ser Ser Ser Thr Thr Ser Ser Ser Ser Ser Ser Ser
35 40 45

Ser Ser Ser Thr Ala Ala Thr Ser Glu Glu Ser Ser Ala Val Glu Glu

```
     50                  55                  60

Pro Ala Val Glu Ala Pro Val Glu Glu Ala Pro Val Glu Ala Pro Val
 65                  70                  75                  80

Glu Gln Ala Pro Val Val Glu Gln Ala Pro Val Glu Gln Ala Pro Ala
                85                  90                  95

Pro Val Gln Glu Ala Pro Ala Pro Val Glu Gln Ala Pro Ala Pro Val
            100                 105                 110

Gln Glu Ala Pro Ala Ala Asp Ala Pro Pro Ala Leu Pro Gly Gly Gly
        115                 120                 125

Gly Gly His Ala Gly Tyr
    130
```

<210> 2603
<211> 876
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(853)
<223> RXA02163

<400> 2603

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agcccgtacg atttctgcgc tcccatcctc tgcaccagct gcgcagaaga tctccgaagc 60

caacaccacg acgggccgat tcaccccatt ctattcgcct atg gcg gtg gca aca   115
                                            Met Ala Val Ala Thr
                                              1               5

ttc gga acc atc acc gac atg ttg gaa acc aag ggg atc gtg agc aat   163
Phe Gly Thr Ile Thr Asp Met Leu Glu Thr Lys Gly Ile Val Ser Asn
                10                  15                  20

gta ggc ggc acc gac acc atc gat ttg ggc gcg ttg ttg aat gaa acc   211
Val Gly Gly Thr Asp Thr Ile Asp Leu Gly Ala Leu Leu Asn Glu Thr
            25                  30                  35

caa gcc gga acc cgc tgg agc gaa ctt agc ccc aac tat cag tcc aac   259
Gln Ala Gly Thr Arg Trp Ser Glu Leu Ser Pro Asn Tyr Gln Ser Asn
        40                  45                  50

cgc gtc gtg cag att tct acc acc gat gtg cgc acc tct aac tcg gcg   307
Arg Val Val Gln Ile Ser Thr Thr Asp Val Arg Thr Ser Asn Ser Ala
    55                  60                  65

gcc atg tac cta tca atg atg tcc tgg gtg aaa aat ggc gga aaa acg   355
Ala Met Tyr Leu Ser Met Met Ser Trp Val Lys Asn Gly Gly Lys Thr
70                  75                  80                  85

gtg agc agc act gcg gaa gcc gat gcc atc atc cca gag ctt agc caa   403
Val Ser Ser Thr Ala Glu Ala Asp Ala Ile Ile Pro Glu Leu Ser Gln
                90                  95                  100

ctg ttc gtg ggc cag ggc tat acc gaa agc acc tcc gcc ggc ccg ttt   451
Leu Phe Val Gly Gln Gly Tyr Thr Glu Ser Thr Ser Ala Gly Pro Phe
```

```
            105                 110                 115

gat gaa tac ctc tcc caa gga atg ggt tct aaa cca atg gtg atg atc   499
Asp Glu Tyr Leu Ser Gln Gly Met Gly Ser Lys Pro Met Val Met Ile
        120                 125                 130

tac gaa gcc cag ttc ctc gcg gaa caa aac aag gaa aac tca cgg att   547
Tyr Glu Ala Gln Phe Leu Ala Glu Gln Asn Lys Glu Asn Ser Arg Ile
    135                 140                 145

tcc ggc gat atg gaa cta gtg tat cca agc ccc acc gtg tac agc acg   595
Ser Gly Asp Met Glu Leu Val Tyr Pro Ser Pro Thr Val Tyr Ser Thr
150                 155                 160                 165

cat acg gtg gtt agc ttg agt gac gtc ggc gcg gag atc ggc gaa ctc   643
His Thr Val Val Ser Leu Ser Asp Val Gly Ala Glu Ile Gly Glu Leu
                170                 175                 180

cta gaa acc gac gaa acc ctg cag cag ttg gca gtc aaa cac ggt ttt   691
Leu Glu Thr Asp Glu Thr Leu Gln Gln Leu Ala Val Lys His Gly Phe
            185                 190                 195

agg cca aag aac tcc gca atg atc gcc gat gct ggc atg acc gac cgc   739
Arg Pro Lys Asn Ser Ala Met Ile Ala Asp Ala Gly Met Thr Asp Arg
        200                 205                 210

atg ccc aac aac ctc aat gtc att gat ccg ccg gac tat gac ttc cta   787
Met Pro Asn Asn Leu Asn Val Ile Asp Pro Pro Asp Tyr Asp Phe Leu
    215                 220                 225

gaa cga ctc att gat ggc gtg ggc gca tcg tac agt gcc acc cca gca   835
Glu Arg Leu Ile Asp Gly Val Gly Ala Ser Tyr Ser Ala Thr Pro Ala
230                 235                 240                 245

gaa gag gac aca gat cta tgaaaaatct tgtaaaaggt aca                 876
Glu Glu Asp Thr Asp Leu
                250
```

Substitute Sheet (Rule 26) RO/AU

<210> 2604
<211> 251
<212> PRT
<213> Corynebacterium glutamicum

<400> 2604

```
Met Ala Val Ala Thr Phe Gly Thr Ile Thr Asp Met Leu Glu Thr Lys
  1               5                  10                  15

Gly Ile Val Ser Asn Val Gly Gly Thr Asp Thr Ile Asp Leu Gly Ala
             20                  25                  30

Leu Leu Asn Glu Thr Gln Ala Gly Thr Arg Trp Ser Glu Leu Ser Pro
         35                  40                  45

Asn Tyr Gln Ser Asn Arg Val Val Gln Ile Ser Thr Thr Asp Val Arg
     50                  55                  60

Thr Ser Asn Ser Ala Ala Met Tyr Leu Ser Met Met Ser Trp Val Lys
 65                  70                  75                  80

Asn Gly Gly Lys Thr Val Ser Ser Thr Ala Glu Ala Asp Ala Ile Ile
```

```
                85                  90                  95

Pro Glu Leu Ser Gln Leu Phe Val Gly Gln Gly Tyr Thr Glu Ser Thr
            100                 105                 110

Ser Ala Gly Pro Phe Asp Glu Tyr Leu Ser Gln Gly Met Gly Ser Lys
        115                 120                 125

Pro Met Val Met Ile Tyr Glu Ala Gln Phe Leu Ala Glu Gln Asn Lys
    130                 135                 140

Glu Asn Ser Arg Ile Ser Gly Asp Met Glu Leu Val Tyr Pro Ser Pro
145                 150                 155                 160

Thr Val Tyr Ser Thr His Thr Val Val Ser Leu Ser Asp Val Gly Ala
                165                 170                 175

Glu Ile Gly Glu Leu Leu Glu Thr Asp Glu Thr Leu Gln Gln Leu Ala
            180                 185                 190

Val Lys His Gly Phe Arg Pro Lys Asn Ser Ala Met Ile Ala Asp Ala
        195                 200                 205

Gly Met Thr Asp Arg Met Pro Asn Asn Leu Asn Val Ile Asp Pro Pro
    210                 215                 220

Asp Tyr Asp Phe Leu Glu Arg Leu Ile Asp Gly Val Gly Ala Ser Tyr
225                 230                 235                 240

Ser Ala Thr Pro Ala Glu Glu Asp Thr Asp Leu
                245                 250


<210> 2605
<211> 1698
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1675)
<223> RXA02164

<400> 2605
tcaatgtcat tgatccgccg gactatgact tcctagaacg actcattgat ggcgtgggcg 60

catcgtacag tgccacccca gcagaagagg acacagatct atg aaa aat ctt gta   115
                                              Met Lys Asn Leu Val
                                                1               5

aaa ggt aca gcg ctg ggc ttg agc ttg gtg ctt ctg gca ggt tgt tca   163
Lys Gly Thr Ala Leu Gly Leu Ser Leu Val Leu Leu Ala Gly Cys Ser
                10                  15                  20

act gtt tcg gat tct atc gat agc ctc ggc ggg ggc ctg ggt ggt tcc   211
Thr Val Ser Asp Ser Ile Asp Ser Leu Gly Gly Gly Leu Gly Gly Ser
            25                  30                  35

tct gag act ttg aag att gtg gcc gcc aca gag ctg gaa gat ctg cag   259
Ser Glu Thr Leu Lys Ile Val Ala Ala Thr Glu Leu Glu Asp Leu Gln
        40                  45                  50
```

```
ccc gcg atc gag caa gcc tcc gac gac ttg ggt ttt gat att gaa ctg   307
Pro Ala Ile Glu Gln Ala Ser Asp Asp Leu Gly Phe Asp Ile Glu Leu
     55                  60                  65

agc ttt cca ggc ggc aca ctc agc aac agc caa gcc ctc atg gat ggc   355
Ser Phe Pro Gly Gly Thr Leu Ser Asn Ser Gln Ala Leu Met Asp Gly
 70                  75                  80                  85

gct ttt gac cag gac tat gat gcc acc tgg ttt gcc acc aac cgt tac   403
Ala Phe Asp Gln Asp Tyr Asp Ala Thr Trp Phe Ala Thr Asn Arg Tyr
                 90                  95                 100

gtc gat ctg atc ggc gct tcc aac aag ctg ggg gag acc acc aaa atc   451
Val Asp Leu Ile Gly Ala Ser Asn Lys Leu Gly Glu Thr Thr Lys Ile
            105                 110                 115

gcg acc tct ccc gtg gcg ttc ggt gtg aaa act tcc atg gcc cag gag   499
Ala Thr Ser Pro Val Ala Phe Gly Val Lys Thr Ser Met Ala Gln Glu
        120                 125                 130

ctc ggc tgg gat cag cgc cag cca acc tgg gaa gag ctg ggc cag gcc   547
Leu Gly Trp Asp Gln Arg Gln Pro Thr Trp Glu Glu Leu Gly Gln Ala
    135                 140                 145

tcg cag acc caa gat ttc acc ttc ggt atg acc gat ccg gcc act tcc   595
Ser Gln Thr Gln Asp Phe Thr Phe Gly Met Thr Asp Pro Ala Thr Ser
150                 155                 160                 165

aac tcc gga ttt tcc gcg ctc gtt gcc atg gcc acg gca tat gct gat   643
Asn Ser Gly Phe Ser Ala Leu Val Ala Met Ala Thr Ala Tyr Ala Asp
                170                 175                 180

acc ggc cag gcc tta aca acc aac gac atc ccc gcg atc gcc gag ccg   691
Thr Gly Gln Ala Leu Thr Thr Asn Asp Ile Pro Ala Ile Ala Glu Pro
            185                 190                 195

atg tcc aca tcc ctt tcc ggc caa acc atc acc tcc ggt tcc tct ggc   739
Met Ser Thr Ser Leu Ser Gly Gln Thr Ile Thr Ser Gly Ser Ser Gly
        200                 205                 210

tgg ctc aaa gac act ttc ctg gaa cag cct gac cgc gcg aat gcg atc   787
Trp Leu Lys Asp Thr Phe Leu Glu Gln Pro Asp Arg Ala Asn Ala Ile
    215                 220                 225

atc aac tac gag tcc gtc ctg cac acc atg atc agc gaa gac ggc gcc   835
Ile Asn Tyr Glu Ser Val Leu His Thr Met Ile Ser Glu Asp Gly Ala
230                 235                 240                 245

gat atc acc gtc gtg gtg ccc gcc gat ggc gtg gtc agc gcc gat tac   883
Asp Ile Thr Val Val Val Pro Ala Asp Gly Val Val Ser Ala Asp Tyr
                250                 255                 260

ccg ctc tct acg atc acg ggc tcc gac cag ggc gag cat gta gca gag   931
Pro Leu Ser Thr Ile Thr Gly Ser Asp Gln Gly Glu His Val Ala Glu
            265                 270                 275

ctg gcc ggc tgg ttc gct gag cac ccc gac gct tta aca gat act tat   979
Leu Ala Gly Trp Phe Ala Glu His Pro Asp Ala Leu Thr Asp Thr Tyr
        280                 285                 290
```

```
cga cgt ccg acc acc gcg aac gca acg ctc cca gcg gag ctt agc tcg   1027
Arg Arg Pro Thr Thr Ala Asn Ala Thr Leu Pro Ala Glu Leu Ser Ser
    295                 300                 305

cag acc atc atc gaa gct ccc ttc cca ggg agc aag acg gtc acc gac   1075
Gln Thr Ile Ile Glu Ala Pro Phe Pro Gly Ser Lys Thr Val Thr Asp
310                 315                 320                 325

gcg ctt atc gac gcc tac acc aat caa ttc cgc gtc cca ggc gaa acc   1123
Ala Leu Ile Asp Ala Tyr Thr Asn Gln Phe Arg Val Pro Gly Glu Thr
                330                 335                 340

acc ttt gtg ctc gac gtt tcc gga tcc atg ctg ggc cag cgc atc acc   1171
Thr Phe Val Leu Asp Val Ser Gly Ser Met Leu Gly Gln Arg Ile Thr
            345                 350                 355

ttg ctc aaa gac acc atg tca gac ctg atc agc ggc ggc gcg acc act   1219
Leu Leu Lys Asp Thr Met Ser Asp Leu Ile Ser Gly Gly Ala Thr Thr
        360                 365                 370

gac ctt gcc aac gtg tcc ctg cgc gac cgc gaa aaa gta tcg atc att   1267
Asp Leu Ala Asn Val Ser Leu Arg Asp Arg Glu Lys Val Ser Ile Ile
    375                 380                 385

cct ttc agc ttc ggg cca cac gaa gta atc agc gaa acc ctc ggt gcg   1315
Pro Phe Ser Phe Gly Pro His Glu Val Ile Ser Glu Thr Leu Gly Ala
390                 395                 400                 405

gtg ggc agc cca agc cgc acc gat ctg cag cag cgc gtt gaa gcc ttg   1363
Val Gly Ser Pro Ser Arg Thr Asp Leu Gln Gln Arg Val Glu Ala Leu
                410                 415                 420

caa gca gac ggc gga acc gga att tac gac gca gtg ctc gcc gcc tac   1411
Gln Ala Asp Gly Gly Thr Gly Ile Tyr Asp Ala Val Leu Ala Ala Tyr
            425                 430                 435

gca gag tcc gct ggt ggc gac tac atc cca tcc atc gtg ctc atg acc   1459
Ala Glu Ser Ala Gly Gly Asp Tyr Ile Pro Ser Ile Val Leu Met Thr
        440                 445                 450

gac ggc gaa ctc acc gca gga cga acc tac gat caa ttc ctc acc gaa   1507
Asp Gly Glu Leu Thr Ala Gly Arg Thr Tyr Asp Gln Phe Leu Thr Glu
    455                 460                 465

tgg aac gcg ctt cct agc aat atc cga tca att cca gtg ttt gtc atc   1555
Trp Asn Ala Leu Pro Ser Asn Ile Arg Ser Ile Pro Val Phe Val Ile
470                 475                 480                 485

ctt tac ggt gaa gcc aat gtt gcg gat atg gaa caa ttg gca gca aca   1603
Leu Tyr Gly Glu Ala Asn Val Ala Asp Met Glu Gln Leu Ala Ala Thr
                490                 495                 500

acc ggc ggt gag acc ttt gac gcc atc aac ggt gac cta gac gaa gca   1651
Thr Gly Gly Glu Thr Phe Asp Ala Ile Asn Gly Asp Leu Asp Glu Ala
            505                 510                 515

ttt aag gag att cgt gcc tac caa taatggagga tccttctttt tct        1698
Phe Lys Glu Ile Arg Ala Tyr Gln
        520                 525
```

<210> 2606
<211> 525
<212> PRT
<213> Corynebacterium glutamicum

<400> 2606
Met Lys Asn Leu Val Lys Gly Thr Ala Leu Gly Leu Ser Leu Val Leu
1 5 10 15

Leu Ala Gly Cys Ser Thr Val Ser Asp Ser Ile Asp Ser Leu Gly Gly
20 25 30

Gly Leu Gly Gly Ser Ser Glu Thr Leu Lys Ile Val Ala Ala Thr Glu
35 40 45

Leu Glu Asp Leu Gln Pro Ala Ile Glu Gln Ala Ser Asp Asp Leu Gly
50 55 60

Phe Asp Ile Glu Leu Ser Phe Pro Gly Gly Thr Leu Ser Asn Ser Gln
65 70 75 80

Ala Leu Met Asp Gly Ala Phe Asp Gln Asp Tyr Asp Ala Thr Trp Phe
85 90 95

Ala Thr Asn Arg Tyr Val Asp Leu Ile Gly Ala Ser Asn Lys Leu Gly
100 105 110

Glu Thr Thr Lys Ile Ala Thr Ser Pro Val Ala Phe Gly Val Lys Thr
115 120 125

Ser Met Ala Gln Glu Leu Gly Trp Asp Gln Arg Gln Pro Thr Trp Glu
130 135 140

Glu Leu Gly Gln Ala Ser Gln Thr Gln Asp Phe Thr Phe Gly Met Thr
145 150 155 160

Asp Pro Ala Thr Ser Asn Ser Gly Phe Ser Ala Leu Val Ala Met Ala
165 170 175

Thr Ala Tyr Ala Asp Thr Gly Gln Ala Leu Thr Thr Asn Asp Ile Pro
180 185 190

Ala Ile Ala Glu Pro Met Ser Thr Ser Leu Ser Gly Gln Thr Ile Thr
195 200 205

Ser Gly Ser Ser Gly Trp Leu Lys Asp Thr Phe Leu Glu Gln Pro Asp
210 215 220

Arg Ala Asn Ala Ile Ile Asn Tyr Glu Ser Val Leu His Thr Met Ile
225 230 235 240

Ser Glu Asp Gly Ala Asp Ile Thr Val Val Val Pro Ala Asp Gly Val
245 250 255

Val Ser Ala Asp Tyr Pro Leu Ser Thr Ile Thr Gly Ser Asp Gln Gly
260 265 270

Glu His Val Ala Glu Leu Ala Gly Trp Phe Ala Glu His Pro Asp Ala
275 280 285

Leu Thr Asp Thr Tyr Arg Arg Pro Thr Thr Ala Asn Ala Thr Leu Pro

```
    290                 295                 300

Ala Glu Leu Ser Ser Gln Thr Ile Ile Glu Ala Pro Phe Pro Gly Ser
305                 310                 315                 320

Lys Thr Val Thr Asp Ala Leu Ile Asp Ala Tyr Thr Asn Gln Phe Arg
                325                 330                 335

Val Pro Gly Glu Thr Thr Phe Val Leu Asp Val Ser Gly Ser Met Leu
            340                 345                 350

Gly Gln Arg Ile Thr Leu Leu Lys Asp Thr Met Ser Asp Leu Ile Ser
        355                 360                 365

Gly Gly Ala Thr Thr Asp Leu Ala Asn Val Ser Leu Arg Asp Arg Glu
    370                 375                 380

Lys Val Ser Ile Ile Pro Phe Ser Phe Gly Pro His Glu Val Ile Ser
385                 390                 395                 400

Glu Thr Leu Gly Ala Val Gly Ser Pro Ser Arg Thr Asp Leu Gln Gln
                405                 410                 415

Arg Val Glu Ala Leu Gln Ala Asp Gly Gly Thr Gly Ile Tyr Asp Ala
            420                 425                 430

Val Leu Ala Ala Tyr Ala Glu Ser Ala Gly Gly Asp Tyr Ile Pro Ser
        435                 440                 445

Ile Val Leu Met Thr Asp Gly Glu Leu Thr Ala Gly Arg Thr Tyr Asp
    450                 455                 460

Gln Phe Leu Thr Glu Trp Asn Ala Leu Pro Ser Asn Ile Arg Ser Ile
465                 470                 475                 480

Pro Val Phe Val Ile Leu Tyr Gly Glu Ala Asn Val Ala Asp Met Glu
                485                 490                 495

Gln Leu Ala Ala Thr Thr Gly Gly Glu Thr Phe Asp Ala Ile Asn Gly
            500                 505                 510

Asp Leu Asp Glu Ala Phe Lys Glu Ile Arg Ala Tyr Gln
        515                 520                 525


<210> 2607
<211> 735
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(712)
<223> RXA02165

<400> 2607
gaagccaatg ttgcggatat ggaacaattg gcagcaacaa ccggcggtga gacctttgac 60

gccatcaacg gtgacctaga cgaagcattt aaggagattc gtg cct acc aat aat   115
                                              Val Pro Thr Asn Asn
                                                1               5
```

```
gga gga tcc ttc ttt ttc tcc cgc aag aat ctc gcg ggt atc gct att   163
Gly Gly Ser Phe Phe Phe Ser Arg Lys Asn Leu Ala Gly Ile Ala Ile
                 10                  15                  20

gca acg ctg att atc gcg ctg cac tta gtg atc gga ctc gga gca ttt   211
Ala Thr Leu Ile Ile Ala Leu His Leu Val Ile Gly Leu Gly Ala Phe
             25                  30                  35

tgg cct gtt gtc gcc atc gcc gga tac ggc gct gcg gtg gca ctt aca   259
Trp Pro Val Val Ala Ile Ala Gly Tyr Gly Ala Ala Val Ala Leu Thr
         40                  45                  50

cct aaa aac cct ccg aag aag gaa ctc cct ccg gtt cag gca act ccc   307
Pro Lys Asn Pro Pro Lys Lys Glu Leu Pro Pro Val Gln Ala Thr Pro
     55                  60                  65

gaa tta gat agc ccg ggt ctg ctt gca gcc agg tct caa gaa ctc gtg   355
Glu Leu Asp Ser Pro Gly Leu Leu Ala Ala Arg Ser Gln Glu Leu Val
 70                  75                  80                  85

aga act atg tat agc cac ggt gct gca gca cca gtg atc gaa gcg att   403
Arg Thr Met Tyr Ser His Gly Ala Ala Ala Pro Val Ile Glu Ala Ile
                 90                  95                 100

aag agg cta gac agc tca ctg caa ttg gtc att ggt aac tgg aca agc   451
Lys Arg Leu Asp Ser Ser Leu Gln Leu Val Ile Gly Asn Trp Thr Ser
            105                 110                 115

ctg acc aat ttt ccc gag cac caa gtc acc att cgc tca att atc aac   499
Leu Thr Asn Phe Pro Glu His Gln Val Thr Ile Arg Ser Ile Ile Asn
        120                 125                 130

cag tac atc cca ggc att atc gac gct tac ctg aag atc ccc acc cgc   547
Gln Tyr Ile Pro Gly Ile Ile Asp Ala Tyr Leu Lys Ile Pro Thr Arg
    135                 140                 145

aac gat cct cgg gca gtc gaa gac ctc att gaa tcc ttc gac ctc ctg   595
Asn Asp Pro Arg Ala Val Glu Asp Leu Ile Glu Ser Phe Asp Leu Leu
150                 155                 160                 165

aac tcc gag acg atg aag atc ttc aat gcg atc caa gaa caa ggc ctt   643
Asn Ser Glu Thr Met Lys Ile Phe Asn Ala Ile Gln Glu Gln Gly Leu
                170                 175                 180

aat aac ctt gaa gat cac ggt cgc gca ctg cgc atg caa ttt ggt caa   691
Asn Asn Leu Glu Asp His Gly Arg Ala Leu Arg Met Gln Phe Gly Gln
            185                 190                 195

ctg cca gaa gaa ttc cgg gaa tagccactca atgcagttaa gtt            735
Leu Pro Glu Glu Phe Arg Glu
        200
```

<210> 2608
<211> 204
<212> PRT
<213> Corynebacterium glutamicum

<400> 2608
Val Pro Thr Asn Asn Gly Gly Ser Phe Phe Phe Ser Arg Lys Asn Leu

```
  1               5                  10                  15

Ala Gly Ile Ala Ile Ala Thr Leu Ile Ile Ala Leu His Leu Val Ile
            20                  25                  30

Gly Leu Gly Ala Phe Trp Pro Val Val Ala Ile Ala Gly Tyr Gly Ala
        35                  40                  45

Ala Val Ala Leu Thr Pro Lys Asn Pro Pro Lys Lys Glu Leu Pro Pro
    50                  55                  60

Val Gln Ala Thr Pro Glu Leu Asp Ser Pro Gly Leu Leu Ala Ala Arg
65                  70                  75                  80

Ser Gln Glu Leu Val Arg Thr Met Tyr Ser His Gly Ala Ala Ala Pro
                85                  90                  95

Val Ile Glu Ala Ile Lys Arg Leu Asp Ser Ser Leu Gln Leu Val Ile
            100                 105                 110

Gly Asn Trp Thr Ser Leu Thr Asn Phe Pro Glu His Gln Val Thr Ile
        115                 120                 125

Arg Ser Ile Ile Asn Gln Tyr Ile Pro Gly Ile Ile Asp Ala Tyr Leu
    130                 135                 140

Lys Ile Pro Thr Arg Asn Asp Pro Arg Ala Val Glu Asp Leu Ile Glu
145                 150                 155                 160

Ser Phe Asp Leu Leu Asn Ser Glu Thr Met Lys Ile Phe Asn Ala Ile
                165                 170                 175

Gln Glu Gln Gly Leu Asn Asn Leu Glu Asp His Gly Arg Ala Leu Arg
            180                 185                 190

Met Gln Phe Gly Gln Leu Pro Glu Glu Phe Arg Glu
        195                 200


<210> 2609
<211> 300
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(277)
<223> RXA02166

<400> 2609
cggtcgcgca ctgcgcatgc aatttggtca actgccagaa gaattccggg aatagccact 60

caatgcagtt aagtttttcc tgcccggtag gatggtccgt atg agt ctt gat cca   115
                                            Met Ser Leu Asp Pro
                                              1               5

cag ctt ctt gaa gtc ctg gcc tgc cca aag gac aag ggc cca ctt cga   163
Gln Leu Leu Glu Val Leu Ala Cys Pro Lys Asp Lys Gly Pro Leu Arg
                10                  15                  20

tat ctg gag agc gaa cag ctc ttg gtc aac gaa cgc ctc aac ctg gcc   211
```

```
Tyr Leu Glu Ser Glu Gln Leu Leu Val Asn Glu Arg Leu Asn Leu Ala
            25                  30                  35

tat cgc att gac gac gga att ccg gtg ctt ctc atc gac gaa gcc acc   259
Tyr Arg Ile Asp Asp Gly Ile Pro Val Leu Leu Ile Asp Glu Ala Thr
        40                  45                  50

gag tgg acc ccc aac aac tagaagtaca tcaaggacat ttt                 300
Glu Trp Thr Pro Asn Asn
    55


<210> 2610
<211> 59
<212> PRT
<213> Corynebacterium glutamicum

<400> 2610
Met Ser Leu Asp Pro Gln Leu Leu Glu Val Leu Ala Cys Pro Lys Asp
  1               5                  10                  15

Lys Gly Pro Leu Arg Tyr Leu Glu Ser Glu Gln Leu Leu Val Asn Glu
            20                  25                  30

Arg Leu Asn Leu Ala Tyr Arg Ile Asp Asp Gly Ile Pro Val Leu Leu
        35                  40                  45

Ile Asp Glu Ala Thr Glu Trp Thr Pro Asn Asn
    50                  55


<210> 2611
<211> 2937
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2914)
<223> RXA02168

<400> 2611
agggtttagt catctatttc ggctacgctc acgtaaccta cgcattcgta agtggtcatg 60

ggtccaagaa gcccattcca agacttagga gctttatttc gtg agt att tct tca   115
                                        Val Ser Ile Ser Ser
                                          1               5

ctg aca ccg ctg cac tct ttc aaa gag cca gca att ctg tac gcc ggt   163
Leu Thr Pro Leu His Ser Phe Lys Glu Pro Ala Ile Leu Tyr Ala Gly
                10                  15                  20

cag gct tct gcc tgg cag cag gtg atc gct gat tcc agc gaa gac cac   211
Gln Ala Ser Ala Trp Gln Gln Val Ile Ala Asp Ser Ser Glu Asp His
            25                  30                  35

atc acc gca acg cac ctg cgc gag ctc ctg tct cgc tcc cgt gca aag   259
Ile Thr Ala Thr His Leu Arg Glu Leu Leu Ser Arg Ser Arg Ala Lys
        40                  45                  50

act gca cct ttc gct cgc caa atc acc gcc atc gtg cct ggc tca ctt   307
```

```
Thr Ala Pro Phe Ala Arg Gln Ile Thr Ala Ile Val Pro Gly Ser Leu
     55                  60                  65

gct cgt ctt gag gaa ctg acc cgc gaa gac gca caa atc ggt gca gac   355
Ala Arg Leu Glu Glu Leu Thr Arg Glu Asp Ala Gln Ile Gly Ala Asp
 70                  75                  80                  85

atc gac gca cag cct gcc gtt tcc att cca ggc att ctg ctg gga cag   403
Ile Asp Ala Gln Pro Ala Val Ser Ile Pro Gly Ile Leu Leu Gly Gln
                 90                  95                 100

atc gct gca acc cgt cag ctg cgt gac ctc gga ctc gat gtc gca gca   451
Ile Ala Ala Thr Arg Gln Leu Arg Asp Leu Gly Leu Asp Val Ala Ala
            105                 110                 115

gct tcc cgc ctt gga cac tcc cag ggc att ttg ggc gtt gaa gca gta   499
Ala Ser Arg Leu Gly His Ser Gln Gly Ile Leu Gly Val Glu Ala Val
        120                 125                 130

gac aat gaa gaa gac gtt tta gct ttc gcc atc ctg ctg ggc gca gca   547
Asp Asn Glu Glu Asp Val Leu Ala Phe Ala Ile Leu Leu Gly Ala Ala
    135                 140                 145

gct tcc cag ttc gct ggc aag ggc gca cat atg ctc tct gtt cgc ggc   595
Ala Ser Gln Phe Ala Gly Lys Gly Ala His Met Leu Ser Val Arg Gly
150                 155                 160                 165

ctg tcc cgt gag atc atc cag gac acc atc gct ggt gtc gat ggg gta   643
Leu Ser Arg Glu Ile Ile Gln Asp Thr Ile Ala Gly Val Asp Gly Val
                170                 175                 180

gag gtc tcc ctg cgc aac gct cgt gca cac ttt gtt gtc tct ggt aag   691
Glu Val Ser Leu Arg Asn Ala Arg Ala His Phe Val Val Ser Gly Lys
            185                 190                 195

cca gag gca ctg aag aag gct gct gct gct cta cag cgc gca gct gat   739
Pro Glu Ala Leu Lys Lys Ala Ala Ala Ala Leu Gln Arg Ala Ala Asp
        200                 205                 210

gtt tac aac gaa gac atc aac gaa aag cgc aag ggt gga tcc ctg gca   787
Val Tyr Asn Glu Asp Ile Asn Glu Lys Arg Lys Gly Gly Ser Leu Ala
    215                 220                 225

gag cct aag ttt gac tac ttg gat gtg gcc att cct ttc cac cac tcc   835
Glu Pro Lys Phe Asp Tyr Leu Asp Val Ala Ile Pro Phe His His Ser
230                 235                 240                 245

tcc atg cag gac gca gcc gac ttg gct gtc gag tgg gca acc acc tgt   883
Ser Met Gln Asp Ala Ala Asp Leu Ala Val Glu Trp Ala Thr Thr Cys
                250                 255                 260

ggc cta aac gtc aac gcg cgc gcg ttg gca gaa gca att cta gtt aac   931
Gly Leu Asn Val Asn Ala Arg Ala Leu Ala Glu Ala Ile Leu Val Asn
            265                 270                 275

cca gct gac tgg gtt gag cag atc gca aac ctc aag gct gat tac gtt   979
Pro Ala Asp Trp Val Glu Gln Ile Ala Asn Leu Lys Ala Asp Tyr Val
        280                 285                 290

ctt tcc ctc gat gca ggc gtc agc cgt ttc acc gct cca ttg cta gac   1027
Leu Ser Leu Asp Ala Gly Val Ser Arg Phe Thr Ala Pro Leu Leu Asp
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    295                 300                 305

ggt cgc gga atc tct ttg gtt cct gcg ttc tcc gct gca gag cgc gac   1075
Gly Arg Gly Ile Ser Leu Val Pro Ala Phe Ser Ala Ala Glu Arg Asp
310                 315                 320                 325

aac ttg gct cgc cct ggc ttc cac gtt cct acc gct gag gat tgg tcc   1123
Asn Leu Ala Arg Pro Gly Phe His Val Pro Thr Ala Glu Asp Trp Ser
                330                 335                 340

gag ttc gct cca aag ctg gtt aag ctt cca aac ggt gag cac aag gtt   1171
Glu Phe Ala Pro Lys Leu Val Lys Leu Pro Asn Gly Glu His Lys Val
            345                 350                 355

ctc acc ggg ttc tcc cgc ctg act ggt tat tcc cca atc gtc ctg gct   1219
Leu Thr Gly Phe Ser Arg Leu Thr Gly Tyr Ser Pro Ile Val Leu Ala
        360                 365                 370

ggc atg acc cca acc acc gtt gat cct gag atc gtt gca gct gca gcg   1267
Gly Met Thr Pro Thr Thr Val Asp Pro Glu Ile Val Ala Ala Ala Ala
    375                 380                 385

aac gct gga cac tgg gcc gaa atg gcc ggt ggc gga cag tac tct gaa   1315
Asn Ala Gly His Trp Ala Glu Met Ala Gly Gly Gly Gln Tyr Ser Glu
390                 395                 400                 405

gaa gtc ttc acc aag aac aag gaa aag ctc gtt tcc ctg ctc aag gtt   1363
Glu Val Phe Thr Lys Asn Lys Glu Lys Leu Val Ser Leu Leu Lys Val
                410                 415                 420

gga cgc tcc gca cag ttc aac tcc atg ttc ttc gac cgc tac atg tgg   1411
Gly Arg Ser Ala Gln Phe Asn Ser Met Phe Phe Asp Arg Tyr Met Trp
            425                 430                 435

aac ctg cag ttc ggt gca cag cgc atc gtt tcc aag gca cgt gca acc   1459
Asn Leu Gln Phe Gly Ala Gln Arg Ile Val Ser Lys Ala Arg Ala Thr
        440                 445                 450

ggt acc tcc atc aac ggt gtt gtt gtc tcc gct ggt atc cca gag gtt   1507
Gly Thr Ser Ile Asn Gly Val Val Val Ser Ala Gly Ile Pro Glu Val
    455                 460                 465

gag gaa gca act gag ctg atc aac gat ctg aac gct gat ggc ttc cca   1555
Glu Glu Ala Thr Glu Leu Ile Asn Asp Leu Asn Ala Asp Gly Phe Pro
470                 475                 480                 485

tac gtt gca ttc aag cca ggc acc gtg gat cag atc cgc gca acc ctg   1603
Tyr Val Ala Phe Lys Pro Gly Thr Val Asp Gln Ile Arg Ala Thr Leu
                490                 495                 500

aag att gct gat gca aac cca gag acc aag atc atc atc cag atc gag   1651
Lys Ile Ala Asp Ala Asn Pro Glu Thr Lys Ile Ile Ile Gln Ile Glu
            505                 510                 515

gac gga cac gct ggt ggc cac cac tcc tgg gtc aac ttg gac gat ctg   1699
Asp Gly His Ala Gly Gly His His Ser Trp Val Asn Leu Asp Asp Leu
        520                 525                 530

ctc ctg acc acc tac gca gag ctg cgt tcc cgc aag aac gtt gtc gtc   1747
Leu Leu Thr Thr Tyr Ala Glu Leu Arg Ser Arg Lys Asn Val Val Val
    535                 540                 545
```

```
atg atc ggt ggc ggc atc gga acc cct gca aag gct gct tac tac ctg   1795
Met Ile Gly Gly Gly Ile Gly Thr Pro Ala Lys Ala Ala Tyr Tyr Leu
550                 555                 560                 565

acc ggt gaa tgg tcc acc gat ttg ggc ttc cca gca atg cca gtg gac   1843
Thr Gly Glu Trp Ser Thr Asp Leu Gly Phe Pro Ala Met Pro Val Asp
                570                 575                 580

ggc atc ctc gtg ggt acc gct gcc atg gca acc aag gaa gca acc act   1891
Gly Ile Leu Val Gly Thr Ala Ala Met Ala Thr Lys Glu Ala Thr Thr
            585                 590                 595

tct cct cag gtc aag cag gca ctg gtc gac acc cca ggt gtt gat cca   1939
Ser Pro Gln Val Lys Gln Ala Leu Val Asp Thr Pro Gly Val Asp Pro
        600                 605                 610

cac gac gct ggc ggc tgg gtt ggc cgt ggc gat gct cgt ggt ggc gtg   1987
His Asp Ala Gly Gly Trp Val Gly Arg Gly Asp Ala Arg Gly Gly Val
    615                 620                 625

acc tct ggt ctg tca cac ctg cac gct gac atg tac gag ctg gac aac   2035
Thr Ser Gly Leu Ser His Leu His Ala Asp Met Tyr Glu Leu Asp Asn
630                 635                 640                 645

gat tct gct gca gct tcc cgc ctg atc tct tcc atc gat tct gat gat   2083
Asp Ser Ala Ala Ala Ser Arg Leu Ile Ser Ser Ile Asp Ser Asp Asp
                650                 655                 660

tac gca gat cac cgc gaa gag ctc atc gag gct atc aac aag acc gct   2131
Tyr Ala Asp His Arg Glu Glu Leu Ile Glu Ala Ile Asn Lys Thr Ala
            665                 670                 675

aag cct ttc ttc ggc gag gtc gaa gag atg act tac gca gag tgg atc   2179
Lys Pro Phe Phe Gly Glu Val Glu Glu Met Thr Tyr Ala Glu Trp Ile
        680                 685                 690

cag cgt tgg gtt gag ctt gct tac cca act cag gac cca acc tgg gat   2227
Gln Arg Trp Val Glu Leu Ala Tyr Pro Thr Gln Asp Pro Thr Trp Asp
    695                 700                 705

gat cgt ttc ctc gat ttg gtt cac cgc att gaa gct cgt ctc aac gag   2275
Asp Arg Phe Leu Asp Leu Val His Arg Ile Glu Ala Arg Leu Asn Glu
710                 715                 720                 725

gca gag cac ggc gcc atc acc aca ctg ttc cca gac cat gcg tct gtg   2323
Ala Glu His Gly Ala Ile Thr Thr Leu Phe Pro Asp His Ala Ser Val
                730                 735                 740

gaa aat gag gaa gag gcc gtc gaa aag ctt ctt gct gct tac ccg cag   2371
Glu Asn Glu Glu Glu Ala Val Glu Lys Leu Leu Ala Ala Tyr Pro Gln
            745                 750                 755

gcc cgc gag atc cag gtc tct gcg cgc gac gcc gcg tgg ttt att ggt   2419
Ala Arg Glu Ile Gln Val Ser Ala Arg Asp Ala Ala Trp Phe Ile Gly
        760                 765                 770

ctg tgc cgc aag cac cac aag cct atg cct tgg gtt cca gca atc gat   2467
Leu Cys Arg Lys His His Lys Pro Met Pro Trp Val Pro Ala Ile Asp
    775                 780                 785
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gct gac cta gca cgc tgg tgg ggc ctt gac acc ctg tgg cag tcc cag   2515
Ala Asp Leu Ala Arg Trp Trp Gly Leu Asp Thr Leu Trp Gln Ser Gln
790                 795                 800                 805

aac gag cgc tac ggc gcg aac tca gtc cgc gtt atc cca gga cca gtc   2563
Asn Glu Arg Tyr Gly Ala Asn Ser Val Arg Val Ile Pro Gly Pro Val
                810                 815                 820

tcc gtc gcc ggc atc gac cgt gtt gac gag cca gtt gca gag ctg ctc   2611
Ser Val Ala Gly Ile Asp Arg Val Asp Glu Pro Val Ala Glu Leu Leu
            825                 830                 835

ggc cgc ttc gaa gct gcc tgc gtt gac gct ctc gac ggc gag cca gaa   2659
Gly Arg Phe Glu Ala Ala Cys Val Asp Ala Leu Asp Gly Glu Pro Glu
        840                 845                 850

gag atc ttc gct cgc ctc aat gag tcc aag aac gag cgc gaa ttc ctg   2707
Glu Ile Phe Ala Arg Leu Asn Glu Ser Lys Asn Glu Arg Glu Phe Leu
    855                 860                 865

ctg gct acc cca cac atc gtg tgg cac ggc aac ctg atc gac aac cca   2755
Leu Ala Thr Pro His Ile Val Trp His Gly Asn Leu Ile Asp Asn Pro
870                 875                 880                 885

gct cac gtc ctc aac gag ggt gct ttc gag ctc atc gag gag gat ggc   2803
Ala His Val Leu Asn Glu Gly Ala Phe Glu Leu Ile Glu Glu Asp Gly
                890                 895                 900

tac tgg gtc atc cgt atc ctg gct gat tcc tac ttc gac gat ctg cca   2851
Tyr Trp Val Ile Arg Ile Leu Ala Asp Ser Tyr Phe Asp Asp Leu Pro
            905                 910                 915

gtt gag cag cgc cca tac ctg gtt cag cat gtt gac atc cca gtt gag   2899
Val Glu Gln Arg Pro Tyr Leu Val Gln His Val Asp Ile Pro Val Glu
        920                 925                 930

ctg ggt gac gct ggt tgaaccggtg gtttcccaat tgg                    2937
Leu Gly Asp Ala Gly
    935
```

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<210> 2612
<211> 938
<212> PRT
<213> Corynebacterium glutamicum

<400> 2612

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Val Ser Ile Ser Ser Leu Thr Pro Leu His Ser Phe Lys Glu Pro Ala
  1               5                  10                  15

Ile Leu Tyr Ala Gly Gln Ala Ser Ala Trp Gln Gln Val Ile Ala Asp
             20                  25                  30

Ser Ser Glu Asp His Ile Thr Ala Thr His Leu Arg Glu Leu Leu Ser
         35                  40                  45

Arg Ser Arg Ala Lys Thr Ala Pro Phe Ala Arg Gln Ile Thr Ala Ile
     50                  55                  60

Val Pro Gly Ser Leu Ala Arg Leu Glu Glu Leu Thr Arg Glu Asp Ala
 65                  70                  75                  80
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Gln Ile Gly Ala Asp Ile Asp Ala Gln Pro Ala Val Ser Ile Pro Gly
                 85                  90                  95

Ile Leu Leu Gly Gln Ile Ala Ala Thr Arg Gln Leu Arg Asp Leu Gly
            100                 105                 110

Leu Asp Val Ala Ala Ala Ser Arg Leu Gly His Ser Gln Gly Ile Leu
        115                 120                 125

Gly Val Glu Ala Val Asp Asn Glu Glu Asp Val Leu Ala Phe Ala Ile
    130                 135                 140

Leu Leu Gly Ala Ala Ala Ser Gln Phe Ala Gly Lys Gly Ala His Met
145                 150                 155                 160

Leu Ser Val Arg Gly Leu Ser Arg Glu Ile Ile Gln Asp Thr Ile Ala
                165                 170                 175

Gly Val Asp Gly Val Glu Val Ser Leu Arg Asn Ala Arg Ala His Phe
            180                 185                 190

Val Val Ser Gly Lys Pro Glu Ala Leu Lys Lys Ala Ala Ala Ala Leu
        195                 200                 205

Gln Arg Ala Ala Asp Val Tyr Asn Glu Asp Ile Asn Glu Lys Arg Lys
    210                 215                 220

Gly Gly Ser Leu Ala Glu Pro Lys Phe Asp Tyr Leu Asp Val Ala Ile
225                 230                 235                 240

Pro Phe His His Ser Ser Met Gln Asp Ala Ala Asp Leu Ala Val Glu
                245                 250                 255

Trp Ala Thr Thr Cys Gly Leu Asn Val Asn Ala Arg Ala Leu Ala Glu
            260                 265                 270

Ala Ile Leu Val Asn Pro Ala Asp Trp Val Glu Gln Ile Ala Asn Leu
        275                 280                 285

Lys Ala Asp Tyr Val Leu Ser Leu Asp Ala Gly Val Ser Arg Phe Thr
    290                 295                 300

Ala Pro Leu Leu Asp Gly Arg Gly Ile Ser Leu Val Pro Ala Phe Ser
305                 310                 315                 320

Ala Ala Glu Arg Asp Asn Leu Ala Arg Pro Gly Phe His Val Pro Thr
                325                 330                 335

Ala Glu Asp Trp Ser Glu Phe Ala Pro Lys Leu Val Lys Leu Pro Asn
            340                 345                 350

Gly Glu His Lys Val Leu Thr Gly Phe Ser Arg Leu Thr Gly Tyr Ser
        355                 360                 365

Pro Ile Val Leu Ala Gly Met Thr Pro Thr Thr Val Asp Pro Glu Ile
    370                 375                 380

Val Ala Ala Ala Ala Asn Ala Gly His Trp Ala Glu Met Ala Gly Gly
385                 390                 395                 400
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Gly Gln Tyr Ser Glu Glu Val Phe Thr Lys Asn Lys Glu Lys Leu Val
                405                 410                 415

Ser Leu Leu Lys Val Gly Arg Ser Ala Gln Phe Asn Ser Met Phe Phe
            420                 425                 430

Asp Arg Tyr Met Trp Asn Leu Gln Phe Gly Ala Gln Arg Ile Val Ser
        435                 440                 445

Lys Ala Arg Ala Thr Gly Thr Ser Ile Asn Gly Val Val Val Ser Ala
    450                 455                 460

Gly Ile Pro Glu Val Glu Glu Ala Thr Glu Leu Ile Asn Asp Leu Asn
465                 470                 475                 480

Ala Asp Gly Phe Pro Tyr Val Ala Phe Lys Pro Gly Thr Val Asp Gln
                485                 490                 495

Ile Arg Ala Thr Leu Lys Ile Ala Asp Ala Asn Pro Glu Thr Lys Ile
            500                 505                 510

Ile Ile Gln Ile Glu Asp Gly His Ala Gly Gly His His Ser Trp Val
        515                 520                 525

Asn Leu Asp Asp Leu Leu Leu Thr Thr Tyr Ala Glu Leu Arg Ser Arg
    530                 535                 540

Lys Asn Val Val Val Met Ile Gly Gly Gly Ile Gly Thr Pro Ala Lys
545                 550                 555                 560

Ala Ala Tyr Tyr Leu Thr Gly Glu Trp Ser Thr Asp Leu Gly Phe Pro
                565                 570                 575

Ala Met Pro Val Asp Gly Ile Leu Val Gly Thr Ala Ala Met Ala Thr
            580                 585                 590

Lys Glu Ala Thr Thr Ser Pro Gln Val Lys Gln Ala Leu Val Asp Thr
        595                 600                 605

Pro Gly Val Asp Pro His Asp Ala Gly Gly Trp Val Gly Arg Gly Asp
    610                 615                 620

Ala Arg Gly Gly Val Thr Ser Gly Leu Ser His Leu His Ala Asp Met
625                 630                 635                 640

Tyr Glu Leu Asp Asn Asp Ser Ala Ala Ala Ser Arg Leu Ile Ser Ser
                645                 650                 655

Ile Asp Ser Asp Asp Tyr Ala Asp His Arg Glu Glu Leu Ile Glu Ala
            660                 665                 670

Ile Asn Lys Thr Ala Lys Pro Phe Phe Gly Glu Val Glu Glu Met Thr
        675                 680                 685

Tyr Ala Glu Trp Ile Gln Arg Trp Val Glu Leu Ala Tyr Pro Thr Gln
    690                 695                 700

Asp Pro Thr Trp Asp Asp Arg Phe Leu Asp Leu Val His Arg Ile Glu
705                 710                 715                 720

Ala Arg Leu Asn Glu Ala Glu His Gly Ala Ile Thr Thr Leu Phe Pro
```

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                725                 730                 735

Asp His Ala Ser Val Glu Asn Glu Glu Glu Ala Val Glu Lys Leu Leu
            740                 745                 750

Ala Ala Tyr Pro Gln Ala Arg Glu Ile Gln Val Ser Ala Arg Asp Ala
        755                 760                 765

Ala Trp Phe Ile Gly Leu Cys Arg Lys His His Lys Pro Met Pro Trp
    770                 775                 780

Val Pro Ala Ile Asp Ala Asp Leu Ala Arg Trp Trp Gly Leu Asp Thr
785                 790                 795                 800

Leu Trp Gln Ser Gln Asn Glu Arg Tyr Gly Ala Asn Ser Val Arg Val
                805                 810                 815

Ile Pro Gly Pro Val Ser Val Ala Gly Ile Asp Arg Val Asp Glu Pro
            820                 825                 830

Val Ala Glu Leu Leu Gly Arg Phe Glu Ala Ala Cys Val Asp Ala Leu
        835                 840                 845

Asp Gly Glu Pro Glu Glu Ile Phe Ala Arg Leu Asn Glu Ser Lys Asn
    850                 855                 860

Glu Arg Glu Phe Leu Leu Ala Thr Pro His Ile Val Trp His Gly Asn
865                 870                 875                 880

Leu Ile Asp Asn Pro Ala His Val Leu Asn Glu Gly Ala Phe Glu Leu
                885                 890                 895

Ile Glu Glu Asp Gly Tyr Trp Val Ile Arg Ile Leu Ala Asp Ser Tyr
            900                 905                 910

Phe Asp Asp Leu Pro Val Glu Gln Arg Pro Tyr Leu Val Gln His Val
        915                 920                 925

Asp Ile Pro Val Glu Leu Gly Asp Ala Gly
    930                 935


<210> 2613
<211> 897
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(874)
<223> RXA02170

<400> 2613
atttaaaccg cccactctcc agtcggagga tgggcggttt tcgcatgcag tactattagt 60

ggacgtgtca agaacttcta aggttcaccc gggatggcgg gtg tct act gtc ctt   115
                                            Val Ser Thr Val Leu
                                              1               5

tta gca gga gta gtt att att ggc gga att ttt act ctc cct cag aag   163
Leu Ala Gly Val Val Ile Ile Gly Gly Ile Phe Thr Leu Pro Gln Lys
```

```
                    10                  15                  20

gag gaa gta aag gtt tcc gaa ttg cag cca cag gcc agc gct gca tcc   211
Glu Glu Val Lys Val Ser Glu Leu Gln Pro Gln Ala Ser Ala Ala Ser
            25                  30                  35

atc ccg tct tca tct tcc aca gct ggg aaa gca gtg gaa gaa agc cct   259
Ile Pro Ser Ser Ser Ser Thr Ala Gly Lys Ala Val Glu Glu Ser Pro
        40                  45                  50

cta acg cag ttt gtg gaa aac tcg aca ggc tcc caa att acg tac atg   307
Leu Thr Gln Phe Val Glu Asn Ser Thr Gly Ser Gln Ile Thr Tyr Met
    55                  60                  65

agc ctg aaa gac gat ttc cat act ggc acg tct acg gaa cgt ttt gcg   355
Ser Leu Lys Asp Asp Phe His Thr Gly Thr Ser Thr Glu Arg Phe Ala
70                  75                  80                  85

cgc cca gcg tta agt ttg tct aag ctc tac atc gct gaa tat gtg ctc   403
Arg Pro Ala Leu Ser Leu Ser Lys Leu Tyr Ile Ala Glu Tyr Val Leu
                90                  95                  100

gag cac ggc acg aat aat gag aag tct ttg gcg atg gaa atg atc aaa   451
Glu His Gly Thr Asn Asn Glu Lys Ser Leu Ala Met Glu Met Ile Lys
            105                 110                 115

gat tcc tcc gac gta tcc gcc gaa atc ttg tat gag gcg tac cca gaa   499
Asp Ser Ser Asp Val Ser Ala Glu Ile Leu Tyr Glu Ala Tyr Pro Glu
        120                 125                 130

tca att gag gag att gcg gat caa tac gga ttg ctc tcc aca agg gga   547
Ser Ile Glu Glu Ile Ala Asp Gln Tyr Gly Leu Leu Ser Thr Arg Gly
    135                 140                 145

gac gcg cac tgg gga tac tcg gtg aca tcc act tac gat ttg gtg aaa   595
Asp Ala His Trp Gly Tyr Ser Val Thr Ser Thr Tyr Asp Leu Val Lys
150                 155                 160                 165

ttt gtc agc gct ctc att atc gat gat cca gat tca ccg atc ctt gaa   643
Phe Val Ser Ala Leu Ile Ile Asp Asp Pro Asp Ser Pro Ile Leu Glu
                170                 175                 180

gcg atg cgt aat gcc agc gca gtc gcg gct gac ggt tat ccg caa gac   691
Ala Met Arg Asn Ala Ser Ala Val Ala Ala Asp Gly Tyr Pro Gln Asp
            185                 190                 195

tgg ggg aca gcg gtg ctt gat gag gca gaa gga tcc aaa tgg gga tgg   739
Trp Gly Thr Ala Val Leu Asp Glu Ala Glu Gly Ser Lys Trp Gly Trp
        200                 205                 210

tct gat gat ctc atg ctg cac tcc tct gtg acc ttt ggc gaa gac tat   787
Ser Asp Asp Leu Met Leu His Ser Ser Val Thr Phe Gly Glu Asp Tyr
    215                 220                 225

gtt gtg gca gct gct gtg act gga tca aaa gaa gac ctc acc caa ttg   835
Val Val Ala Ala Ala Val Thr Gly Ser Lys Glu Asp Leu Thr Gln Leu
230                 235                 240                 245

gtg gaa aac caa ttg ggt gag gtt gtg agt cag cac ggc tagtttagct    884
Val Glu Asn Gln Leu Gly Glu Val Val Ser Gln His Gly
                250                 255
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agatagggtg cca 897

<210> 2614
<211> 258
<212> PRT
<213> Corynebacterium glutamicum

<400> 2614

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Val Ser Thr Val Leu Leu Ala Gly Val Val Ile Ile Gly Gly Ile Phe
  1               5                  10                  15

Thr Leu Pro Gln Lys Glu Glu Val Lys Val Ser Glu Leu Gln Pro Gln
             20                  25                  30

Ala Ser Ala Ala Ser Ile Pro Ser Ser Ser Ser Thr Ala Gly Lys Ala
         35                  40                  45

Val Glu Glu Ser Pro Leu Thr Gln Phe Val Glu Asn Ser Thr Gly Ser
     50                  55                  60

Gln Ile Thr Tyr Met Ser Leu Lys Asp Asp Phe His Thr Gly Thr Ser
 65                  70                  75                  80

Thr Glu Arg Phe Ala Arg Pro Ala Leu Ser Leu Ser Lys Leu Tyr Ile
                 85                  90                  95

Ala Glu Tyr Val Leu Glu His Gly Thr Asn Asn Glu Lys Ser Leu Ala
            100                 105                 110

Met Glu Met Ile Lys Asp Ser Ser Asp Val Ser Ala Glu Ile Leu Tyr
        115                 120                 125

Glu Ala Tyr Pro Glu Ser Ile Glu Glu Ile Ala Asp Gln Tyr Gly Leu
    130                 135                 140

Leu Ser Thr Arg Gly Asp Ala His Trp Gly Tyr Ser Val Thr Ser Thr
145                 150                 155                 160

Tyr Asp Leu Val Lys Phe Val Ser Ala Leu Ile Ile Asp Asp Pro Asp
                165                 170                 175

Ser Pro Ile Leu Glu Ala Met Arg Asn Ala Ser Ala Val Ala Ala Asp
            180                 185                 190

Gly Tyr Pro Gln Asp Trp Gly Thr Ala Val Leu Asp Glu Ala Glu Gly
        195                 200                 205

Ser Lys Trp Gly Trp Ser Asp Asp Leu Met Leu His Ser Ser Val Thr
    210                 215                 220

Phe Gly Glu Asp Tyr Val Val Ala Ala Ala Val Thr Gly Ser Lys Glu
225                 230                 235                 240

Asp Leu Thr Gln Leu Val Glu Asn Gln Leu Gly Glu Val Val Ser Gln
                245                 250                 255

His Gly
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<210> 2615
<211> 462
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(439)
<223> RXA02172

<400> 2615
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gactcccgct cgagggatat gaaagcgaga taagtttcca gtg aat gca gaa caa 115
Val Asn Ala Glu Gln
1 5

atc acc cag ggg cgt cgc cag ccg acg gct caa gag ttt cgg gac atg 163
Ile Thr Gln Gly Arg Arg Gln Pro Thr Ala Gln Glu Phe Arg Asp Met
10 15 20

cag gcg agc cca gaa ttt gga gag ctc cgc agc aag ttc cgt tcc ttt 211
Gln Ala Ser Pro Glu Phe Gly Glu Leu Arg Ser Lys Phe Arg Ser Phe
25 30 35

gct ttc cca atg acc gtt gcc ttc ttc ttg tgg tac gtc gtc tac gtt 259
Ala Phe Pro Met Thr Val Ala Phe Phe Leu Trp Tyr Val Val Tyr Val
40 45 50

ctg gtt gca tcc ttt gca tca gag tgg atg gca acc cca gtt ttc ggc 307
Leu Val Ala Ser Phe Ala Ser Glu Trp Met Ala Thr Pro Val Phe Gly
55 60 65

gca atc aac att ggc cta atc ttc ggc ttc ctt cag ttc gta acc aca 355
Ala Ile Asn Ile Gly Leu Ile Phe Gly Phe Leu Gln Phe Val Thr Thr
70 75 80 85

ttc gtc att act tac atc tat gtc atg ttt gcg aac aag aac ttg gag 403
Phe Val Ile Thr Tyr Ile Tyr Val Met Phe Ala Asn Lys Asn Leu Glu
90 95 100

cct cgt cag gct gct att cgc cag aag atg gaa ggt taatcagata 449
Pro Arg Gln Ala Ala Ile Arg Gln Lys Met Glu Gly
105 110

tgaattccac tat 462

<210> 2616
<211> 113
<212> PRT
<213> Corynebacterium glutamicum

<400> 2616
Val Asn Ala Glu Gln Ile Thr Gln Gly Arg Arg Gln Pro Thr Ala Gln
1 5 10 15

Glu Phe Arg Asp Met Gln Ala Ser Pro Glu Phe Gly Glu Leu Arg Ser
20 25 30

```
Lys Phe Arg Ser Phe Ala Phe Pro Met Thr Val Ala Phe Phe Leu Trp
         35                  40                  45

Tyr Val Val Tyr Val Leu Val Ala Ser Phe Ala Ser Glu Trp Met Ala
     50                  55                  60

Thr Pro Val Phe Gly Ala Ile Asn Ile Gly Leu Ile Phe Gly Phe Leu
 65                  70                  75                  80

Gln Phe Val Thr Thr Phe Val Ile Thr Tyr Ile Tyr Val Met Phe Ala
                 85                  90                  95

Asn Lys Asn Leu Glu Pro Arg Gln Ala Ala Ile Arg Gln Lys Met Glu
            100                 105                 110

Gly
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<210> 2617
<211> 1056
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1033)
<223> RXA02177

<400> 2617

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aagcttgggt gatcacttaa cccagctaga aggagtcaac atg cgg gaa ata ttc   115
                                            Met Arg Glu Ile Phe
                                              1               5

ctg atc agc ggt gat tcc acc gaa tca tcc ttg gtt ttc aag acc tcc   163
Leu Ile Ser Gly Asp Ser Thr Glu Ser Ser Leu Val Phe Lys Thr Ser
                10                  15                  20

gaa gag gac ggc gct gag gaa ttt ttc att gct gta aca gat gaa ctc   211
Glu Glu Asp Gly Ala Glu Glu Phe Phe Ile Ala Val Thr Asp Glu Leu
            25                  30                  35

cac gcc att ctt gca ggt cat agc gag att aag agc gcc cca gaa ccc   259
His Ala Ile Leu Ala Gly His Ser Glu Ile Lys Ser Ala Pro Glu Pro
        40                  45                  50

gaa gaa cac aaa gag gtc cca cct cct gtt cta gag ccg gtc gct gcg   307
Glu Glu His Lys Glu Val Pro Pro Pro Val Leu Glu Pro Val Ala Ala
    55                  60                  65

gta gaa gag ccc cgt gag gaa aaa gaa att gac cct cgt atc agc gct   355
Val Glu Glu Pro Arg Glu Glu Lys Glu Ile Asp Pro Arg Ile Ser Ala
70                  75                  80                  85

ccc ctg acg atg tca ccc cgc gaa att cag att cgg gtt cgc tca ggc   403
Pro Leu Thr Met Ser Pro Arg Glu Ile Gln Ile Arg Val Arg Ser Gly
                90                  95                 100

gcc acc atc gaa gaa tta gcc gaa gaa atc ggc gtc acc gaa gcc cgc   451
```

```
Ala Thr Ile Glu Glu Leu Ala Glu Glu Ile Gly Val Thr Glu Ala Arg
            105                 110                 115

gtt gag ccc tat gcc cac ccc gtt ttg ctg gaa cgt gcc cgc att gcc   499
Val Glu Pro Tyr Ala His Pro Val Leu Leu Glu Arg Ala Arg Ile Ala
        120                 125                 130

gac ttg gct aag caa tca cac ccc atc agg gaa aat ggt cct gca aaa   547
Asp Leu Ala Lys Gln Ser His Pro Ile Arg Glu Asn Gly Pro Ala Lys
    135                 140                 145

ctg act ctc tgg gaa att ctt gca acg gcg ttt gcc act cgc ggc cac   595
Leu Thr Leu Trp Glu Ile Leu Ala Thr Ala Phe Ala Thr Arg Gly His
150                 155                 160                 165

gat ctc acc aca gca cgc tgg gac gcc tac aaa gac gcc acc aac cag   643
Asp Leu Thr Thr Ala Arg Trp Asp Ala Tyr Lys Asp Ala Thr Asn Gln
                170                 175                 180

tgg atc gtg cga gtt gat tgg aaa gca gga ctc agc gac aac tac gcg   691
Trp Ile Val Arg Val Asp Trp Lys Ala Gly Leu Ser Asp Asn Tyr Ala
            185                 190                 195

gag tgg acg tta aac ctg cac aac acc agc aat ccc acc gct gat ccg   739
Glu Trp Thr Leu Asn Leu His Asn Thr Ser Asn Pro Thr Ala Asp Pro
        200                 205                 210

cgg acc cca gtc gca gcc gat ttg atc gat cct gaa ttc att cag ccg   787
Arg Thr Pro Val Ala Ala Asp Leu Ile Asp Pro Glu Phe Ile Gln Pro
    215                 220                 225

gta cgt acc ttg acg tcc gta aac tcc acc cag gaa cag tac gac gac   835
Val Arg Thr Leu Thr Ser Val Asn Ser Thr Gln Glu Gln Tyr Asp Asp
230                 235                 240                 245

gaa acc gat gtt ttc gac acc gta cca agc cct gac gac gca cca gac   883
Glu Thr Asp Val Phe Asp Thr Val Pro Ser Pro Asp Asp Ala Pro Asp
                250                 255                 260

tca gaa tcc gat gcc gtt gct gaa atc acc aac gac aac gaa cct gaa   931
Ser Glu Ser Asp Ala Val Ala Glu Ile Thr Asn Asp Asn Glu Pro Glu
            265                 270                 275

gtc gat gcg gaa ggc cca cgc aac agg cgt cga aaa gca gta acc cca   979
Val Asp Ala Glu Gly Pro Arg Asn Arg Arg Arg Lys Ala Val Thr Pro
        280                 285                 290

cac tgg gaa gat gtt ctt tta gga gtt cgc gca aac aca aag cgc ccg   1027
His Trp Glu Asp Val Leu Leu Gly Val Arg Ala Asn Thr Lys Arg Pro
    295                 300                 305

aag aaa taggatgtgc tgatgccaag tca                                1056
Lys Lys
310
```

<210> 2618
<211> 311
<212> PRT
<213> Corynebacterium glutamicum

<400> 2618

```
Met Arg Glu Ile Phe Leu Ile Ser Gly Asp Ser Thr Glu Ser Ser Leu
  1               5                  10                  15

Val Phe Lys Thr Ser Glu Glu Asp Gly Ala Glu Glu Phe Phe Ile Ala
             20                  25                  30

Val Thr Asp Glu Leu His Ala Ile Leu Ala Gly His Ser Glu Ile Lys
         35                  40                  45

Ser Ala Pro Glu Pro Glu Glu His Lys Glu Val Pro Pro Pro Val Leu
     50                  55                  60

Glu Pro Val Ala Ala Val Glu Glu Pro Arg Glu Glu Lys Glu Ile Asp
 65                  70                  75                  80

Pro Arg Ile Ser Ala Pro Leu Thr Met Ser Pro Arg Glu Ile Gln Ile
                 85                  90                  95

Arg Val Arg Ser Gly Ala Thr Ile Glu Glu Leu Ala Glu Glu Ile Gly
            100                 105                 110

Val Thr Glu Ala Arg Val Glu Pro Tyr Ala His Pro Val Leu Leu Glu
        115                 120                 125

Arg Ala Arg Ile Ala Asp Leu Ala Lys Gln Ser His Pro Ile Arg Glu
    130                 135                 140

Asn Gly Pro Ala Lys Leu Thr Leu Trp Glu Ile Leu Ala Thr Ala Phe
145                 150                 155                 160

Ala Thr Arg Gly His Asp Leu Thr Thr Ala Arg Trp Asp Ala Tyr Lys
                165                 170                 175

Asp Ala Thr Asn Gln Trp Ile Val Arg Val Asp Trp Lys Ala Gly Leu
            180                 185                 190

Ser Asp Asn Tyr Ala Glu Trp Thr Leu Asn Leu His Asn Thr Ser Asn
        195                 200                 205

Pro Thr Ala Asp Pro Arg Thr Pro Val Ala Ala Asp Leu Ile Asp Pro
    210                 215                 220

Glu Phe Ile Gln Pro Val Arg Thr Leu Thr Ser Val Asn Ser Thr Gln
225                 230                 235                 240

Glu Gln Tyr Asp Asp Glu Thr Asp Val Phe Asp Thr Val Pro Ser Pro
                245                 250                 255

Asp Asp Ala Pro Asp Ser Glu Ser Asp Ala Val Ala Glu Ile Thr Asn
            260                 265                 270

Asp Asn Glu Pro Glu Val Asp Ala Glu Gly Pro Arg Asn Arg Arg Arg
        275                 280                 285

Lys Ala Val Thr Pro His Trp Glu Asp Val Leu Leu Gly Val Arg Ala
    290                 295                 300

Asn Thr Lys Arg Pro Lys Lys
305                 310
```

<210> 2619
<211> 993
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(970)
<223> RXA02178

<400> 2619
cccacgcaac aggcgtcgaa aagcagtaac ccacactgg gaagatgttc ttttaggagt 60

tcgcgcaaac acaaagcgcc cgaagaaata ggatgtgctg atg cca agt caa ttg 115
Met Pro Ser Gln Leu
1 5

gga gaa aac gcg gcg atc gtc acc ctc tgg ttt gtt agc gca tcc gat 163
Gly Glu Asn Ala Ala Ile Val Thr Leu Trp Phe Val Ser Ala Ser Asp
10 15 20

ccc caa tcc atc atc cgc tcg gaa cct cgg gcg gat cgt gga tat ggc 211
Pro Gln Ser Ile Ile Arg Ser Glu Pro Arg Ala Asp Arg Gly Tyr Gly
25 30 35

cga aaa ctg ttg gca cag ctc aac cca acg tgg cca att acc ccc atc 259
Arg Lys Leu Leu Ala Gln Leu Asn Pro Thr Trp Pro Ile Thr Pro Ile
40 45 50

ggg cag ttc gcc ctc aac aga tcc gtt cct gct agt gcc aac gag ttc 307
Gly Gln Phe Ala Leu Asn Arg Ser Val Pro Ala Ser Ala Asn Glu Phe
55 60 65

tac atc gct ggt ttt ccc ggc atc acc atc att caa acc gtg ttg gaa 355
Tyr Ile Ala Gly Phe Pro Gly Ile Thr Ile Ile Gln Thr Val Leu Glu
70 75 80 85

gat gtc acc tct tta tcc aag ctg aat cct cgg tta ctg cgc agc gtc 403
Asp Val Thr Ser Leu Ser Lys Leu Asn Pro Arg Leu Leu Arg Ser Val
90 95 100

ccg gca aca gat gtc tac att ttc gcc gtc aat gaa gaa acc acc ctt 451
Pro Ala Thr Asp Val Tyr Ile Phe Ala Val Asn Glu Glu Thr Thr Leu
105 110 115

ggt ggc ttc gca cac atc tac aac ggt gag atc aaa cga tcc ttc atc 499
Gly Gly Phe Ala His Ile Tyr Asn Gly Glu Ile Lys Arg Ser Phe Ile
120 125 130

gcc tat gaa gag cgc gtc ttc gaa gac aac ggc atc ccc ggc ggc ttt 547
Ala Tyr Glu Glu Arg Val Phe Glu Asp Asn Gly Ile Pro Gly Gly Phe
135 140 145

gaa acc ccc tac tgg gca ggc aaa aaa ggc acc cgg aaa act gcg ctg 595
Glu Thr Pro Tyr Trp Ala Gly Lys Lys Gly Thr Arg Lys Thr Ala Leu
150 155 160 165

tcg ttg ccc ttc aac ccc atc gaa cta gtc cac gaa gca caa cgt gca 643
Ser Leu Pro Phe Asn Pro Ile Glu Leu Val His Glu Ala Gln Arg Ala
170 175 180

```
tgg ctc gga ttc gac gcc acc acc tcc cct gac atc aac gtc gtt gcc   691
Trp Leu Gly Phe Asp Ala Thr Thr Ser Pro Asp Ile Asn Val Val Ala
            185                 190                 195

tat gcc acc gat ggt cgc ccc gag ccg cgc atc gct gca ccc cgc ata   739
Tyr Ala Thr Asp Gly Arg Pro Glu Pro Arg Ile Ala Ala Pro Arg Ile
        200                 205                 210

att aac agc gag gaa gtg aca agg tcc gcc gtc gaa aag cta gga ctg   787
Ile Asn Ser Glu Glu Val Thr Arg Ser Ala Val Glu Lys Leu Gly Leu
    215                 220                 225

cgc gaa tcc gcc ttc tac gac gac tac gaa gaa tac gag gca ccc gat   835
Arg Glu Ser Ala Phe Tyr Asp Asp Tyr Glu Glu Tyr Glu Ala Pro Asp
230                 235                 240                 245

cga gtg gtg tcc aag cgc att acc tca aac gcg aaa aaa gcg gcc agc   883
Arg Val Val Ser Lys Arg Ile Thr Ser Asn Ala Lys Lys Ala Ala Ser
                250                 255                 260

tca gca cag aaa ttt ggt aaa tct ctg tgg cga gcc agc cgc gaa ttc   931
Ser Ala Gln Lys Phe Gly Lys Ser Leu Trp Arg Ala Ser Arg Glu Phe
            265                 270                 275

ggg tca aac atg gcg gaa aga ctc cgc cac act gac cgc tagcgctact    980
Gly Ser Asn Met Ala Glu Arg Leu Arg His Thr Asp Arg
        280                 285                 290

acttagcgct gtt                                                   993


<210> 2620
<211> 290
<212> PRT
<213> Corynebacterium glutamicum

<400> 2620
Met Pro Ser Gln Leu Gly Glu Asn Ala Ala Ile Val Thr Leu Trp Phe
  1               5                  10                  15

Val Ser Ala Ser Asp Pro Gln Ser Ile Ile Arg Ser Glu Pro Arg Ala
             20                  25                  30

Asp Arg Gly Tyr Gly Arg Lys Leu Leu Ala Gln Leu Asn Pro Thr Trp
         35                  40                  45

Pro Ile Thr Pro Ile Gly Gln Phe Ala Leu Asn Arg Ser Val Pro Ala
     50                  55                  60

Ser Ala Asn Glu Phe Tyr Ile Ala Gly Phe Pro Gly Ile Thr Ile Ile
 65                  70                  75                  80

Gln Thr Val Leu Glu Asp Val Thr Ser Leu Ser Lys Leu Asn Pro Arg
                 85                  90                  95

Leu Leu Arg Ser Val Pro Ala Thr Asp Val Tyr Ile Phe Ala Val Asn
            100                 105                 110

Glu Glu Thr Thr Leu Gly Gly Phe Ala His Ile Tyr Asn Gly Glu Ile
        115                 120                 125
```

```
Lys Arg Ser Phe Ile Ala Tyr Glu Glu Arg Val Phe Glu Asp Asn Gly
    130                 135                 140

Ile Pro Gly Gly Phe Glu Thr Pro Tyr Trp Ala Gly Lys Lys Gly Thr
145                 150                 155                 160

Arg Lys Thr Ala Leu Ser Leu Pro Phe Asn Pro Ile Glu Leu Val His
                165                 170                 175

Glu Ala Gln Arg Ala Trp Leu Gly Phe Asp Ala Thr Thr Ser Pro Asp
            180                 185                 190

Ile Asn Val Val Ala Tyr Ala Thr Asp Gly Arg Pro Glu Pro Arg Ile
        195                 200                 205

Ala Ala Pro Arg Ile Ile Asn Ser Glu Glu Val Thr Arg Ser Ala Val
    210                 215                 220

Glu Lys Leu Gly Leu Arg Glu Ser Ala Phe Tyr Asp Asp Tyr Glu Glu
225                 230                 235                 240

Tyr Glu Ala Pro Asp Arg Val Val Ser Lys Arg Ile Thr Ser Asn Ala
                245                 250                 255

Lys Lys Ala Ala Ser Ser Ala Gln Lys Phe Gly Lys Ser Leu Trp Arg
            260                 265                 270

Ala Ser Arg Glu Phe Gly Ser Asn Met Ala Glu Arg Leu Arg His Thr
        275                 280                 285

Asp Arg
    290


<210> 2621
<211> 801
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(778)
<223> RXA02181

<400> 2621
tttggctagt agggtgataa tctcaaataa aatgcacttt caccagcttt ttcgattccg 60

gaaggtctaa ctacacgtcg tggtgaccac aagttttctc atg gtt gac gga cac   115
                                            Met Val Asp Gly His
                                              1               5

atc cgc aat ctt cag ggc cac atc gat cgc ctc gag gcg gca gcc cct   163
Ile Arg Asn Leu Gln Gly His Ile Asp Arg Leu Glu Ala Ala Ala Pro
                10                  15                  20

act gct tca cag ttc cat gat cgc atc atc act caa ttg cgt gaa gct   211
Thr Ala Ser Gln Phe His Asp Arg Ile Ile Thr Gln Leu Arg Glu Ala
            25                  30                  35

ccg ggc agt gtt cag gca gct gtc acg att gaa aat aac cac tat aac   259
```

```
Pro Gly Ser Val Gln Ala Ala Val Thr Ile Glu Asn Asn His Tyr Asn
         40                  45                  50

gtc gag ctg cgc ccg ccc cgc aag tta aat tca ctg gtc acc ctt gat   307
Val Glu Leu Arg Pro Pro Arg Lys Leu Asn Ser Leu Val Thr Leu Asp
     55                  60                  65

acc cac ggc cac cgc gat gag cgc cta cat cca aag att aaa ggc cac   355
Thr His Gly His Arg Asp Glu Arg Leu His Pro Lys Ile Lys Gly His
 70                  75                  80                  85

gat atc gcg tgg cag aac acg gcc acc gca aac agc cgc cgc cag ggc   403
Asp Ile Ala Trp Gln Asn Thr Ala Thr Ala Asn Ser Arg Arg Gln Gly
                 90                  95                 100

gcc gat gat gga ttg ctt gtc gac gag tcc ggc cag gtg atc atg gct   451
Ala Asp Asp Gly Leu Leu Val Asp Glu Ser Gly Gln Val Ile Met Ala
            105                 110                 115

atc aat gcc tct ctc ttg gcg att aag ggc gac acc gtg ttt cat tcc   499
Ile Asn Ala Ser Leu Leu Ala Ile Lys Gly Asp Thr Val Phe His Ser
        120                 125                 130

acg cac ccc agg tcg ctg ccg tct gtt ctg gaa tca acg gtc att gcc   547
Thr His Pro Arg Ser Leu Pro Ser Val Leu Glu Ser Thr Val Ile Ala
    135                 140                 145

tac ctg cag gaa caa ggc tgt aat gca aag cct cga gag caa ggc ttc   595
Tyr Leu Gln Glu Gln Gly Cys Asn Ala Lys Pro Arg Glu Gln Gly Phe
150                 155                 160                 165

aac atc aat gat ttg cgc tct tcg gaa gtg tgg ctg gtg gat tct ttg   643
Asn Ile Asn Asp Leu Arg Ser Ser Glu Val Trp Leu Val Asp Ser Leu
                170                 175                 180

tcc ggc atc cgt cgc gtc gct gca tgg ctc gaa tac ggt tcc aaa ttc   691
Ser Gly Ile Arg Arg Val Ala Ala Trp Leu Glu Tyr Gly Ser Lys Phe
            185                 190                 195

cca gtc tca gaa acg cga cct gtg gca gct ttc gtg ccg acg ttt tct   739
Pro Val Ser Glu Thr Arg Pro Val Ala Ala Phe Val Pro Thr Phe Ser
        200                 205                 210

gaa gtc aat gac tac cta tgg agc act gca cag caa gtg taggtcgctc    788
Glu Val Asn Asp Tyr Leu Trp Ser Thr Ala Gln Gln Val
    215                 220                 225

gactgttatt ctc                                                   801


<210> 2622
<211> 226
<212> PRT
<213> Corynebacterium glutamicum

<400> 2622
Met Val Asp Gly His Ile Arg Asn Leu Gln Gly His Ile Asp Arg Leu
  1               5                  10                  15

Glu Ala Ala Ala Pro Thr Ala Ser Gln Phe His Asp Arg Ile Ile Thr
             20                  25                  30
```

```
Gln Leu Arg Glu Ala Pro Gly Ser Val Gln Ala Ala Val Thr Ile Glu
         35                  40                  45

Asn Asn His Tyr Asn Val Glu Leu Arg Pro Pro Arg Lys Leu Asn Ser
     50                  55                  60

Leu Val Thr Leu Asp Thr His Gly His Arg Asp Glu Arg Leu His Pro
 65                  70                  75                  80

Lys Ile Lys Gly His Asp Ile Ala Trp Gln Asn Thr Ala Thr Ala Asn
                 85                  90                  95

Ser Arg Arg Gln Gly Ala Asp Asp Gly Leu Leu Val Asp Glu Ser Gly
            100                 105                 110

Gln Val Ile Met Ala Ile Asn Ala Ser Leu Leu Ala Ile Lys Gly Asp
        115                 120                 125

Thr Val Phe His Ser Thr His Pro Arg Ser Leu Pro Ser Val Leu Glu
    130                 135                 140

Ser Thr Val Ile Ala Tyr Leu Gln Glu Gln Gly Cys Asn Ala Lys Pro
145                 150                 155                 160

Arg Glu Gln Gly Phe Asn Ile Asn Asp Leu Arg Ser Ser Glu Val Trp
                165                 170                 175

Leu Val Asp Ser Leu Ser Gly Ile Arg Arg Val Ala Ala Trp Leu Glu
            180                 185                 190

Tyr Gly Ser Lys Phe Pro Val Ser Glu Thr Arg Pro Val Ala Ala Phe
        195                 200                 205

Val Pro Thr Phe Ser Glu Val Asn Asp Tyr Leu Trp Ser Thr Ala Gln
    210                 215                 220

Gln Val
225
```

Sequence Listing - Page 2981 - 2623 - 648 - DNA - Corynebacterium glutamicum

<210> 2623
<211> 648
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(625)
<223> RXA02183

<400> 2623

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ttgcacatat tccggattcc gatcgttttt atatcactgg taagcgttgg cctgacctct 60

atgaggttag attcgtccct gctgactaga atcaagactc atg gca agc cgg aag   115
                                              Met Ala Ser Arg Lys
                                                1               5

acc aag cgt aaa aac ctc att cag att ctc agc ctt atc gtt gct gtg   163
Thr Lys Arg Lys Asn Leu Ile Gln Ile Leu Ser Leu Ile Val Ala Val
                10                  15                  20
```

```
tta ttg gtg gtg att ttg tct gtg gtg ttc cag caa tgg tgg aac aat   211
Leu Leu Val Val Ile Leu Ser Val Val Phe Gln Gln Trp Trp Asn Asn
            25                  30                  35

cgc cca gag cca ctc ccc caa gag atc tct atc tca gca tct tct ccc   259
Arg Pro Glu Pro Leu Pro Gln Glu Ile Ser Ile Ser Ala Ser Ser Pro
        40                  45                  50

gct ggt gaa atc gag gta ttc cca ttc agc atg tgt gaa cca ggt gtt   307
Ala Gly Glu Ile Glu Val Phe Pro Phe Ser Met Cys Glu Pro Gly Val
    55                  60                  65

gaa tgc gaa gag aac gag gtg cca acg ctg gaa gtt ggt gct gat gaa   355
Glu Cys Glu Glu Asn Glu Val Pro Thr Leu Glu Val Gly Ala Asp Glu
70                  75                  80                  85

gag ttg cac ctg acg att cca gag gca att cat gat cat gac tgg tac   403
Glu Leu His Leu Thr Ile Pro Glu Ala Ile His Asp His Asp Trp Tyr
                90                  95                  100

ttg ttg acc att tat gat gat ccg gct gca aat gac gag ttc tac cac   451
Leu Leu Thr Ile Tyr Asp Asp Pro Ala Ala Asn Asp Glu Phe Tyr His
            105                 110                 115

acc agt tac gac gcc acc gag gca acc gtt cct ggt tct gtg gat cca   499
Thr Ser Tyr Asp Ala Thr Glu Ala Thr Val Pro Gly Ser Val Asp Pro
        120                 125                 130

acc gaa gag ggt gcg gag cgc cca cgt ctg gtc gta gtg gaa gtg tcc   547
Thr Glu Glu Gly Ala Glu Arg Pro Arg Leu Val Val Val Glu Val Ser
    135                 140                 145

gct gtg atg atc ggt gag gat gaa aat ggt gag gaa agc cct tac acc   595
Ala Val Met Ile Gly Glu Asp Glu Asn Gly Glu Glu Ser Pro Tyr Thr
150                 155                 160                 165

gtc acg tgg tcg cta tcc acg atg aac gag taactcactc acaaacaata     645
Val Thr Trp Ser Leu Ser Thr Met Asn Glu
                170                 175

agg                                                               648
```

<210> 2624
<211> 175
<212> PRT
<213> Corynebacterium glutamicum

<400> 2624

```
Met Ala Ser Arg Lys Thr Lys Arg Lys Asn Leu Ile Gln Ile Leu Ser
  1               5                  10                  15

Leu Ile Val Ala Val Leu Leu Val Val Ile Leu Ser Val Val Phe Gln
            20                  25                  30

Gln Trp Trp Asn Asn Arg Pro Glu Pro Leu Pro Gln Glu Ile Ser Ile
        35                  40                  45

Ser Ala Ser Ser Pro Ala Gly Glu Ile Glu Val Phe Pro Phe Ser Met
    50                  55                  60
```

```
Cys Glu Pro Gly Val Glu Cys Glu Glu Asn Glu Val Pro Thr Leu Glu
 65                  70                  75                  80

Val Gly Ala Asp Glu Glu Leu His Leu Thr Ile Pro Glu Ala Ile His
                85                  90                  95

Asp His Asp Trp Tyr Leu Leu Thr Ile Tyr Asp Asp Pro Ala Ala Asn
            100                 105                 110

Asp Glu Phe Tyr His Thr Ser Tyr Asp Ala Thr Glu Ala Thr Val Pro
        115                 120                 125

Gly Ser Val Asp Pro Thr Glu Glu Gly Ala Glu Arg Pro Arg Leu Val
    130                 135                 140

Val Val Glu Val Ser Ala Val Met Ile Gly Glu Asp Glu Asn Gly Glu
145                 150                 155                 160

Glu Ser Pro Tyr Thr Val Thr Trp Ser Leu Ser Thr Met Asn Glu
                165                 170                 175
```

Sequence Listing Free Text

<210> 2625
<211> 2322
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2299)
<223> RXA02187

<400> 2625

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ggatcgacga agtgcttctt ctctacgttt gccatgtcat acattctttc aaactctggg 60

aacaaaagtc acctcaacaa ggcttaaact taacaacatc atg aaa aaa gac tcc   115
                                            Met Lys Lys Asp Ser
                                              1               5

ccc atc ccc acc ctc aag ggg tgg ttg gat act caa agt gat gat cag   163
Pro Ile Pro Thr Leu Lys Gly Trp Leu Asp Thr Gln Ser Asp Asp Gln
                10                  15                  20

ctc tcc aca atc ctt aga aat cga ccc gat acg gtt ctc cct tta cca   211
Leu Ser Thr Ile Leu Arg Asn Arg Pro Asp Thr Val Leu Pro Leu Pro
            25                  30                  35

cct aat ttg gcc tct ctt gct gcg cgt tta cag ctg agg gcg tct gcg   259
Pro Asn Leu Ala Ser Leu Ala Ala Arg Leu Gln Leu Arg Ala Ser Ala
        40                  45                  50

att cgc gcg gtg ttg aaa ctc aat gcg ttg gaa ctt ggt gtg ttg gag   307
Ile Arg Ala Val Leu Lys Leu Asn Ala Leu Glu Leu Gly Val Leu Glu
    55                  60                  65

gcc gtg gcc aac ctt ggt ggt gaa ctc cac ccg gtt act gcc ccc gaa   355
Ala Val Ala Asn Leu Gly Gly Glu Leu His Pro Val Thr Ala Pro Glu
 70                  75                  80                  85

gtg gtg gaa tat ttg cat gtg gcg ttg gca gag gat ctt cca gcg caa   403
```

```
Val Val Glu Tyr Leu His Val Ala Leu Ala Glu Asp Leu Pro Ala Gln
                 90                  95                 100

gac acg att ggt gcg gct ctt gcc acg ctg aaa aat ttc gcg ttg gtt   451
Asp Thr Ile Gly Ala Ala Leu Ala Thr Leu Lys Asn Phe Ala Leu Val
            105                 110                 115

tat ggc gat gac cag ttg atg att gct cag gag acg atg gct gcg ttg   499
Tyr Gly Asp Asp Gln Leu Met Ile Ala Gln Glu Thr Met Ala Ala Leu
        120                 125                 130

cct gtt cat tgg cgg ttg ctt ccg gag gta agt gat cgc ggg cag agt   547
Pro Val His Trp Arg Leu Leu Pro Glu Val Ser Asp Arg Gly Gln Ser
    135                 140                 145

gag gaa cag gtg agg gaa agc gtc gat aag ctt tct gat agg cac cgc   595
Glu Glu Gln Val Arg Glu Ser Val Asp Lys Leu Ser Asp Arg His Arg
150                 155                 160                 165

aaa ctt ttg cac acg ctt gcg gcc tcg ggt ggc ttc ggt ctg acg cgc   643
Lys Leu Leu His Thr Leu Ala Ala Ser Gly Gly Phe Gly Leu Thr Arg
                170                 175                 180

gat gcg gcg cct gat gcg gat ccg tcg cgg ccg att ccg cag ttg ctg   691
Asp Ala Ala Pro Asp Ala Asp Pro Ser Arg Pro Ile Pro Gln Leu Leu
            185                 190                 195

gcg tcg ggg ttg ttg gcg cgc gtg gat gag cag acc gtg cgc ctg ccg   739
Ala Ser Gly Leu Leu Ala Arg Val Asp Glu Gln Thr Val Arg Leu Pro
        200                 205                 210

gcg atg gtg cgg cgt gtg att gag ggc cgc gag cag ctg ccc gct cag   787
Ala Met Val Arg Arg Val Ile Glu Gly Arg Glu Gln Leu Pro Ala Gln
    215                 220                 225

gtg cgc cca att ccg cgc acg gcg gcg cca ggt tcg aat gat ggc ggc   835
Val Arg Pro Ile Pro Arg Thr Ala Ala Pro Gly Ser Asn Asp Gly Gly
230                 235                 240                 245

att gca gcc ggc ctt gag gtg gtg cgg cac atg cga ttg ctt atc gac   883
Ile Ala Ala Gly Leu Glu Val Val Arg His Met Arg Leu Leu Ile Asp
                250                 255                 260

gcc ctc agc cac gtt ccc gcc ccc acg ctg aaa gtc gga gcc ctc ggt   931
Ala Leu Ser His Val Pro Ala Pro Thr Leu Lys Val Gly Ala Leu Gly
            265                 270                 275

gtg cgc gtg gtg act cgc ctg agc aag gaa tta gac ctt gat gag acc   979
Val Arg Val Val Thr Arg Leu Ser Lys Glu Leu Asp Leu Asp Glu Thr
        280                 285                 290

gag ctg gca cgt cta ctg agt ttg ggt atg gcc agc ggt cta atc cgt   1027
Glu Leu Ala Arg Leu Leu Ser Leu Gly Met Ala Ser Gly Leu Ile Arg
    295                 300                 305

aaa ggc gtg ccc gat cca ttg ccc atg gat gat gat ggc ggc gat tac   1075
Lys Gly Val Pro Asp Pro Leu Pro Met Asp Asp Asp Gly Gly Asp Tyr
310                 315                 320                 325

gtc gct ccc acc ccg ctg gct gac gaa tgg atg gaa tat gat ctg gcg   1123
Val Ala Pro Thr Pro Leu Ala Asp Glu Trp Met Glu Tyr Asp Leu Ala
```

```
                330                 335                 340

cac caa ttg ggc acg ttg atg tct ggt tgg tgg aag caa act tac gcg   1171
His Gln Leu Gly Thr Leu Met Ser Gly Trp Trp Lys Gln Thr Tyr Ala
            345                 350                 355

ccg tgg ttg gtg ggt cgg gct gat gat aag gac aag ccg atc cat gtt   1219
Pro Trp Leu Val Gly Arg Ala Asp Asp Lys Asp Lys Pro Ile His Val
        360                 365                 370

ctc agt aaa aca agc atc att gat tcg ctt cct gat gct cgt gcg aag   1267
Leu Ser Lys Thr Ser Ile Ile Asp Ser Leu Pro Asp Ala Arg Ala Lys
    375                 380                 385

atc ctg tcc tct tta tct agg gtt tta gtg gac aat ctg cac gcg gat   1315
Ile Leu Ser Ser Leu Ser Arg Val Leu Val Asp Asn Leu His Ala Asp
390                 395                 400                 405

tta gca ttc cat tat ccc ctt gcg gcg agt cgg atg aat cct gac acc   1363
Leu Ala Phe His Tyr Pro Leu Ala Ala Ser Arg Met Asn Pro Asp Thr
                410                 415                 420

atc aca cag ctg gta cag gaa gcc cag tgg atc gga gca tat tct caa   1411
Ile Thr Gln Leu Val Gln Glu Ala Gln Trp Ile Gly Ala Tyr Ser Gln
            425                 430                 435

ggc gtg acc gca gcg ggt cag gcc tta att gat ggc gaa aac cct acg   1459
Gly Val Thr Ala Ala Gly Gln Ala Leu Ile Asp Gly Glu Asn Pro Thr
        440                 445                 450

gag gta atc aag gct cct gcg ccg gtg gag aat ttc atc gtg caa ggc   1507
Glu Val Ile Lys Ala Pro Ala Pro Val Glu Asn Phe Ile Val Gln Gly
    455                 460                 465

gat ttc acc atc atg gtt cca gga cca cta acc cct gcg atg caa aaa   1555
Asp Phe Thr Ile Met Val Pro Gly Pro Leu Thr Pro Ala Met Gln Lys
470                 475                 480                 485

acc atg gat tcg atc gca tcg ttg gaa tca cct ggt ttg gcc tcg gtg   1603
Thr Met Asp Ser Ile Ala Ser Leu Glu Ser Pro Gly Leu Ala Ser Val
                490                 495                 500

tat cga ctc agc gag aaa tcc atc agg cat gct ctg gat ctt ggg ctc   1651
Tyr Arg Leu Ser Glu Lys Ser Ile Arg His Ala Leu Asp Leu Gly Leu
            505                 510                 515

acc acc ccg gaa atc ttg gag ttt ctc aaa gaa cat tcc atg aca gat   1699
Thr Thr Pro Glu Ile Leu Glu Phe Leu Lys Glu His Ser Met Thr Asp
        520                 525                 530

ctg ccc caa tct gtg ggc tat ttg ctc agc gat atc gcc aga aag cac   1747
Leu Pro Gln Ser Val Gly Tyr Leu Leu Ser Asp Ile Ala Arg Lys His
    535                 540                 545

ggc acc ctc cga ggc ggc cct gca ctg tcc tat atc cgt agc gac gat   1795
Gly Thr Leu Arg Gly Gly Pro Ala Leu Ser Tyr Ile Arg Ser Asp Asp
550                 555                 560                 565

ccc gct ttg ctg cat tcc gca gtg gag gcg ggc gcc gat gtg gcg ctt   1843
Pro Ala Leu Leu His Ser Ala Val Glu Ala Gly Ala Asp Val Ala Leu
                570                 575                 580
```

```
cgg cag atc gct ccc acc gtt gcg att gct caa gca ccc ctg ctt cag   1891
Arg Gln Ile Ala Pro Thr Val Ala Ile Ala Gln Ala Pro Leu Leu Gln
            585                 590                 595

gtg atc act gtg ctg cgt gct gcc ggg ttc caa cct gtg gca gaa gac   1939
Val Ile Thr Val Leu Arg Ala Ala Gly Phe Gln Pro Val Ala Glu Asp
        600                 605                 610

ggc gaa ggc gca agt ctg aat atc tcg cca tcc cct gca cgt gtg ccc   1987
Gly Glu Gly Ala Ser Leu Asn Ile Ser Pro Ser Pro Ala Arg Val Pro
    615                 620                 625

gca gct tcc cca cca cca gtt gtt ccg gca ctg gat gaa agc cgg gta   2035
Ala Ala Ser Pro Pro Pro Val Val Pro Ala Leu Asp Glu Ser Arg Val
630                 635                 640                 645

cag gca gca gtc aaa gca atc cga cgg gaa aat tca gca tct caa gga   2083
Gln Ala Ala Val Lys Ala Ile Arg Arg Glu Asn Ser Ala Ser Gln Gly
                650                 655                 660

act gtt tcc aca cag cca act ctt tcg gtg ctg cag gct gca gtg cga   2131
Thr Val Ser Thr Gln Pro Thr Leu Ser Val Leu Gln Ala Ala Val Arg
            665                 670                 675

ggg cag cgc acg gtg acg ttg ggg ttc gtc gat aag caa ggc gtg gcc   2179
Gly Gln Arg Thr Val Thr Leu Gly Phe Val Asp Lys Gln Gly Val Ala
        680                 685                 690

gtg cac cgc gtc gtc aag cct tta acc gtc aac gcc ggg cag gtg gac   2227
Val His Arg Val Val Lys Pro Leu Thr Val Asn Ala Gly Gln Val Asp
    695                 700                 705

gct gtg gat gaa gcc aca ggt gcg gtg cat cgt ttc atg ttg cac agg   2275
Ala Val Asp Glu Ala Thr Gly Ala Val His Arg Phe Met Leu His Arg
710                 715                 720                 725

atc aca gaa gta ata gtg gat aac tagcctagaa gtgacataat gga         2322
Ile Thr Glu Val Ile Val Asp Asn
                730
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<210> 2626
<211> 733
<212> PRT
<213> Corynebacterium glutamicum

<400> 2626

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Met Lys Lys Asp Ser Pro Ile Pro Thr Leu Lys Gly Trp Leu Asp Thr
  1               5                  10                  15

Gln Ser Asp Asp Gln Leu Ser Thr Ile Leu Arg Asn Arg Pro Asp Thr
             20                  25                  30

Val Leu Pro Leu Pro Pro Asn Leu Ala Ser Leu Ala Ala Arg Leu Gln
         35                  40                  45

Leu Arg Ala Ser Ala Ile Arg Ala Val Leu Lys Leu Asn Ala Leu Glu
     50                  55                  60

Leu Gly Val Leu Glu Ala Val Ala Asn Leu Gly Gly Glu Leu His Pro
```

```
 65                  70                  75                  80

Val Thr Ala Pro Glu Val Val Glu Tyr Leu His Val Ala Leu Ala Glu
                 85                  90                  95

Asp Leu Pro Ala Gln Asp Thr Ile Gly Ala Ala Leu Ala Thr Leu Lys
            100                 105                 110

Asn Phe Ala Leu Val Tyr Gly Asp Asp Gln Leu Met Ile Ala Gln Glu
        115                 120                 125

Thr Met Ala Ala Leu Pro Val His Trp Arg Leu Leu Pro Glu Val Ser
    130                 135                 140

Asp Arg Gly Gln Ser Glu Glu Gln Val Arg Glu Ser Val Asp Lys Leu
145                 150                 155                 160

Ser Asp Arg His Arg Lys Leu Leu His Thr Leu Ala Ala Ser Gly Gly
                165                 170                 175

Phe Gly Leu Thr Arg Asp Ala Ala Pro Asp Ala Asp Pro Ser Arg Pro
            180                 185                 190

Ile Pro Gln Leu Leu Ala Ser Gly Leu Leu Ala Arg Val Asp Glu Gln
        195                 200                 205

Thr Val Arg Leu Pro Ala Met Val Arg Arg Val Ile Glu Gly Arg Glu
    210                 215                 220

Gln Leu Pro Ala Gln Val Arg Pro Ile Pro Arg Thr Ala Ala Pro Gly
225                 230                 235                 240

Ser Asn Asp Gly Gly Ile Ala Ala Gly Leu Glu Val Val Arg His Met
                245                 250                 255

Arg Leu Leu Ile Asp Ala Leu Ser His Val Pro Ala Pro Thr Leu Lys
            260                 265                 270

Val Gly Ala Leu Gly Val Arg Val Val Thr Arg Leu Ser Lys Glu Leu
        275                 280                 285

Asp Leu Asp Glu Thr Glu Leu Ala Arg Leu Leu Ser Leu Gly Met Ala
    290                 295                 300

Ser Gly Leu Ile Arg Lys Gly Val Pro Asp Pro Leu Pro Met Asp Asp
305                 310                 315                 320

Asp Gly Gly Asp Tyr Val Ala Pro Thr Pro Leu Ala Asp Glu Trp Met
                325                 330                 335

Glu Tyr Asp Leu Ala His Gln Leu Gly Thr Leu Met Ser Gly Trp Trp
            340                 345                 350

Lys Gln Thr Tyr Ala Pro Trp Leu Val Gly Arg Ala Asp Asp Lys Asp
        355                 360                 365

Lys Pro Ile His Val Leu Ser Lys Thr Ser Ile Ile Asp Ser Leu Pro
    370                 375                 380

Asp Ala Arg Ala Lys Ile Leu Ser Ser Leu Ser Arg Val Leu Val Asp
385                 390                 395                 400
```

```
Asn Leu His Ala Asp Leu Ala Phe His Tyr Pro Leu Ala Ala Ser Arg
                405                 410                 415

Met Asn Pro Asp Thr Ile Thr Gln Leu Val Gln Glu Ala Gln Trp Ile
            420                 425                 430

Gly Ala Tyr Ser Gln Gly Val Thr Ala Ala Gly Gln Ala Leu Ile Asp
        435                 440                 445

Gly Glu Asn Pro Thr Glu Val Ile Lys Ala Pro Ala Pro Val Glu Asn
    450                 455                 460

Phe Ile Val Gln Gly Asp Phe Thr Ile Met Val Pro Gly Pro Leu Thr
465                 470                 475                 480

Pro Ala Met Gln Lys Thr Met Asp Ser Ile Ala Ser Leu Glu Ser Pro
                485                 490                 495

Gly Leu Ala Ser Val Tyr Arg Leu Ser Glu Lys Ser Ile Arg His Ala
            500                 505                 510

Leu Asp Leu Gly Leu Thr Thr Pro Glu Ile Leu Glu Phe Leu Lys Glu
        515                 520                 525

His Ser Met Thr Asp Leu Pro Gln Ser Val Gly Tyr Leu Leu Ser Asp
    530                 535                 540

Ile Ala Arg Lys His Gly Thr Leu Arg Gly Gly Pro Ala Leu Ser Tyr
545                 550                 555                 560

Ile Arg Ser Asp Asp Pro Ala Leu Leu His Ser Ala Val Glu Ala Gly
                565                 570                 575

Ala Asp Val Ala Leu Arg Gln Ile Ala Pro Thr Val Ala Ile Ala Gln
            580                 585                 590

Ala Pro Leu Leu Gln Val Ile Thr Val Leu Arg Ala Ala Gly Phe Gln
        595                 600                 605

Pro Val Ala Glu Asp Gly Glu Gly Ala Ser Leu Asn Ile Ser Pro Ser
    610                 615                 620

Pro Ala Arg Val Pro Ala Ala Ser Pro Pro Pro Val Val Pro Ala Leu
625                 630                 635                 640

Asp Glu Ser Arg Val Gln Ala Ala Val Lys Ala Ile Arg Arg Glu Asn
                645                 650                 655

Ser Ala Ser Gln Gly Thr Val Ser Thr Gln Pro Thr Leu Ser Val Leu
            660                 665                 670

Gln Ala Ala Val Arg Gly Gln Arg Thr Val Thr Leu Gly Phe Val Asp
        675                 680                 685

Lys Gln Gly Val Ala Val His Arg Val Val Lys Pro Leu Thr Val Asn
    690                 695                 700

Ala Gly Gln Val Asp Ala Val Asp Glu Ala Thr Gly Ala Val His Arg
705                 710                 715                 720
```

Phe Met Leu His Arg Ile Thr Glu Val Ile Val Asp Asn
725 730

<210> 2627
<211> 693
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(670)
<223> RXA02199

<400> 2627
acagcttagt acggattaga caattcccga acttttcatt cgtagttcat tttcaacgcc 60

gcctaagcaa cacaggcaaa gcgccactag tctcggtcgc atg act gac tcc act 115
Met Thr Asp Ser Thr
1 5

ccg caa ggc tca aca cca ggc atg tcc cct gaa gct atc ctc aac ggc 163
Pro Gln Gly Ser Thr Pro Gly Met Ser Pro Glu Ala Ile Leu Asn Gly
10 15 20

acc gga aag ccg tgg gaa gag tgg cta aaa ttg ctt gac gac gta aaa 211
Thr Gly Lys Pro Trp Glu Glu Trp Leu Lys Leu Leu Asp Asp Val Lys
25 30 35

gcc acc tct tgg act cac acc cac atc gca aag cac atc gtg gac aac 259
Ala Thr Ser Trp Thr His Thr His Ile Ala Lys His Ile Val Asp Asn
40 45 50

ttt gat gtc agt ggc tgg tgg gct caa ggc atc gcg att ggt tat gaa 307
Phe Asp Val Ser Gly Trp Trp Ala Gln Gly Ile Ala Ile Gly Tyr Glu
55 60 65

tac gaa cgt ggc atg cgc aaa ccc ggg atg acc agc gat ggg ttc gcg 355
Tyr Glu Arg Gly Met Arg Lys Pro Gly Met Thr Ser Asp Gly Phe Ala
70 75 80 85

gcc aat gcc tcc aaa acc ctt aac ctg ccg gtc gaa aaa gtg tgg aag 403
Ala Asn Ala Ser Lys Thr Leu Asn Leu Pro Val Glu Lys Val Trp Lys
90 95 100

ctc ttc gga gac gat gac ctg cgg gcg cag tgg ctc gat ccc gca cta 451
Leu Phe Gly Asp Asp Asp Leu Arg Ala Gln Trp Leu Asp Pro Ala Leu
105 110 115

att gag aaa acc tcc gcc tcc gaa cct aga aca ttc aat gcc aaa tgg 499
Ile Glu Lys Thr Ser Ala Ser Glu Pro Arg Thr Phe Asn Ala Lys Trp
120 125 130

ttg gcc gat gat tct cga gtg agc gtc aac ttc acc tcc aaa ggc gac 547
Leu Ala Asp Asp Ser Arg Val Ser Val Asn Phe Thr Ser Lys Gly Asp
135 140 145

aat aaa tcc agc ttc ggc atc cag cac aga cgc ctg cct gat caa gac 595
Asn Lys Ser Ser Phe Gly Ile Gln His Arg Arg Leu Pro Asp Gln Asp
150 155 160 165

```
agc atc cct gtc atg aaa gca ttc tgg aaa gaa cgc atc gct gca tta   643
Ser Ile Pro Val Met Lys Ala Phe Trp Lys Glu Arg Ile Ala Ala Leu
                170                 175                 180

gtt gag gtg tca aaa caa ttt tcg ctt taacattaag ttcttagcct         690
Val Glu Val Ser Lys Gln Phe Ser Leu
            185                 190

tca                                                               693
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<210> 2628
<211> 190
<212> PRT
<213> Corynebacterium glutamicum

<400> 2628

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Met Thr Asp Ser Thr Pro Gln Gly Ser Thr Pro Gly Met Ser Pro Glu
  1               5                  10                  15

Ala Ile Leu Asn Gly Thr Gly Lys Pro Trp Glu Glu Trp Leu Lys Leu
             20                  25                  30

Leu Asp Asp Val Lys Ala Thr Ser Trp Thr His Thr His Ile Ala Lys
         35                  40                  45

His Ile Val Asp Asn Phe Asp Val Ser Gly Trp Trp Ala Gln Gly Ile
     50                  55                  60

Ala Ile Gly Tyr Glu Tyr Glu Arg Gly Met Arg Lys Pro Gly Met Thr
 65                  70                  75                  80

Ser Asp Gly Phe Ala Ala Asn Ala Ser Lys Thr Leu Asn Leu Pro Val
                 85                  90                  95

Glu Lys Val Trp Lys Leu Phe Gly Asp Asp Asp Leu Arg Ala Gln Trp
            100                 105                 110

Leu Asp Pro Ala Leu Ile Glu Lys Thr Ser Ala Ser Glu Pro Arg Thr
        115                 120                 125

Phe Asn Ala Lys Trp Leu Ala Asp Asp Ser Arg Val Ser Val Asn Phe
    130                 135                 140

Thr Ser Lys Gly Asp Asn Lys Ser Ser Phe Gly Ile Gln His Arg Arg
145                 150                 155                 160

Leu Pro Asp Gln Asp Ser Ile Pro Val Met Lys Ala Phe Trp Lys Glu
                165                 170                 175

Arg Ile Ala Ala Leu Val Glu Val Ser Lys Gln Phe Ser Leu
            180                 185                 190
```

<210> 2629
<211> 501
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(478)
<223> RXA02203

<400> 2629
cgattcaaaa gagttcaccg aggtaggaaa catcgtggtc gcagccattg atgccctcct 60

gggcgtgcag ctctaggaaa tttcaggaac aatacatctc atg acc att cgc gcc 115
Met Thr Ile Arg Ala
1 5

act ttc cag cct tcc gta gat gaa ttc atc tcc act ctc gaa gag ttt 163
Thr Phe Gln Pro Ser Val Asp Glu Phe Ile Ser Thr Leu Glu Glu Phe
10 15 20

gca aca ggt tca tac ctt aaa gag gac gaa aag gaa ttc tgg gac gaa 211
Ala Thr Gly Ser Tyr Leu Lys Glu Asp Glu Lys Glu Phe Trp Asp Glu
25 30 35

cct ttc gat gtc aag gca ctt cca gat ctt cgt ttc atc ttg gaa aac 259
Pro Phe Asp Val Lys Ala Leu Pro Asp Leu Arg Phe Ile Leu Glu Asn
40 45 50

tac ctt gat tcc cta gat aag ctc ggt gaa gca cca gac ctt gat gct 307
Tyr Leu Asp Ser Leu Asp Lys Leu Gly Glu Ala Pro Asp Leu Asp Ala
55 60 65

gtt aac gcc tcc gct cag tcc acc ctt gat gag ctg gag aag ttc aac 355
Val Asn Ala Ser Ala Gln Ser Thr Leu Asp Glu Leu Glu Lys Phe Asn
70 75 80 85

aca aag cac cac ggt gct gtt gtt gag cct gaa gaa aaa gaa gag atc 403
Thr Lys His His Gly Ala Val Val Glu Pro Glu Glu Lys Glu Glu Ile
90 95 100

act aaa ttg atg ttt gat gct gca aag cag act ggt gca gat gat ctt 451
Thr Lys Leu Met Phe Asp Ala Ala Lys Gln Thr Gly Ala Asp Asp Leu
105 110 115

tct gca gag gct ttc cct gag ttt gag taaatttcag tagaagtttt 498
Ser Ala Glu Ala Phe Pro Glu Phe Glu
120 125

tta 501

<210> 2630
<211> 126
<212> PRT
<213> Corynebacterium glutamicum

<400> 2630
Met Thr Ile Arg Ala Thr Phe Gln Pro Ser Val Asp Glu Phe Ile Ser
1 5 10 15

Thr Leu Glu Glu Phe Ala Thr Gly Ser Tyr Leu Lys Glu Asp Glu Lys
20 25 30

Glu Phe Trp Asp Glu Pro Phe Asp Val Lys Ala Leu Pro Asp Leu Arg
35 40 45

Phe Ile Leu Glu Asn Tyr Leu Asp Ser Leu Asp Lys Leu Gly Glu Ala

```
     50                  55                  60

Pro Asp Leu Asp Ala Val Asn Ala Ser Ala Gln Ser Thr Leu Asp Glu
 65                  70                  75                  80

Leu Glu Lys Phe Asn Thr Lys His His Gly Ala Val Val Glu Pro Glu
                85                  90                  95

Glu Lys Glu Glu Ile Thr Lys Leu Met Phe Asp Ala Ala Lys Gln Thr
            100                 105                 110

Gly Ala Asp Asp Leu Ser Ala Glu Ala Phe Pro Glu Phe Glu
        115                 120                 125


<210> 2631
<211> 1059
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1036)
<223> RXA02206

<400> 2631
ggcaggatct gctgctgcgg ctaggagggt tatctcttca ttcacccgat ctaccgtact 60

accttatgac ctcagtagtg tggtgggcgt gaaacagcga atg gtc ggt tca agt   115
                                            Met Val Gly Ser Ser
                                              1               5

ggt ttg cgg gta tcc agg ctc ggt ttg ggc acc tca aca tgg ggc tcg   163
Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr Ser Thr Trp Gly Ser
                10                  15                  20

ggc acc gag ctg gct gag gca ggc gat atc ttt aag gcg ttc atc aat   211
Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe Lys Ala Phe Ile Asn
            25                  30                  35

tct ggt ggc acg ctt atc gac gtc tcc ccc aac tac acc acc ggc gtc   259
Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn Tyr Thr Thr Gly Val
        40                  45                  50

gcg gaa gaa atg ctc ggc acg atg ttg gat gcg gaa gtc tct cgt tcg   307
Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala Glu Val Ser Arg Ser
    55                  60                  65

gct gtc gtc att tcc tcc agc gca ggt gtc aac ccc gct ctg ccg ctc   355
Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn Pro Ala Leu Pro Leu
70                  75                  80                  85

ggc cga cgt gtg gat tgc tcc cgc cgc aat ttg att gcc caa tta gat   403
Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu Ile Ala Gln Leu Asp
                90                  95                  100

gtc acc ctg cgg gca tta aac act gac tat ttg gat ttg tgg tct gtg   451
Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu Asp Leu Trp Ser Val
            105                 110                 115

ggc tat tgg gat gag ggc acc cca ccg cat gag gtg gcc gat act ttg   499
```

```
Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu Val Ala Asp Thr Leu
        120                 125                 130

gat tac gcc gtg cgc acc ggc cga gtc cga tat gcc ggt gtc cga gga   547
Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr Ala Gly Val Arg Gly
    135                 140                 145

tat tcc ggt tgg cag tta gcg gtc acc cac gct gca tcc aat cat gca   595
Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala Ala Ser Asn His Ala
150                 155                 160                 165

gcg gcc tcc gcc cgc ccc gtg gtc gtt gca caa aat gaa tac agc ctg   643
Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln Asn Glu Tyr Ser Leu
                170                 175                 180

ctg gaa cgc cgc gca gaa caa gaa ctc ctc cct gcc acc caa cac cta   691
Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro Ala Thr Gln His Leu
            185                 190                 195

ggt gtc gga ttc ttt gct ggc gct ccg ctg ggg caa ggc gtg ctg act   739
Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly Gln Gly Val Leu Thr
        200                 205                 210

gct aaa tac cgc tcc gaa att ccc cat gat tcc aga gct gca tcc aca   787
Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser Arg Ala Ala Ser Thr
    215                 220                 225

gga cgc gac gca gaa gtc caa agc tac cta gat aat cga ggc cgc atc   835
Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp Asn Arg Gly Arg Ile
230                 235                 240                 245

att gtc gat gct ctt gat act gca gcc aaa gga tta ggc att agc ccc   883
Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly Leu Gly Ile Ser Pro
                250                 255                 260

gct gtc aca gcc acc acc tgg gtg cgt gat cgt ccc gga gtg aca gct   931
Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg Pro Gly Val Thr Ala
            265                 270                 275

gtc atc gtg ggc gct cgc aca cat gaa cag ctg tca cat ctt ctc aag   979
Val Ile Val Gly Ala Arg Thr His Glu Gln Leu Ser His Leu Leu Lys
        280                 285                 290

gcg gaa tcg gtg act ttg cca aca cca atc aca caa gcc ctt gat gat  1027
Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr Gln Ala Leu Asp Asp
    295                 300                 305

gtc tcc ctg tgacttggtc caattacatt cac                           1059
Val Ser Leu
310


<210> 2632
<211> 312
<212> PRT
<213> Corynebacterium glutamicum

<400> 2632
Met Val Gly Ser Ser Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr
  1               5                  10                  15
```

```
Ser Thr Trp Gly Ser Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe
            20                  25                  30

Lys Ala Phe Ile Asn Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn
        35                  40                  45

Tyr Thr Thr Gly Val Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala
    50                  55                  60

Glu Val Ser Arg Ser Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn
65                  70                  75                  80

Pro Ala Leu Pro Leu Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu
                85                  90                  95

Ile Ala Gln Leu Asp Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu
            100                 105                 110

Asp Leu Trp Ser Val Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu
        115                 120                 125

Val Ala Asp Thr Leu Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr
    130                 135                 140

Ala Gly Val Arg Gly Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala
145                 150                 155                 160

Ala Ser Asn His Ala Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln
                165                 170                 175

Asn Glu Tyr Ser Leu Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro
            180                 185                 190

Ala Thr Gln His Leu Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly
        195                 200                 205

Gln Gly Val Leu Thr Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser
    210                 215                 220

Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp
225                 230                 235                 240

Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly
                245                 250                 255

Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg
            260                 265                 270

Pro Gly Val Thr Ala Val Ile Val Gly Ala Arg Thr His Glu Gln Leu
        275                 280                 285

Ser His Leu Leu Lys Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr
    290                 295                 300

Gln Ala Leu Asp Asp Val Ser Leu
305                 310
```

<210> 2633
<211> 553
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(553)
<223> RXA02211

<400> 2633
actgtccgaa gtattggatc tggtcgaggg aactgtccgt aaacgcgact aaacgacccc 60

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tgattcacac tttcagacta caagaactag actaagcggt atg gtt tca gtt ctt   115
                                            Met Val Ser Val Leu
                                              1               5

tta att cag ccc cgt cag gga gaa gca gtc gcc gca gct gag cga cgt   163
Leu Ile Gln Pro Arg Gln Gly Glu Ala Val Ala Ala Ala Glu Arg Arg
                10                  15                  20

gac ttt ttg cag gcc acc ggt ctt aag cct caa gaa ctg acc tcc cga   211
Asp Phe Leu Gln Ala Thr Gly Leu Lys Pro Gln Glu Leu Thr Ser Arg
            25                  30                  35

atg ttg gat acc acc act tct cga att ggc agt ctg gaa ggt ttc gac   259
Met Leu Asp Thr Thr Thr Ser Arg Ile Gly Ser Leu Glu Gly Phe Asp
        40                  45                  50

ggc gtg att gtg ggc gga agc cca ctg aat gcc acc aac ttt gag tac   307
Gly Val Ile Val Gly Gly Ser Pro Leu Asn Ala Thr Asn Phe Glu Tyr
    55                  60                  65

agc gat tgg caa cgc cac gtc cac cgc gaa ttg tcc ttg ctg atc aat   355
Ser Asp Trp Gln Arg His Val His Arg Glu Leu Ser Leu Leu Ile Asn
70                  75                  80                  85

cac cca ctg cca aca atc ttt gtc tgc tac ggc aat acc ttt ttg acc   403
His Pro Leu Pro Thr Ile Phe Val Cys Tyr Gly Asn Thr Phe Leu Thr
                90                  95                  100

ttc ttc tct ggc gga cag att ggt cgc aca cac ccc gaa gat tcc ggc   451
Phe Phe Ser Gly Gly Gln Ile Gly Arg Thr His Pro Glu Asp Ser Gly
            105                 110                 115

gcc acc aca gtg ttg cta act gac gcc ggc aaa cga gac gta ctc act   499
Ala Thr Thr Val Leu Leu Thr Asp Ala Gly Lys Arg Asp Val Leu Thr
        120                 125                 130

caa gac cta ccg gat agc ttt acg tcc ttt act ggt cac acg gaa aac   547
Gln Asp Leu Pro Asp Ser Phe Thr Ser Phe Thr Gly His Thr Glu Asn
    135                 140                 145

tcc gta                                                          553
Ser Val
150
```

<210> 2634
<211> 151
<212> PRT
<213> Corynebacterium glutamicum

<400> 2634

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Met Val Ser Val Leu Leu Ile Gln Pro Arg Gln Gly Glu Ala Val Ala
  1               5                  10                  15

Ala Ala Glu Arg Arg Asp Phe Leu Gln Ala Thr Gly Leu Lys Pro Gln
             20                  25                  30

Glu Leu Thr Ser Arg Met Leu Asp Thr Thr Thr Ser Arg Ile Gly Ser
         35                  40                  45

Leu Glu Gly Phe Asp Gly Val Ile Val Gly Gly Ser Pro Leu Asn Ala
     50                  55                  60

Thr Asn Phe Glu Tyr Ser Asp Trp Gln Arg His Val His Arg Glu Leu
 65                  70                  75                  80

Ser Leu Leu Ile Asn His Pro Leu Pro Thr Ile Phe Val Cys Tyr Gly
                 85                  90                  95

Asn Thr Phe Leu Thr Phe Phe Ser Gly Gly Gln Ile Gly Arg Thr His
            100                 105                 110

Pro Glu Asp Ser Gly Ala Thr Thr Val Leu Leu Thr Asp Ala Gly Lys
        115                 120                 125

Arg Asp Val Leu Thr Gln Asp Leu Pro Asp Ser Phe Thr Ser Phe Thr
    130                 135                 140

Gly His Thr Glu Asn Ser Val
145                 150


<210> 2635
<211> 621
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(598)
<223> RXA02212

<400> 2635
gtgatgtgac tttctatcac ccccttactc acccccattg cttattgagt aaagtcggtt 60

cccgctcttt cgtgagcccg acactaatga aggtttttag atg att cca gaa aat   115
                                            Met Ile Pro Glu Asn
                                              1               5

att gat ctc aag cag ctc gct tcg gag ctt ggt gat gat gcc gtg gca   163
Ile Asp Leu Lys Gln Leu Ala Ser Glu Leu Gly Asp Asp Ala Val Ala
                 10                  15                  20

atg ggg gag cac aca ggc aac cag ttt ccg act ttg gaa aaa gac ctt   211
Met Gly Glu His Thr Gly Asn Gln Phe Pro Thr Leu Glu Lys Asp Leu
             25                  30                  35

att aat gtt gtg aca gat gca aag gaa tca gat ttt gga tct tta ggg   259
Ile Asn Val Val Thr Asp Ala Lys Glu Ser Asp Phe Gly Ser Leu Gly
         40                  45                  50

gtc gtg att ctt gat gaa act cca gtg atg act tcc aac ctg agg gat   307
```

```
Val Val Ile Leu Asp Glu Thr Pro Val Met Thr Ser Asn Leu Arg Asp
     55                  60                  65

att gcg cag gag ctg ttg att caa acg gat ctg gac acc gtt gtg gtg   355
Ile Ala Gln Glu Leu Leu Ile Gln Thr Asp Leu Asp Thr Val Val Val
 70                  75                  80                  85

cgg gct cca atg tcg gct gcg gtg gtg agt gat gtt cat tcg agg gcg   403
Arg Ala Pro Met Ser Ala Ala Val Val Ser Asp Val His Ser Arg Ala
                90                  95                 100

gcg ctt gag tca ggg cag cat gat ttg ctt ggg acc act gat tac gtg   451
Ala Leu Glu Ser Gly Gln His Asp Leu Leu Gly Thr Thr Asp Tyr Val
            105                 110                 115

ctg gga acg gag ctt ttg gta cag gat gta acg gaa tcg acg gtg ggg   499
Leu Gly Thr Glu Leu Leu Val Gln Asp Val Thr Glu Ser Thr Val Gly
        120                 125                 130

aat att gat tgg ggt caa ttg ctg att tgg ggg ttg gtt gct ttg gca   547
Asn Ile Asp Trp Gly Gln Leu Leu Ile Trp Gly Leu Val Ala Leu Ala
    135                 140                 145

atc gcc gtg gtt gtt gcg ggt gcg tct gtg cgt cga aaa gca ata tct   595
Ile Ala Val Val Val Ala Gly Ala Ser Val Arg Arg Lys Ala Ile Ser
150                 155                 160                 165

tta taagtaaagt tctaaagctt tac                                    621
Leu
```

<210> 2636
<211> 166
<212> PRT
<213> Corynebacterium glutamicum

<400> 2636

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Met Ile Pro Glu Asn Ile Asp Leu Lys Gln Leu Ala Ser Glu Leu Gly
  1               5                  10                  15

Asp Asp Ala Val Ala Met Gly Glu His Thr Gly Asn Gln Phe Pro Thr
             20                  25                  30

Leu Glu Lys Asp Leu Ile Asn Val Val Thr Asp Ala Lys Glu Ser Asp
         35                  40                  45

Phe Gly Ser Leu Gly Val Val Ile Leu Asp Glu Thr Pro Val Met Thr
     50                  55                  60

Ser Asn Leu Arg Asp Ile Ala Gln Glu Leu Leu Ile Gln Thr Asp Leu
 65                  70                  75                  80

Asp Thr Val Val Val Arg Ala Pro Met Ser Ala Ala Val Val Ser Asp
                 85                  90                  95

Val His Ser Arg Ala Ala Leu Glu Ser Gly Gln His Asp Leu Leu Gly
            100                 105                 110

Thr Thr Asp Tyr Val Leu Gly Thr Glu Leu Leu Val Gln Asp Val Thr
        115                 120                 125
```

```
Glu Ser Thr Val Gly Asn Ile Asp Trp Gly Gln Leu Leu Ile Trp Gly
    130                 135                 140

Leu Val Ala Leu Ala Ile Ala Val Val Val Ala Gly Ala Ser Val Arg
145                 150                 155                 160

Arg Lys Ala Ile Ser Leu
                165
```

<210> 2637
<211> 329
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(306)
<223> RXA02216

<400> 2637

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gta gcg ccc gcc cct gga cac gtg gtg ttg gca acg gga cca acc tgc   48
Val Ala Pro Ala Pro Gly His Val Val Leu Ala Thr Gly Pro Thr Cys
  1               5                  10                  15

ccc atc cag atg ctg cgc gcc aac aag aac acc tgg tca gtt caa ttc   96
Pro Ile Gln Met Leu Arg Ala Asn Lys Asn Thr Trp Ser Val Gln Phe
             20                  25                  30

cat gcg gat atg gat gcc gta ggc atg aaa aac cgc atg gat ttt tac   144
His Ala Asp Met Asp Ala Val Gly Met Lys Asn Arg Met Asp Phe Tyr
         35                  40                  45

tcc aac tac cgg ttc ttc tcc cca gaa gat tat gac cgc atc att gca   192
Ser Asn Tyr Arg Phe Phe Ser Pro Glu Asp Tyr Asp Arg Ile Ile Ala
     50                  55                  60

gag cta ccc tct gtt gac tcc att tat gcc aac agg gtg ctc cgc aac   240
Glu Leu Pro Ser Val Asp Ser Ile Tyr Ala Asn Arg Val Leu Arg Asn
 65                  70                  75                  80

ttc gtg gag gtc tgc gaa gga att cgt gtt gct gat ggt gct gag cac   288
Phe Val Glu Val Cys Glu Gly Ile Arg Val Ala Asp Gly Ala Glu His
                 85                  90                  95

caa ctc cca aag ctt aac taatcgagga gactggtgat tcg                 329
Gln Leu Pro Lys Leu Asn
            100
```

<210> 2638
<211> 102
<212> PRT
<213> Corynebacterium glutamicum

<400> 2638

```
Val Ala Pro Ala Pro Gly His Val Val Leu Ala Thr Gly Pro Thr Cys
  1               5                  10                  15

Pro Ile Gln Met Leu Arg Ala Asn Lys Asn Thr Trp Ser Val Gln Phe
```

```
            20                  25                  30

His Ala Asp Met Asp Ala Val Gly Met Lys Asn Arg Met Asp Phe Tyr
         35                  40                  45

Ser Asn Tyr Arg Phe Phe Ser Pro Glu Asp Tyr Asp Arg Ile Ile Ala
     50                  55                  60

Glu Leu Pro Ser Val Asp Ser Ile Tyr Ala Asn Arg Val Leu Arg Asn
 65                  70                  75                  80

Phe Val Glu Val Cys Glu Gly Ile Arg Val Ala Asp Gly Ala Glu His
                 85                  90                  95

Gln Leu Pro Lys Leu Asn
            100


<210> 2639
<211> 786
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(763)
<223> RXA02217

<400> 2639
ccaaatgggt atgggcgctt ttgaccatcg tcaatggtgt tggccccgct gcctactggg 60

ctttcggcag gaaaaactaa gagttgttag ggtggcgctc atg act aat aaa aca   115
                                            Met Thr Asn Lys Thr
                                              1               5

cga gct cta ctc att ggt ggc cac ggc aag gtg gcc ctc cta gca acc   163
Arg Ala Leu Leu Ile Gly Gly His Gly Lys Val Ala Leu Leu Ala Thr
                 10                  15                  20

ccc atg ctt atc gac gcc tcg gtg cag gtc act tcc atg tac cgc aat   211
Pro Met Leu Ile Asp Ala Ser Val Gln Val Thr Ser Met Tyr Arg Asn
             25                  30                  35

ccg gac cac agg tcc gaa att gag gcg ctg ggc gcc aca act tta gag   259
Pro Asp His Arg Ser Glu Ile Glu Ala Leu Gly Ala Thr Thr Leu Glu
         40                  45                  50

cgt gac gtc acc aca ctc agc gtg gag gat tgg gca gat ctg ctc aag   307
Arg Asp Val Thr Thr Leu Ser Val Glu Asp Trp Ala Asp Leu Leu Lys
     55                  60                  65

gac ttc gac gta gtg gtg tgg agc gcc gga aac ggt ggc aag aac ggc   355
Asp Phe Asp Val Val Val Trp Ser Ala Gly Asn Gly Gly Lys Asn Gly
 70                  75                  80                  85

gcg gat gca act tat gcc att gat cgt gat gcc gcg atc gca tcc att   403
Ala Asp Ala Thr Tyr Ala Ile Asp Arg Asp Ala Ala Ile Ala Ser Ile
                 90                  95                 100

gat ggt gca gct agc cta ggg gag aag gca cct cgc tac atc atg gtg   451
Asp Gly Ala Ala Ser Leu Gly Glu Lys Ala Pro Arg Tyr Ile Met Val
```

```
            105                 110                 115

agc tac att gga tcc tcc acg cac acc att gat cct tca gca tcc ttc   499
Ser Tyr Ile Gly Ser Ser Thr His Thr Ile Asp Pro Ser Ala Ser Phe
        120                 125                 130

tac cca tat gca gaa tcc aaa aag gcc gct gat gag cac cta agc tcc   547
Tyr Pro Tyr Ala Glu Ser Lys Lys Ala Ala Asp Glu His Leu Ser Ser
    135                 140                 145

acc aac ctg gat tac ctt atc ctc gca cca gca gcc tta act ctg gat   595
Thr Asn Leu Asp Tyr Leu Ile Leu Ala Pro Ala Ala Leu Thr Leu Asp
150                 155                 160                 165

gaa gtc aat ggc gtt gag gtg atc gcc gat acc aac gaa gca gcc gca   643
Glu Val Asn Gly Val Glu Val Ile Ala Asp Thr Asn Glu Ala Ala Ala
                170                 175                 180

ggc cgc acc aca tca aga gtc ctc gtt gcg gaa gtt atc acc gag ttg   691
Gly Arg Thr Thr Ser Arg Val Leu Val Ala Glu Val Ile Thr Glu Leu
            185                 190                 195

gtg gtt cgc gac ttc cca caa acc cgt gtg ctg cct ttc gtg gat ggc   739
Val Val Arg Asp Phe Pro Gln Thr Arg Val Leu Pro Phe Val Asp Gly
        200                 205                 210

gaa tca cca gtc tcc tcg att agt taagctttgg gagttggtgc tca         786
Glu Ser Pro Val Ser Ser Ile Ser
    215                 220
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<210> 2640
<211> 221
<212> PRT
<213> Corynebacterium glutamicum

<400> 2640

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Met Thr Asn Lys Thr Arg Ala Leu Leu Ile Gly Gly His Gly Lys Val
  1               5                  10                  15

Ala Leu Leu Ala Thr Pro Met Leu Ile Asp Ala Ser Val Gln Val Thr
             20                  25                  30

Ser Met Tyr Arg Asn Pro Asp His Arg Ser Glu Ile Glu Ala Leu Gly
         35                  40                  45

Ala Thr Thr Leu Glu Arg Asp Val Thr Thr Leu Ser Val Glu Asp Trp
     50                  55                  60

Ala Asp Leu Leu Lys Asp Phe Asp Val Val Val Trp Ser Ala Gly Asn
 65                  70                  75                  80

Gly Gly Lys Asn Gly Ala Asp Ala Thr Tyr Ala Ile Asp Arg Asp Ala
                 85                  90                  95

Ala Ile Ala Ser Ile Asp Gly Ala Ala Ser Leu Gly Glu Lys Ala Pro
            100                 105                 110

Arg Tyr Ile Met Val Ser Tyr Ile Gly Ser Ser Thr His Thr Ile Asp
        115                 120                 125
```

```
Pro Ser Ala Ser Phe Tyr Pro Tyr Ala Glu Ser Lys Lys Ala Ala Asp
    130                 135                 140

Glu His Leu Ser Ser Thr Asn Leu Asp Tyr Leu Ile Leu Ala Pro Ala
145                 150                 155                 160

Ala Leu Thr Leu Asp Glu Val Asn Gly Val Glu Val Ile Ala Asp Thr
                165                 170                 175

Asn Glu Ala Ala Ala Gly Arg Thr Thr Ser Arg Val Leu Val Ala Glu
            180                 185                 190

Val Ile Thr Glu Leu Val Val Arg Asp Phe Pro Gln Thr Arg Val Leu
        195                 200                 205

Pro Phe Val Asp Gly Glu Ser Pro Val Ser Ser Ile Ser
    210                 215                 220


<210> 2641
<211> 390
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(367)
<223> RXA02218

<400> 2641
caatgattta tatgtcttgg acgagcgatt aaatagagtt ggcatacccc aaatgataga 60

cccaaagtgt cgtgtccacc gctcgttgta gcatgaaccc atg ttt gca atc atg   115
                                            Met Phe Ala Ile Met
                                              1               5

act gtc aca ggg cag gac cac acc gga att atc gcc gca gtt tcc acc   163
Thr Val Thr Gly Gln Asp His Thr Gly Ile Ile Ala Ala Val Ser Thr
                10                  15                  20

gcg ttg gct gag cta gat gtc aat att cac aac gtt tcc caa acc atc   211
Ala Leu Ala Glu Leu Asp Val Asn Ile His Asn Val Ser Gln Thr Ile
            25                  30                  35

atg gat caa tgg ttc acc atg atc ttg cac gtt ggt ttc gat gaa tcg   259
Met Asp Gln Trp Phe Thr Met Ile Leu His Val Gly Phe Asp Glu Ser
        40                  45                  50

gtc ttg gat atc gcc aca gtt cag gaa cgc atg aag cca gtg gaa aag   307
Val Leu Asp Ile Ala Thr Val Gln Glu Arg Met Lys Pro Val Glu Lys
    55                  60                  65

gaa cag ggc ttg gtt att cgt atc cag tct gaa gcc ttg ttc aac gcg   355
Glu Gln Gly Leu Val Ile Arg Ile Gln Ser Glu Ala Leu Phe Asn Ala
70                  75                  80                  85

gtt aat gag atc taggggtgc acatggatga ttt                         390
Val Asn Glu Ile
```

<210> 2642
<211> 89
<212> PRT
<213> Corynebacterium glutamicum

<400> 2642
Met Phe Ala Ile Met Thr Val Thr Gly Gln Asp His Thr Gly Ile Ile
1 5 10 15

Ala Ala Val Ser Thr Ala Leu Ala Glu Leu Asp Val Asn Ile His Asn
20 25 30

Val Ser Gln Thr Ile Met Asp Gln Trp Phe Thr Met Ile Leu His Val
35 40 45

Gly Phe Asp Glu Ser Val Leu Asp Ile Ala Thr Val Gln Glu Arg Met
50 55 60

Lys Pro Val Glu Lys Glu Gln Gly Leu Val Ile Arg Ile Gln Ser Glu
65 70 75 80

Ala Leu Phe Asn Ala Val Asn Glu Ile
85

<210> 2643
<211> 1509
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1486)
<223> RXA02219

<400> 2643
tcaggaacgc atgaagccag tggaaaagga acagggcttg gttattcgta tccagtctga 60

agccttgttc aacgcggtta atgagatcta gggggtgcac atg gat gat ttt tct 115
Met Asp Asp Phe Ser
1 5

gca tcg cta ggt ttt act gac cgt tcc tcg agg gga att ctg gac acc 163
Ala Ser Leu Gly Phe Thr Asp Arg Ser Ser Arg Gly Ile Leu Asp Thr
10 15 20

atc gag atg att gag aag tat cgt ctt gat att cgc acc gtg acc atg 211
Ile Glu Met Ile Glu Lys Tyr Arg Leu Asp Ile Arg Thr Val Thr Met
25 30 35

gga atc agc ctg ttg gaa tgc gcg cgt ggc tcg atg gaa gag acc gcg 259
Gly Ile Ser Leu Leu Glu Cys Ala Arg Gly Ser Met Glu Glu Thr Ala
40 45 50

acg gct gtt tat gat cgc gtg acg tca cag gct gca cgt ctg gtt gag 307
Thr Ala Val Tyr Asp Arg Val Thr Ser Gln Ala Ala Arg Leu Val Glu
55 60 65

gtt tgt gaa ggc att gag cgt gaa ttg ggc att ccc att gtg aat aag 355
Val Cys Glu Gly Ile Glu Arg Glu Leu Gly Ile Pro Ile Val Asn Lys
70 75 80 85

```
cgc atc tcg gtg act cca att gcc ctg gtg act gct ggt tgc agt ggc   403
Arg Ile Ser Val Thr Pro Ile Ala Leu Val Thr Ala Gly Cys Ser Gly
                 90                  95                 100

gat ccc gtt gac gtt gct cga gcc tta gat aag gca gca aaa gat gtc   451
Asp Pro Val Asp Val Ala Arg Ala Leu Asp Lys Ala Ala Lys Asp Val
            105                 110                 115

gga gtg aac ttc atc ggc ggg tat tca gca ctg gtt gaa aaa ggt gga   499
Gly Val Asn Phe Ile Gly Gly Tyr Ser Ala Leu Val Glu Lys Gly Gly
        120                 125                 130

acc acc tcc gat att cgg ctg atc cgc tcc att ccc gag gca ttg agc   547
Thr Thr Ser Asp Ile Arg Leu Ile Arg Ser Ile Pro Glu Ala Leu Ser
    135                 140                 145

aca acc gat gtg gtg tgt gga tcc gtc aat gtg gcg tcg tct cgc gcg   595
Thr Thr Asp Val Val Cys Gly Ser Val Asn Val Ala Ser Ser Arg Ala
150                 155                 160                 165

ggt atc aac atg aac gca gtc aat gag atg ggc aag gtg gtc aag caa   643
Gly Ile Asn Met Asn Ala Val Asn Glu Met Gly Lys Val Val Lys Gln
                170                 175                 180

gca gct gaa ttg acc aaa gat cgc tcc gcc atc gca tgt gca aag cta   691
Ala Ala Glu Leu Thr Lys Asp Arg Ser Ala Ile Ala Cys Ala Lys Leu
            185                 190                 195

gtg gtc ttt gcc aat tct gtg ggc gat aat cca ttc atg gct ggc gct   739
Val Val Phe Ala Asn Ser Val Gly Asp Asn Pro Phe Met Ala Gly Ala
        200                 205                 210

ttc cac ggc att gag gag ccg gat tgt gtg gtc agc gtt ggt gtc tca   787
Phe His Gly Ile Glu Glu Pro Asp Cys Val Val Ser Val Gly Val Ser
    215                 220                 225

gga cca ggc gtg gtt agt cgc gcg ctg ggc aat ctt caa ggt gcc acc   835
Gly Pro Gly Val Val Ser Arg Ala Leu Gly Asn Leu Gln Gly Ala Thr
230                 235                 240                 245

ctt gat caa gtc gca gaa gag atc aag aaa gcg gcc ttc aag atc act   883
Leu Asp Gln Val Ala Glu Glu Ile Lys Lys Ala Ala Phe Lys Ile Thr
                250                 255                 260

cgt act gga caa ctg gtt ggt gcg atg gcc tca gaa cgc cta gga gtt   931
Arg Thr Gly Gln Leu Val Gly Ala Met Ala Ser Glu Arg Leu Gly Val
            265                 270                 275

cct ttc ggc atc gtt gat ctt tcg ctc gct ccc act gct gaa gtg ggc   979
Pro Phe Gly Ile Val Asp Leu Ser Leu Ala Pro Thr Ala Glu Val Gly
        280                 285                 290

gat tcc gtg gca aat atc ctt gag gtc atg ggt ctt gac cag gtg ggc   1027
Asp Ser Val Ala Asn Ile Leu Glu Val Met Gly Leu Asp Gln Val Gly
    295                 300                 305

aca cat ggc acc acc gcg gca ctc gca ctg ctc aac gac gcg gtg aaa   1075
Thr His Gly Thr Thr Ala Ala Leu Ala Leu Leu Asn Asp Ala Val Lys
310                 315                 320                 325
```

```
aag ggt ggc atg atg gcc tgc tca cgt gtc ggc ggc ttg tcc gga tcc   1123
Lys Gly Gly Met Met Ala Cys Ser Arg Val Gly Gly Leu Ser Gly Ser
                330                 335                 340

ttc att cca gtt tct gaa gat aaa ggc atg atc gat gcg gtt cgc aca   1171
Phe Ile Pro Val Ser Glu Asp Lys Gly Met Ile Asp Ala Val Arg Thr
            345                 350                 355

gga gca att tct att gac aag ctc gaa gcg atg acc gcg atc tgc tca   1219
Gly Ala Ile Ser Ile Asp Lys Leu Glu Ala Met Thr Ala Ile Cys Ser
        360                 365                 370

gtt ggt ttg gat atg att gcg atc cct ggc gac acc ccg gcg gaa act   1267
Val Gly Leu Asp Met Ile Ala Ile Pro Gly Asp Thr Pro Ala Glu Thr
    375                 380                 385

att tcg ggc atg atc gcg gac gaa gca gcc atc ggt gtg atg aat cat   1315
Ile Ser Gly Met Ile Ala Asp Glu Ala Ala Ile Gly Val Met Asn His
390                 395                 400                 405

aag act aca gct gtg cgt gtt att cct gtt cca gga act gtc cct ggc   1363
Lys Thr Thr Ala Val Arg Val Ile Pro Val Pro Gly Thr Val Pro Gly
                410                 415                 420

gat gag gta gat ttc ggt ggc ttg ctg ggt tac gcg ccg gtc att cca   1411
Asp Glu Val Asp Phe Gly Gly Leu Leu Gly Tyr Ala Pro Val Ile Pro
            425                 430                 435

gta aat acc gtg gga aat agt gag ttt att cac cgc ggc ggc ttc att   1459
Val Asn Thr Val Gly Asn Ser Glu Phe Ile His Arg Gly Gly Phe Ile
        440                 445                 450

cca gca ccc gtt cac ggg ttt aga aac taggagatcc ggggcctttta       1506
Pro Ala Pro Val His Gly Phe Arg Asn
    455                 460

cct                                                              1509
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<210> 2644
<211> 462
<212> PRT
<213> Corynebacterium glutamicum

<400> 2644

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Met Asp Asp Phe Ser Ala Ser Leu Gly Phe Thr Asp Arg Ser Ser Arg
  1               5                  10                  15

Gly Ile Leu Asp Thr Ile Glu Met Ile Glu Lys Tyr Arg Leu Asp Ile
             20                  25                  30

Arg Thr Val Thr Met Gly Ile Ser Leu Leu Glu Cys Ala Arg Gly Ser
         35                  40                  45

Met Glu Glu Thr Ala Thr Ala Val Tyr Asp Arg Val Thr Ser Gln Ala
     50                  55                  60

Ala Arg Leu Val Glu Val Cys Glu Gly Ile Glu Arg Glu Leu Gly Ile
 65                  70                  75                  80

Pro Ile Val Asn Lys Arg Ile Ser Val Thr Pro Ile Ala Leu Val Thr
```

```
                  85                  90                  95

Ala Gly Cys Ser Gly Asp Pro Val Asp Val Ala Arg Ala Leu Asp Lys
            100                 105                 110

Ala Ala Lys Asp Val Gly Val Asn Phe Ile Gly Gly Tyr Ser Ala Leu
        115                 120                 125

Val Glu Lys Gly Gly Thr Thr Ser Asp Ile Arg Leu Ile Arg Ser Ile
    130                 135                 140

Pro Glu Ala Leu Ser Thr Thr Asp Val Val Cys Gly Ser Val Asn Val
145                 150                 155                 160

Ala Ser Ser Arg Ala Gly Ile Asn Met Asn Ala Val Asn Glu Met Gly
                165                 170                 175

Lys Val Val Lys Gln Ala Ala Glu Leu Thr Lys Asp Arg Ser Ala Ile
            180                 185                 190

Ala Cys Ala Lys Leu Val Val Phe Ala Asn Ser Val Gly Asp Asn Pro
        195                 200                 205

Phe Met Ala Gly Ala Phe His Gly Ile Glu Glu Pro Asp Cys Val Val
    210                 215                 220

Ser Val Gly Val Ser Gly Pro Gly Val Val Ser Arg Ala Leu Gly Asn
225                 230                 235                 240

Leu Gln Gly Ala Thr Leu Asp Gln Val Ala Glu Glu Ile Lys Lys Ala
                245                 250                 255

Ala Phe Lys Ile Thr Arg Thr Gly Gln Leu Val Gly Ala Met Ala Ser
            260                 265                 270

Glu Arg Leu Gly Val Pro Phe Gly Ile Val Asp Leu Ser Leu Ala Pro
        275                 280                 285

Thr Ala Glu Val Gly Asp Ser Val Ala Asn Ile Leu Glu Val Met Gly
    290                 295                 300

Leu Asp Gln Val Gly Thr His Gly Thr Thr Ala Ala Leu Ala Leu Leu
305                 310                 315                 320

Asn Asp Ala Val Lys Lys Gly Gly Met Met Ala Cys Ser Arg Val Gly
                325                 330                 335

Gly Leu Ser Gly Ser Phe Ile Pro Val Ser Glu Asp Lys Gly Met Ile
            340                 345                 350

Asp Ala Val Arg Thr Gly Ala Ile Ser Ile Asp Lys Leu Glu Ala Met
        355                 360                 365

Thr Ala Ile Cys Ser Val Gly Leu Asp Met Ile Ala Ile Pro Gly Asp
    370                 375                 380

Thr Pro Ala Glu Thr Ile Ser Gly Met Ile Ala Asp Glu Ala Ala Ile
385                 390                 395                 400

Gly Val Met Asn His Lys Thr Thr Ala Val Arg Val Ile Pro Val Pro
                405                 410                 415
```

```
Gly Thr Val Pro Gly Asp Glu Val Asp Phe Gly Gly Leu Leu Gly Tyr
            420                 425                 430

Ala Pro Val Ile Pro Val Asn Thr Val Gly Asn Ser Glu Phe Ile His
        435                 440                 445

Arg Gly Gly Phe Ile Pro Ala Pro Val His Gly Phe Arg Asn
    450                 455                 460


<210> 2645
<211> 1485
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1462)
<223> RXA02221

<400> 2645
ttcaatgata tttgctctga tttttggttc tcgtctaatt tcattatttt gtcacgccag 60

ccatcacgac ttcataccca ccaattgaaa gtaaagtcca atg ttt acc gca tcc   115
                                          Met Phe Thr Ala Ser
                                            1               5

att cct act tat gaa tta ggg tct ttc agc aag ggc tcc tac gtt gag   163
Ile Pro Thr Tyr Glu Leu Gly Ser Phe Ser Lys Gly Ser Tyr Val Glu
                10                  15                  20

atc aaa gga act tac ttc tac cct gac acg cta aat act tta ttt aga   211
Ile Lys Gly Thr Tyr Phe Tyr Pro Asp Thr Leu Asn Thr Leu Phe Arg
            25                  30                  35

aat tct ggg gca aaa gac aac gaa gag ttc ttt gta gac gta act ctt   259
Asn Ser Gly Ala Lys Asp Asn Glu Glu Phe Phe Val Asp Val Thr Leu
        40                  45                  50

gtt cca gaa cca gat aat ccg cat agc act cga ggc cat gcc att tca   307
Val Pro Glu Pro Asp Asn Pro His Ser Thr Arg Gly His Ala Ile Ser
    55                  60                  65

gtc cgc tgg aat gat ctc gta ata gga cat att gcc tcg gat atg act   355
Val Arg Trp Asn Asp Leu Val Ile Gly His Ile Ala Ser Asp Met Thr
70                  75                  80                  85

gaa aaa ttc caa caa gtg cga cga gtt gca gct agt ggc tac gat gct   403
Glu Lys Phe Gln Gln Val Arg Arg Val Ala Ala Ser Gly Tyr Asp Ala
                90                  95                  100

cga gtc tct gct cgg att tgg acg aat aca aac tat aag aat gaa cga   451
Arg Val Ser Ala Arg Ile Trp Thr Asn Thr Asn Tyr Lys Asn Glu Arg
            105                 110                 115

gat ttt tgg gta tct gtt aag ctc ccc gat cca gat ttc ctt gtt cct   499
Asp Phe Trp Val Ser Val Lys Leu Pro Asp Pro Asp Phe Leu Val Pro
        120                 125                 130

ctt aat gat cct ccc cat gac ggg ttt acc ctc ctc cct tat gga aca   547
```

```
Leu Asn Asp Pro Pro His Asp Gly Phe Thr Leu Leu Pro Tyr Gly Thr
    135                 140                 145

gca atc caa gtc acc aag gaa tct gat cac atg gac gtg ctc tca gaa   595
Ala Ile Gln Val Thr Lys Glu Ser Asp His Met Asp Val Leu Ser Glu
150                 155                 160                 165

ttc gtg cct cca tct gga caa ggt cag att ctc gta tcg cta cac atc   643
Phe Val Pro Pro Ser Gly Gln Gly Gln Ile Leu Val Ser Leu His Ile
                170                 175                 180

att aac gca ggc gtg aga aaa gaa tgg gat ggc att gaa gtt cgg ctc   691
Ile Asn Ala Gly Val Arg Lys Glu Trp Asp Gly Ile Glu Val Arg Leu
            185                 190                 195

gat aat caa cgg atc gga gag ctt aca aag gcc agt tca gaa aaa ttc   739
Asp Asn Gln Arg Ile Gly Glu Leu Thr Lys Ala Ser Ser Glu Lys Phe
        200                 205                 210

gca ccc gta gtg cga cat ttc gat gac cta gga ctt agt aca cta tgt   787
Ala Pro Val Val Arg His Phe Asp Asp Leu Gly Leu Ser Thr Leu Cys
    215                 220                 225

cgt gcg ctc atc aag ggg tca tca cta gct gct gaa gta act cta tat   835
Arg Ala Leu Ile Lys Gly Ser Ser Leu Ala Ala Glu Val Thr Leu Tyr
230                 235                 240                 245

gga gct cgt gca cat gag ctt tcc gaa gaa gac tta gaa cct aaa agc   883
Gly Ala Arg Ala His Glu Leu Ser Glu Glu Asp Leu Glu Pro Lys Ser
                250                 255                 260

tct tcc cca ttg ccc agg ttg gtt gaa tac cag tca aat ccg ttt aat   931
Ser Ser Pro Leu Pro Arg Leu Val Glu Tyr Gln Ser Asn Pro Phe Asn
            265                 270                 275

tat caa gtc ccc aac agg tgg ccc ggc gag cag aat caa cgt gct cct   979
Tyr Gln Val Pro Asn Arg Trp Pro Gly Glu Gln Asn Gln Arg Ala Pro
        280                 285                 290

aag tcg caa aag tct tct tca tca cct ttc gca gcg tat cgc ggg cca   1027
Lys Ser Gln Lys Ser Ser Ser Ser Pro Phe Ala Ala Tyr Arg Gly Pro
    295                 300                 305

tcg caa cct agt aaa tca ctc aca ccg ttt gta gcg cag aca cct gcg   1075
Ser Gln Pro Ser Lys Ser Leu Thr Pro Phe Val Ala Gln Thr Pro Ala
310                 315                 320                 325

cct cag cct agt gat cga ttt att gat tgg gat tca ttg ctt caa ccg   1123
Pro Gln Pro Ser Asp Arg Phe Ile Asp Trp Asp Ser Leu Leu Gln Pro
                330                 335                 340

gac gga act cca aga gct acg cca ttc caa aga gga gta acc cgc ggg   1171
Asp Gly Thr Pro Arg Ala Thr Pro Phe Gln Arg Gly Val Thr Arg Gly
            345                 350                 355

tta att ggc aag cat ttt tcg aat caa aaa tct cca aga att gac ttt   1219
Leu Ile Gly Lys His Phe Ser Asn Gln Lys Ser Pro Arg Ile Asp Phe
        360                 365                 370

gca acg gtg ggg caa tgt gat gca att ctc cga act ttc gga gag ccg   1267
Ala Thr Val Gly Gln Cys Asp Ala Ile Leu Arg Thr Phe Gly Glu Pro
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    375                 380                 385

acc gac aag ctt tat aaa gac ggc agg act tct tgg cct ttg tgg tgg   1315
Thr Asp Lys Leu Tyr Lys Asp Gly Arg Thr Ser Trp Pro Leu Trp Trp
390                 395                 400                 405

gcg ctc atg gcg ata gtc acc ctt ctc gtc atg ttg ctg aac ttt att   1363
Ala Leu Met Ala Ile Val Thr Leu Leu Val Met Leu Leu Asn Phe Ile
                410                 415                 420

cca gga att ggt ccg atc ttc cca ctt atc gga ttg atc gta ctt ggt   1411
Pro Gly Ile Gly Pro Ile Phe Pro Leu Ile Gly Leu Ile Val Leu Gly
            425                 430                 435

cat cac ttt tgg act cgc cga aaa ctt aac cca cca ttc ggt aga tca   1459
His His Phe Trp Thr Arg Arg Lys Leu Asn Pro Pro Phe Gly Arg Ser
        440                 445                 450

aaa tagatattct catcaaatat cgc                                    1485
Lys
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US-10-644-762-2646

<210> 2646
<211> 454
<212> PRT
<213> Corynebacterium glutamicum

<400> 2646

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Gly Ser Tyr Val Glu Ile Lys Gly Thr Tyr Phe Tyr Pro Asp Thr Leu
             20                  25                  30

Asn Thr Leu Phe Arg Asn Ser Gly Ala Lys Asp Asn Glu Glu Phe Phe
         35                  40                  45

Val Asp Val Thr Leu Val Pro Glu Pro Asp Asn Pro His Ser Thr Arg
     50                  55                  60

Gly His Ala Ile Ser Val Arg Trp Asn Asp Leu Val Ile Gly His Ile
 65                  70                  75                  80

Ala Ser Asp Met Thr Glu Lys Phe Gln Gln Val Arg Arg Val Ala Ala
                 85                  90                  95

Ser Gly Tyr Asp Ala Arg Val Ser Ala Arg Ile Trp Thr Asn Thr Asn
            100                 105                 110

Tyr Lys Asn Glu Arg Asp Phe Trp Val Ser Val Lys Leu Pro Asp Pro
        115                 120                 125

Asp Phe Leu Val Pro Leu Asn Asp Pro Pro His Asp Gly Phe Thr Leu
    130                 135                 140

Leu Pro Tyr Gly Thr Ala Ile Gln Val Thr Lys Glu Ser Asp His Met
145                 150                 155                 160

Asp Val Leu Ser Glu Phe Val Pro Pro Ser Gly Gln Gly Gln Ile Leu
                165                 170                 175
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Val Ser Leu His Ile Ile Asn Ala Gly Val Arg Lys Glu Trp Asp Gly
            180                 185                 190

Ile Glu Val Arg Leu Asp Asn Gln Arg Ile Gly Glu Leu Thr Lys Ala
        195                 200                 205

Ser Ser Glu Lys Phe Ala Pro Val Val Arg His Phe Asp Asp Leu Gly
    210                 215                 220

Leu Ser Thr Leu Cys Arg Ala Leu Ile Lys Gly Ser Ser Leu Ala Ala
225                 230                 235                 240

Glu Val Thr Leu Tyr Gly Ala Arg Ala His Glu Leu Ser Glu Glu Asp
                245                 250                 255

Leu Glu Pro Lys Ser Ser Ser Pro Leu Pro Arg Leu Val Glu Tyr Gln
            260                 265                 270

Ser Asn Pro Phe Asn Tyr Gln Val Pro Asn Arg Trp Pro Gly Glu Gln
        275                 280                 285

Asn Gln Arg Ala Pro Lys Ser Gln Lys Ser Ser Ser Ser Pro Phe Ala
    290                 295                 300

Ala Tyr Arg Gly Pro Ser Gln Pro Ser Lys Ser Leu Thr Pro Phe Val
305                 310                 315                 320

Ala Gln Thr Pro Ala Pro Gln Pro Ser Asp Arg Phe Ile Asp Trp Asp
                325                 330                 335

Ser Leu Leu Gln Pro Asp Gly Thr Pro Arg Ala Thr Pro Phe Gln Arg
            340                 345                 350

Gly Val Thr Arg Gly Leu Ile Gly Lys His Phe Ser Asn Gln Lys Ser
        355                 360                 365

Pro Arg Ile Asp Phe Ala Thr Val Gly Gln Cys Asp Ala Ile Leu Arg
    370                 375                 380

Thr Phe Gly Glu Pro Thr Asp Lys Leu Tyr Lys Asp Gly Arg Thr Ser
385                 390                 395                 400

Trp Pro Leu Trp Trp Ala Leu Met Ala Ile Val Thr Leu Leu Val Met
                405                 410                 415

Leu Leu Asn Phe Ile Pro Gly Ile Gly Pro Ile Phe Pro Leu Ile Gly
            420                 425                 430

Leu Ile Val Leu Gly His His Phe Trp Thr Arg Arg Lys Leu Asn Pro
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Pro Phe Gly Arg Ser Lys
    450
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<210> 2647
<211> 741
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(718)
<223> RXA02227

<400> 2647
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ggagaggtgt ttgcccagca atttcggtgg gcaggatagg gtg gaa gac gtg aat 115
Val Glu Asp Val Asn
1 5

gca acg ctg att atc atg cct gga agt ccg gcg ctg gta cct gaa ctg 163
Ala Thr Leu Ile Ile Met Pro Gly Ser Pro Ala Leu Val Pro Glu Leu
10 15 20

gca cca gcg gat gct gcg ggg gcg cgc ttg ttg gcg tcg tta cgt gca 211
Ala Pro Ala Asp Ala Ala Gly Ala Arg Leu Leu Ala Ser Leu Arg Ala
25 30 35

gtt ttt gat gcg gaa ctg gct aat gat gat cgc ccg atc gag ttg gtt 259
Val Phe Asp Ala Glu Leu Ala Asn Asp Asp Arg Pro Ile Glu Leu Val
40 45 50

ggc tcc cgg gat gag gcg tgg ttt acc aag cat gcg gga aat ctg cgg 307
Gly Ser Arg Asp Glu Ala Trp Phe Thr Lys His Ala Gly Asn Leu Arg
55 60 65

gcc tgg ggt gca ccg agc gtg cag gtt tct gac gga cat tat ttg ccg 355
Ala Trp Gly Ala Pro Ser Val Gln Val Ser Asp Gly His Tyr Leu Pro
70 75 80 85

gaa att ttg cag cgt gtc gcg ctg ggt ggt ttc gaa tcg cgt gta act 403
Glu Ile Leu Gln Arg Val Ala Leu Gly Gly Phe Glu Ser Arg Val Thr
90 95 100

cat gtg cgc gat cgg ttg ggt agc gtc aac gac aac acg gtt acg gtg 451
His Val Arg Asp Arg Leu Gly Ser Val Asn Asp Asn Thr Val Thr Val
105 110 115

ctt gcc ctt gac ggc ccc acg ggc ttg acc acc cgc gcg ccg tcc gca 499
Leu Ala Leu Asp Gly Pro Thr Gly Leu Thr Thr Arg Ala Pro Ser Ala
120 125 130

ctc gtg ccc ggc gcg tcc aac atc gac gcc tgg tgc cgc tca ttg ctg 547
Leu Val Pro Gly Ala Ser Asn Ile Asp Ala Trp Cys Arg Ser Leu Leu
135 140 145

tct gga aag ccc ggg gaa gtg ccc agc acc agc acg ctt atc gac gcc 595
Ser Gly Lys Pro Gly Glu Val Pro Ser Thr Ser Thr Leu Ile Asp Ala
150 155 160 165

tcc ctc cgc gaa cca cag ctc tgg ctc gac tta tcc gcc gtg gca aca 643
Ser Leu Arg Glu Pro Gln Leu Trp Leu Asp Leu Ser Ala Val Ala Thr
170 175 180

gaa gcg tca act gct caa ctt ctc gac agc gac gac aca cac ggc gtg 691
Glu Ala Ser Thr Ala Gln Leu Leu Asp Ser Asp Asp Thr His Gly Val
185 190 195

gga cgc tac gtt gct cgc tgg act ttt taacttaagg gagatctaga 738

Gly Arg Tyr Val Ala Arg Trp Thr Phe
200 205

tcg 741

<210> 2648
<211> 206
<212> PRT
<213> Corynebacterium glutamicum

<400> 2648
Val Glu Asp Val Asn Ala Thr Leu Ile Ile Met Pro Gly Ser Pro Ala
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Leu Val Pro Glu Leu Ala Pro Ala Asp Ala Ala Gly Ala Arg Leu Leu
20 25 30

Ala Ser Leu Arg Ala Val Phe Asp Ala Glu Leu Ala Asn Asp Asp Arg
35 40 45

Pro Ile Glu Leu Val Gly Ser Arg Asp Glu Ala Trp Phe Thr Lys His
50 55 60

Ala Gly Asn Leu Arg Ala Trp Gly Ala Pro Ser Val Gln Val Ser Asp
65 70 75 80

Gly His Tyr Leu Pro Glu Ile Leu Gln Arg Val Ala Leu Gly Gly Phe
85 90 95

Glu Ser Arg Val Thr His Val Arg Asp Arg Leu Gly Ser Val Asn Asp
100 105 110

Asn Thr Val Thr Val Leu Ala Leu Asp Gly Pro Thr Gly Leu Thr Thr
115 120 125

Arg Ala Pro Ser Ala Leu Val Pro Gly Ala Ser Asn Ile Asp Ala Trp
130 135 140

Cys Arg Ser Leu Leu Ser Gly Lys Pro Gly Glu Val Pro Ser Thr Ser
145 150 155 160

Thr Leu Ile Asp Ala Ser Leu Arg Glu Pro Gln Leu Trp Leu Asp Leu
165 170 175

Ser Ala Val Ala Thr Glu Ala Ser Thr Ala Gln Leu Leu Asp Ser Asp
180 185 190

Asp Thr His Gly Val Gly Arg Tyr Val Ala Arg Trp Thr Phe
195 200 205

<210> 2649
<211> 660
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(637)
<223> RXA02230

<400> 2649
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gacactttta acgaagcgca gaaggagtga gagcaagaaa atg gga gaa caa ctt 115
Met Gly Glu Gln Leu
1 5

ccg ttt gct aat ggt tca cgc tcc aac aaa ctg ccg ctc atc gtc atc 163
Pro Phe Ala Asn Gly Ser Arg Ser Asn Lys Leu Pro Leu Ile Val Ile
10 15 20

ggt ttg tgc tgc ata atg ctg atc ctg tgg ctt aaa ctt ccc ggc gta 211
Gly Leu Cys Cys Ile Met Leu Ile Leu Trp Leu Lys Leu Pro Gly Val
25 30 35

ctg ctt gcc acc atc att ggg gtt gcc acg atg agt gtg atg cgg atg 259
Leu Leu Ala Thr Ile Ile Gly Val Ala Thr Met Ser Val Met Arg Met
40 45 50

cgc acc tcc acc cca gaa act gcc tcg ctg gtt act tct att cgg ctg 307
Arg Thr Ser Thr Pro Glu Thr Ala Ser Leu Val Thr Ser Ile Arg Leu
55 60 65

tct gcg gaa gat att tcc gat gtg caa cat gag tgg cag cag ttt ttg 355
Ser Ala Glu Asp Ile Ser Asp Val Gln His Glu Trp Gln Gln Phe Leu
70 75 80 85

acc tcc ccc gag gcc gat gcg ctg gct gat cgc acg ctt gtc cgt ccc 403
Thr Ser Pro Glu Ala Asp Ala Leu Ala Asp Arg Thr Leu Val Arg Pro
90 95 100

gca ctg gcg gat cca gat tgt ggc gat aag gct atc gag aaa ttt cat 451
Ala Leu Ala Asp Pro Asp Cys Gly Asp Lys Ala Ile Glu Lys Phe His
105 110 115

tat gaa atc agc aat gcc aat cgc ttc ttg ggc agg ttg gac gct cgt 499
Tyr Glu Ile Ser Asn Ala Asn Arg Phe Leu Gly Arg Leu Asp Ala Arg
120 125 130

ctg caa caa aac ctc gtg gtc agt gag cta gaa aca ctt ctc aaa gta 547
Leu Gln Gln Asn Leu Val Val Ser Glu Leu Glu Thr Leu Leu Lys Val
135 140 145

acg gac gag cgc gca cta gag ctg cgg gaa acg tgg ctg gat gcg cgt 595
Thr Asp Glu Arg Ala Leu Glu Leu Arg Glu Thr Trp Leu Asp Ala Arg
150 155 160 165

aaa gcg gcc cag aaa ctt ggg ccg aac tac aat cgc gaa tct 637
Lys Ala Ala Gln Lys Leu Gly Pro Asn Tyr Asn Arg Glu Ser
170 175

tagatctgca cctcaccgag tgc 660

<210> 2650
<211> 179
<212> PRT
<213> Corynebacterium glutamicum

<400> 2650

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Met Gly Glu Gln Leu Pro Phe Ala Asn Gly Ser Arg Ser Asn Lys Leu
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Pro Leu Ile Val Ile Gly Leu Cys Cys Ile Met Leu Ile Leu Trp Leu
             20                  25                  30

Lys Leu Pro Gly Val Leu Leu Ala Thr Ile Ile Gly Val Ala Thr Met
         35                  40                  45

Ser Val Met Arg Met Arg Thr Ser Thr Pro Glu Thr Ala Ser Leu Val
     50                  55                  60

Thr Ser Ile Arg Leu Ser Ala Glu Asp Ile Ser Asp Val Gln His Glu
 65                  70                  75                  80

Trp Gln Gln Phe Leu Thr Ser Pro Glu Ala Asp Ala Leu Ala Asp Arg
                 85                  90                  95

Thr Leu Val Arg Pro Ala Leu Ala Asp Pro Asp Cys Gly Asp Lys Ala
            100                 105                 110

Ile Glu Lys Phe His Tyr Glu Ile Ser Asn Ala Asn Arg Phe Leu Gly
        115                 120                 125

Arg Leu Asp Ala Arg Leu Gln Gln Asn Leu Val Val Ser Glu Leu Glu
    130                 135                 140

Thr Leu Leu Lys Val Thr Asp Glu Arg Ala Leu Glu Leu Arg Glu Thr
145                 150                 155                 160

Trp Leu Asp Ala Arg Lys Ala Ala Gln Lys Leu Gly Pro Asn Tyr Asn
                165                 170                 175

Arg Glu Ser
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Sequence Listing as filed with the application

<210> 2651
<211> 879
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(856)
<223> RXA02231

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aaagtgacta ttgcctgtta agggagttag actaatcgcc atg act agc gat ctg 115
                                              Met Thr Ser Asp Leu
                                                1   5

aag aca atc ggt atg gat ttc gcc aag tgg caa gat gca gtg gaa gca 163
Lys Thr Ile Gly Met Asp Phe Ala Lys Trp Gln Asp Ala Val Glu Ala
                10   15   20

gca att gct tca cag cgt ctc gag gta aca ggc gag gtc cgt ggc ggc 211
Ala Ile Ala Ser Gln Arg Leu Glu Val Thr Gly Glu Val Arg Gly Gly
            25   30   35

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cag ctc atc cag ttc tcg gat gat tcc ggc gcc caa att aac att ctg   259
Gln Leu Ile Gln Phe Ser Asp Asp Ser Gly Ala Gln Ile Asn Ile Leu
         40                  45                  50

gct gtc gag cct ttt gcc acc ttc gcc ggc ttt aac tcc gca aca gtc   307
Ala Val Glu Pro Phe Ala Thr Phe Ala Gly Phe Asn Ser Ala Thr Val
     55                  60                  65

gct tac ggc cac gtc agc atg atc aat gat gtg ctg tcc ctg gtc gat   355
Ala Tyr Gly His Val Ser Met Ile Asn Asp Val Leu Ser Leu Val Asp
 70                  75                  80                  85

atc atc gat cct ttc ggc acc cct gtt gcc acc att acc tgc aac ctt   403
Ile Ile Asp Pro Phe Gly Thr Pro Val Ala Thr Ile Thr Cys Asn Leu
                90                  95                 100

gct caa ggc cca ctg ctt gtt gat gaa cca gtg cag cgc tgg cag cag   451
Ala Gln Gly Pro Leu Leu Val Asp Glu Pro Val Gln Arg Trp Gln Gln
            105                 110                 115

atc cgc att act gcc ctg ggc att gat gtt gag gtc cac gac aat gca   499
Ile Arg Ile Thr Ala Leu Gly Ile Asp Val Glu Val His Asp Asn Ala
        120                 125                 130

gat gct tac atc cgc aat ggt ggc gaa act gtc ggc atg ctg gtt tct   547
Asp Ala Tyr Ile Arg Asn Gly Gly Glu Thr Val Gly Met Leu Val Ser
    135                 140                 145

gaa ggt gca gag aag att gcc agc ggc agc ggc gct gtc atc ccg gac   595
Glu Gly Ala Glu Lys Ile Ala Ser Gly Ser Gly Ala Val Ile Pro Asp
150                 155                 160                 165

gca tcc gca gag ttt tcc gca cgc gtg ttg tct gcg gag tac cgc acc   643
Ala Ser Ala Glu Phe Ser Ala Arg Val Leu Ser Ala Glu Tyr Arg Thr
                170                 175                 180

aac act ctt acc ggc cag cgt ttt atc cac gca aca gtt gat ggc ctc   691
Asn Thr Leu Thr Gly Gln Arg Phe Ile His Ala Thr Val Asp Gly Leu
            185                 190                 195

ttc gct ttt gat gtg tgc ctt cct gat gca cca gaa cta cct gcc cgt   739
Phe Ala Phe Asp Val Cys Leu Pro Asp Ala Pro Glu Leu Pro Ala Arg
        200                 205                 210

gac agc gtg ttg tct ggc aaa gtc atg ctg act gct gcc gtt atc ccc   787
Asp Ser Val Leu Ser Gly Lys Val Met Leu Thr Ala Ala Val Ile Pro
    215                 220                 225

act gag gtc acc ggc tgc ggt ggc tcc ggt ggc ggc tgt ggc tca ggt   835
Thr Glu Val Thr Gly Cys Gly Gly Ser Gly Gly Gly Cys Gly Ser Gly
230                 235                 240                 245

agc tgt ggc tgc ggc gga cac taaaattctg cacaattttt taa             879
Ser Cys Gly Cys Gly Gly His
                250
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<210> 2652
<211> 252
<212> PRT

<213> Corynebacterium glutamicum

<400> 2652

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Met Thr Ser Asp Leu Lys Thr Ile Gly Met Asp Phe Ala Lys Trp Gln
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Asp Ala Val Glu Ala Ala Ile Ala Ser Gln Arg Leu Glu Val Thr Gly
             20                  25                  30

Glu Val Arg Gly Gly Gln Leu Ile Gln Phe Ser Asp Asp Ser Gly Ala
         35                  40                  45

Gln Ile Asn Ile Leu Ala Val Glu Pro Phe Ala Thr Phe Ala Gly Phe
     50                  55                  60

Asn Ser Ala Thr Val Ala Tyr Gly His Val Ser Met Ile Asn Asp Val
 65                  70                  75                  80

Leu Ser Leu Val Asp Ile Ile Asp Pro Phe Gly Thr Pro Val Ala Thr
                 85                  90                  95

Ile Thr Cys Asn Leu Ala Gln Gly Pro Leu Leu Val Asp Glu Pro Val
            100                 105                 110

Gln Arg Trp Gln Gln Ile Arg Ile Thr Ala Leu Gly Ile Asp Val Glu
        115                 120                 125

Val His Asp Asn Ala Asp Ala Tyr Ile Arg Asn Gly Gly Glu Thr Val
    130                 135                 140

Gly Met Leu Val Ser Glu Gly Ala Glu Lys Ile Ala Ser Gly Ser Gly
145                 150                 155                 160

Ala Val Ile Pro Asp Ala Ser Ala Glu Phe Ser Ala Arg Val Leu Ser
                165                 170                 175

Ala Glu Tyr Arg Thr Asn Thr Leu Thr Gly Gln Arg Phe Ile His Ala
            180                 185                 190

Thr Val Asp Gly Leu Phe Ala Phe Asp Val Cys Leu Pro Asp Ala Pro
        195                 200                 205

Glu Leu Pro Ala Arg Asp Ser Val Leu Ser Gly Lys Val Met Leu Thr
    210                 215                 220

Ala Ala Val Ile Pro Thr Glu Val Thr Gly Cys Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Cys Gly Ser Gly Ser Cys Gly Cys Gly Gly His
                245                 250
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<211> 1656
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1633)
<223> RXA02244

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gggcgcgtgg tgtccaactt gatcaggaag cgaaattcca atg agc cta gaa aaa 115
Met Ser Leu Glu Lys
1 5

tcc ggc gga ttc cgc tcc agg act cca aaa gcg cag cag gaa cct gct 163
Ser Gly Gly Phe Arg Ser Arg Thr Pro Lys Ala Gln Gln Glu Pro Ala
10 15 20

aag cag aag ccg cag gcg cgt aaa tct ccg tca aag aag gcc ccg gct 211
Lys Gln Lys Pro Gln Ala Arg Lys Ser Pro Ser Lys Lys Ala Pro Ala
25 30 35

cgg ggg cag ggg cag agt cag ggg cag cgc cag ggc caa agc agt ggc 259
Arg Gly Gln Gly Gln Ser Gln Gly Gln Arg Gln Gly Gln Ser Ser Gly
40 45 50

aaa ggc ggc gga aac cgc aag ccc cct gcg cag gcc agg gaa gtg agg 307
Lys Gly Gly Gly Asn Arg Lys Pro Pro Ala Gln Ala Arg Glu Val Arg
55 60 65

gct ctg ggc gtc gat aag ccg aga gaa att gcg ttt gag gtg ctt gat 355
Ala Leu Gly Val Asp Lys Pro Arg Glu Ile Ala Phe Glu Val Leu Asp
70 75 80 85

cgt gtg cgt acc ggt gag gcg tat gcc aac ttg gtg ttg cca cga ctg 403
Arg Val Arg Thr Gly Glu Ala Tyr Ala Asn Leu Val Leu Pro Arg Leu
90 95 100

ctg agc aag cac aat ctt tct ggc cgt gac gcg gcc ttt gct acg gaa 451
Leu Ser Lys His Asn Leu Ser Gly Arg Asp Ala Ala Phe Ala Thr Glu
105 110 115

att acc tac ggc acc ttg cgt aat gtc ggc ttg ctg gat gag gtc att 499
Ile Thr Tyr Gly Thr Leu Arg Asn Val Gly Leu Leu Asp Glu Val Ile
120 125 130

aag gct gca tct ggg cgt gaa ctg tct gat att gat cca gag gtt ttg 547
Lys Ala Ala Ser Gly Arg Glu Leu Ser Asp Ile Asp Pro Glu Val Leu
135 140 145

gac gtg ctg cgt ttg ggc gcg tac cag gtg atg ttt acc cgc gtg gag 595
Asp Val Leu Arg Leu Gly Ala Tyr Gln Val Met Phe Thr Arg Val Glu
150 155 160 165

gat cac gct gcg gtc gat act tca gta aag atg gtc ggt ggg ctg aag 643
Asp His Ala Ala Val Asp Thr Ser Val Lys Met Val Gly Gly Leu Lys
170 175 180

aaa ttc cag gcc act ggt ttt gcc aat gca att ttg cgc aac atc acg 691
Lys Phe Gln Ala Thr Gly Phe Ala Asn Ala Ile Leu Arg Asn Ile Thr
185 190 195

cgc aag gaa cca gag cag tgg ttg aag gaa ttg gag ccc gcg gaa gag 739
Arg Lys Glu Pro Glu Gln Trp Leu Lys Glu Leu Glu Pro Ala Glu Glu
200 205 210

ttg gct cgc gtt gcg ttc cgt act gcg cac cca cgc tgg att gcg cag 787

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Leu Ala Arg Val Ala Phe Arg Thr Ala His Pro Arg Trp Ile Ala Gln
    215                 220                 225

agt ttc tca cag gtg ctc ccg gca gat gag ttg gaa gca gcg ctt gct   835
Ser Phe Ser Gln Val Leu Pro Ala Asp Glu Leu Glu Ala Ala Leu Ala
230                 235                 240                 245

gcg gac tct gag cgc cca gtg gtg cac ttg gtg gct cgc cca ggt gag   883
Ala Asp Ser Glu Arg Pro Val Val His Leu Val Ala Arg Pro Gly Glu
                250                 255                 260

atc agt gca gag gaa ttg gcg ctg atc acc ggt ggt gac gag ggc aag   931
Ile Ser Ala Glu Glu Leu Ala Leu Ile Thr Gly Gly Asp Glu Gly Lys
            265                 270                 275

tat tcc cca tac gcg gtg tac ctc gag ggt ggc gac ccg ggt gat att   979
Tyr Ser Pro Tyr Ala Val Tyr Leu Glu Gly Gly Asp Pro Gly Asp Ile
        280                 285                 290

gag cca gtg aag gat ggt ctt gca gca gtg caa gat gag ggt tct cag   1027
Glu Pro Val Lys Asp Gly Leu Ala Ala Val Gln Asp Glu Gly Ser Gln
    295                 300                 305

ctg att gct cgc gcc ttg gtg gaa atc ccc gtg gag ggc acc gat gcc   1075
Leu Ile Ala Arg Ala Leu Val Glu Ile Pro Val Glu Gly Thr Asp Ala
310                 315                 320                 325

ggc cgt tgg ctg gat atg tgt gca ggt cct ggc ggt aaa gcg gcg ctc   1123
Gly Arg Trp Leu Asp Met Cys Ala Gly Pro Gly Gly Lys Ala Ala Leu
                330                 335                 340

att ggt gcg ttg gct cgc atg gat cgt gcc acc gtt gat gcc gtg gag   1171
Ile Gly Ala Leu Ala Arg Met Asp Arg Ala Thr Val Asp Ala Val Glu
            345                 350                 355

gtc tct gat cac cgt gcc cga ctg att gaa aag tcc gtg cgt ggt ttg   1219
Val Ser Asp His Arg Ala Arg Leu Ile Glu Lys Ser Val Arg Gly Leu
        360                 365                 370

ccc gtc aag gtt cat gtg ggc gat ggc cgc acc atc aac ttg acc ggt   1267
Pro Val Lys Val His Val Gly Asp Gly Arg Thr Ile Asn Leu Thr Gly
    375                 380                 385

ggt tac gat cgt gcg cta gtc gat gcg ccg tgt tct ggt ttg ggt gca   1315
Gly Tyr Asp Arg Ala Leu Val Asp Ala Pro Cys Ser Gly Leu Gly Ala
390                 395                 400                 405

ctg cgt cgt cgc cct gag gcg cgt tgg cgc aag cag gaa agc gac att   1363
Leu Arg Arg Arg Pro Glu Ala Arg Trp Arg Lys Gln Glu Ser Asp Ile
                410                 415                 420

gtt gag ctc aac acc ctg cag tac gag ctg ctt gaa tcc gct gtg aac   1411
Val Glu Leu Asn Thr Leu Gln Tyr Glu Leu Leu Glu Ser Ala Val Asn
            425                 430                 435

aag gtg cgt tcc ggt ggc gtg att gtg tac tcc aca tgt tca cct gat   1459
Lys Val Arg Ser Gly Gly Val Ile Val Tyr Ser Thr Cys Ser Pro Asp
        440                 445                 450

ctg cgt gaa acc cgc gga atc gtg gac aag gca ctg ggg gct ctg gag   1507
Leu Arg Glu Thr Arg Gly Ile Val Asp Lys Ala Leu Gly Ala Leu Glu
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    455                 460                 465

atc gaa gag ctt gag gct gcg gag ttc atg cca ggc atg acc gat acc   1555
Ile Glu Glu Leu Glu Ala Ala Glu Phe Met Pro Gly Met Thr Asp Thr
470                 475                 480                 485

ggc gat gag aaa tca gtg cag atg tgg cca cac cgc cac ggc acc gat   1603
Gly Asp Glu Lys Ser Val Gln Met Trp Pro His Arg His Gly Thr Asp
                490                 495                 500

gcg atg ttt gtg gca gtg ctg cga aag aag tagacctgtg agctaagtgg     1653
Ala Met Phe Val Ala Val Leu Arg Lys Lys
            505                 510

ggt                                                               1656


<210> 2654
<211> 511
<212> PRT
<213> Corynebacterium glutamicum

<400> 2654
Met Ser Leu Glu Lys Ser Gly Gly Phe Arg Ser Arg Thr Pro Lys Ala
  1               5                  10                  15

Gln Gln Glu Pro Ala Lys Gln Lys Pro Gln Ala Arg Lys Ser Pro Ser
             20                  25                  30

Lys Lys Ala Pro Ala Arg Gly Gln Gly Gln Ser Gln Gly Gln Arg Gln
         35                  40                  45

Gly Gln Ser Ser Gly Lys Gly Gly Gly Asn Arg Lys Pro Pro Ala Gln
     50                  55                  60

Ala Arg Glu Val Arg Ala Leu Gly Val Asp Lys Pro Arg Glu Ile Ala
 65                  70                  75                  80

Phe Glu Val Leu Asp Arg Val Arg Thr Gly Glu Ala Tyr Ala Asn Leu
                 85                  90                  95

Val Leu Pro Arg Leu Leu Ser Lys His Asn Leu Ser Gly Arg Asp Ala
            100                 105                 110

Ala Phe Ala Thr Glu Ile Thr Tyr Gly Thr Leu Arg Asn Val Gly Leu
        115                 120                 125

Leu Asp Glu Val Ile Lys Ala Ala Ser Gly Arg Glu Leu Ser Asp Ile
    130                 135                 140

Asp Pro Glu Val Leu Asp Val Leu Arg Leu Gly Ala Tyr Gln Val Met
145                 150                 155                 160

Phe Thr Arg Val Glu Asp His Ala Ala Val Asp Thr Ser Val Lys Met
                165                 170                 175

Val Gly Gly Leu Lys Lys Phe Gln Ala Thr Gly Phe Ala Asn Ala Ile
            180                 185                 190

Leu Arg Asn Ile Thr Arg Lys Glu Pro Glu Gln Trp Leu Lys Glu Leu
        195                 200                 205
```

```
Glu Pro Ala Glu Glu Leu Ala Arg Val Ala Phe Arg Thr Ala His Pro
    210                 215                 220

Arg Trp Ile Ala Gln Ser Phe Ser Gln Val Leu Pro Ala Asp Glu Leu
225                 230                 235                 240

Glu Ala Ala Leu Ala Ala Asp Ser Glu Arg Pro Val Val His Leu Val
                245                 250                 255

Ala Arg Pro Gly Glu Ile Ser Ala Glu Glu Leu Ala Leu Ile Thr Gly
            260                 265                 270

Gly Asp Glu Gly Lys Tyr Ser Pro Tyr Ala Val Tyr Leu Glu Gly Gly
        275                 280                 285

Asp Pro Gly Asp Ile Glu Pro Val Lys Asp Gly Leu Ala Ala Val Gln
    290                 295                 300

Asp Glu Gly Ser Gln Leu Ile Ala Arg Ala Leu Val Glu Ile Pro Val
305                 310                 315                 320

Glu Gly Thr Asp Ala Gly Arg Trp Leu Asp Met Cys Ala Gly Pro Gly
                325                 330                 335

Gly Lys Ala Ala Leu Ile Gly Ala Leu Ala Arg Met Asp Arg Ala Thr
            340                 345                 350

Val Asp Ala Val Glu Val Ser Asp His Arg Ala Arg Leu Ile Glu Lys
        355                 360                 365

Ser Val Arg Gly Leu Pro Val Lys Val His Val Gly Asp Gly Arg Thr
    370                 375                 380

Ile Asn Leu Thr Gly Gly Tyr Asp Arg Ala Leu Val Asp Ala Pro Cys
385                 390                 395                 400

Ser Gly Leu Gly Ala Leu Arg Arg Arg Pro Glu Ala Arg Trp Arg Lys
                405                 410                 415

Gln Glu Ser Asp Ile Val Glu Leu Asn Thr Leu Gln Tyr Glu Leu Leu
            420                 425                 430

Glu Ser Ala Val Asn Lys Val Arg Ser Gly Gly Val Ile Val Tyr Ser
        435                 440                 445

Thr Cys Ser Pro Asp Leu Arg Glu Thr Arg Gly Ile Val Asp Lys Ala
    450                 455                 460

Leu Gly Ala Leu Glu Ile Glu Glu Leu Glu Ala Ala Glu Phe Met Pro
465                 470                 475                 480

Gly Met Thr Asp Thr Gly Asp Glu Lys Ser Val Gln Met Trp Pro His
                485                 490                 495

Arg His Gly Thr Asp Ala Met Phe Val Ala Val Leu Arg Lys Lys
            500                 505                 510
```

<210> 2655
<211> 1059

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1036)
<223> RXA02255

<400> 2655
gtgtgcagcg ttgctggcaa gttttgctgg agcacgaaag cgttaaggag taggcgtgtc 60

actgacgagt gatatcaaac aagaattggc gcaggtccat gtg gcc aaa aac agt 115
Val Ala Lys Asn Ser
1 5

gtt cgt gct gcg gaa gtg tct gca att tta agg ttt gct ggt gag atg 163
Val Arg Ala Ala Glu Val Ser Ala Ile Leu Arg Phe Ala Gly Glu Met
10 15 20

caa gct gtc ggc ggc aag ctg gtc atc gaa gca aat ttg gac agc atg 211
Gln Ala Val Gly Gly Lys Leu Val Ile Glu Ala Asn Leu Asp Ser Met
25 30 35

caa gtc ggt atg agg ctt cag gag ttt atc caa ggt ttg tac aac tct 259
Gln Val Gly Met Arg Leu Gln Glu Phe Ile Gln Gly Leu Tyr Asn Ser
40 45 50

cga gtc gat gtg cac acc gtg aac ccg act gtg agc agg aaa acg cca 307
Arg Val Asp Val His Thr Val Asn Pro Thr Val Ser Arg Lys Thr Pro
55 60 65

cgg tat ttg gtg cgc atc att gac aat gcc gat gaa att gcg cga cgc 355
Arg Tyr Leu Val Arg Ile Ile Asp Asn Ala Asp Glu Ile Ala Arg Arg
70 75 80 85

acc gga ctg gtc acc agg tct gga cat gtg gtt aaa ggt cta gcg cct 403
Thr Gly Leu Val Thr Arg Ser Gly His Val Val Lys Gly Leu Ala Pro
90 95 100

tct gtg gtc agc gga aca atc agt gac gct gaa gct gca tgg cgc ggt 451
Ser Val Val Ser Gly Thr Ile Ser Asp Ala Glu Ala Ala Trp Arg Gly
105 110 115

gcg ttt cta gcc aat gga tct tta agt gat cca ggt cgt tcc tct tcg 499
Ala Phe Leu Ala Asn Gly Ser Leu Ser Asp Pro Gly Arg Ser Ser Ser
120 125 130

ttg gag gtg ttg tgt cct ggt caa gaa tca gca ttg gca ctg gtt gga 547
Leu Glu Val Leu Cys Pro Gly Gln Glu Ser Ala Leu Ala Leu Val Gly
135 140 145

tgt gcg cga aga att ggg atc gcg gcg aaa acg aaa gat tct cga gga 595
Cys Ala Arg Arg Ile Gly Ile Ala Ala Lys Thr Lys Asp Ser Arg Gly
150 155 160 165

ttt gat cgc gtc aat gtt cgt gat gcg gaa gca att ggg gca ctg ctc 643
Phe Asp Arg Val Asn Val Arg Asp Ala Glu Ala Ile Gly Ala Leu Leu
170 175 180

act cga atg ggt gcc cag aaa act cgc atg ttg tgg gaa gaa aaa cgc 691
Thr Arg Met Gly Ala Gln Lys Thr Arg Met Leu Trp Glu Glu Lys Arg

```
            185                 190                 195

atc aag cgg gaa agt cga act ccg caa acc ggg ttg gcc aac ttc gac   739
Ile Lys Arg Glu Ser Arg Thr Pro Gln Thr Gly Leu Ala Asn Phe Asp
        200                 205                 210

gat gcc aat ctg cgc agg tca gcc cga gca gca gtt gcc gct gca gcg   787
Asp Ala Asn Leu Arg Arg Ser Ala Arg Ala Ala Val Ala Ala Ala Ala
    215                 220                 225

agg gta gaa cgc gcc atg aag att ctt ggt gat gat gtt cct gag cat   835
Arg Val Glu Arg Ala Met Lys Ile Leu Gly Asp Asp Val Pro Glu His
230                 235                 240                 245

ttg gct gag gct gga cag ctg cgt gtg cag cac cgt cag gca tcg ttg   883
Leu Ala Glu Ala Gly Gln Leu Arg Val Gln His Arg Gln Ala Ser Leu
                250                 255                 260

gag gag ttg ggc cgg ttg gct gat cct caa atg acc aag gat gct gtg   931
Glu Glu Leu Gly Arg Leu Ala Asp Pro Gln Met Thr Lys Asp Ala Val
            265                 270                 275

gcc ggt cgt att cgt cgt ctt ttg acg atg gca gat aag cgc gcc gaa   979
Ala Gly Arg Ile Arg Arg Leu Leu Thr Met Ala Asp Lys Arg Ala Glu
        280                 285                 290

gat ctg aag att cct gat aca aat tct gtt gtg acg gaa gat ttg ttg   1027
Asp Leu Lys Ile Pro Asp Thr Asn Ser Val Val Thr Glu Asp Leu Leu
    295                 300                 305

gaa gaa att tagatgattg aagcctaaaa acg                            1059
Glu Glu Ile
310
```

Sequence Listing.ST25.txt

<210> 2656
<211> 312
<212> PRT
<213> Corynebacterium glutamicum

<400> 2656

```
Val Ala Lys Asn Ser Val Arg Ala Ala Glu Val Ser Ala Ile Leu Arg
  1               5                  10                  15

Phe Ala Gly Glu Met Gln Ala Val Gly Gly Lys Leu Val Ile Glu Ala
             20                  25                  30

Asn Leu Asp Ser Met Gln Val Gly Met Arg Leu Gln Glu Phe Ile Gln
         35                  40                  45

Gly Leu Tyr Asn Ser Arg Val Asp Val His Thr Val Asn Pro Thr Val
     50                  55                  60

Ser Arg Lys Thr Pro Arg Tyr Leu Val Arg Ile Ile Asp Asn Ala Asp
 65                  70                  75                  80

Glu Ile Ala Arg Arg Thr Gly Leu Val Thr Arg Ser Gly His Val Val
                 85                  90                  95

Lys Gly Leu Ala Pro Ser Val Val Ser Gly Thr Ile Ser Asp Ala Glu
            100                 105                 110
```

```
Ala Ala Trp Arg Gly Ala Phe Leu Ala Asn Gly Ser Leu Ser Asp Pro
        115                 120                 125

Gly Arg Ser Ser Ser Leu Glu Val Leu Cys Pro Gly Gln Glu Ser Ala
    130                 135                 140

Leu Ala Leu Val Gly Cys Ala Arg Arg Ile Gly Ile Ala Ala Lys Thr
145                 150                 155                 160

Lys Asp Ser Arg Gly Phe Asp Arg Val Asn Val Arg Asp Ala Glu Ala
                165                 170                 175

Ile Gly Ala Leu Leu Thr Arg Met Gly Ala Gln Lys Thr Arg Met Leu
            180                 185                 190

Trp Glu Glu Lys Arg Ile Lys Arg Glu Ser Arg Thr Pro Gln Thr Gly
        195                 200                 205

Leu Ala Asn Phe Asp Asp Ala Asn Leu Arg Arg Ser Ala Arg Ala Ala
    210                 215                 220

Val Ala Ala Ala Ala Arg Val Glu Arg Ala Met Lys Ile Leu Gly Asp
225                 230                 235                 240

Asp Val Pro Glu His Leu Ala Glu Ala Gly Gln Leu Arg Val Gln His
                245                 250                 255

Arg Gln Ala Ser Leu Glu Glu Leu Gly Arg Leu Ala Asp Pro Gln Met
            260                 265                 270

Thr Lys Asp Ala Val Ala Gly Arg Ile Arg Arg Leu Leu Thr Met Ala
        275                 280                 285

Asp Lys Arg Ala Glu Asp Leu Lys Ile Pro Asp Thr Asn Ser Val Val
    290                 295                 300

Thr Glu Asp Leu Leu Glu Glu Ile
305                 310
```

Replacement Sheet (Rule 26)

<210> 2657
<211> 636
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(613)
<223> RXA02266

<400> 2657
gaggaaagta gcgctacatc tgcatatcta ccccccttaaa aatgaagcat aaaaccgccg 60

tgtaccggcc ttttattgat tttgacgtaa gcttgcaccg atg act caa gat gaa 115
                                            Met Thr Gln Asp Glu
                                              1   5

cac ccc cga cag gcc gac tcc cat ttc aac atg ctt tta ccg gat gga 163
His Pro Arg Gln Ala Asp Ser His Phe Asn Met Leu Leu Pro Asp Gly
                10   15   20

```
aat gaa aac gca cac cag ctt tct gtc gct cta aat cag gtg gca cat   211
Asn Glu Asn Ala His Gln Leu Ser Val Ala Leu Asn Gln Val Ala His
             25                  30                  35

ctg ttg gcc tat gat gcg gac tct tca att cat cgg cct gat ggg cta   259
Leu Leu Ala Tyr Asp Ala Asp Ser Ser Ile His Arg Pro Asp Gly Leu
         40                  45                  50

agt ctg gcg tcc tat aga att ctc ttt tca ctg tgg act gat ggc ccg   307
Ser Leu Ala Ser Tyr Arg Ile Leu Phe Ser Leu Trp Thr Asp Gly Pro
     55                  60                  65

atg agt cca ctc cag gtg act gac aag act gga atg aaa aag tct gcg   355
Met Ser Pro Leu Gln Val Thr Asp Lys Thr Gly Met Lys Lys Ser Ala
 70                  75                  80                  85

att tct aac ctg tta aag cca ttg ctc gct gaa tct ctg att gtg cag   403
Ile Ser Asn Leu Leu Lys Pro Leu Leu Ala Glu Ser Leu Ile Val Gln
                 90                  95                 100

gtg acg gca gaa aat gat cga cgc tca aag gtt tta agc ctt agc gaa   451
Val Thr Ala Glu Asn Asp Arg Arg Ser Lys Val Leu Ser Leu Ser Glu
            105                 110                 115

aaa ggc act aca tac att cag aaa aca gcc acc cgc caa aat gct ttg   499
Lys Gly Thr Thr Tyr Ile Gln Lys Thr Ala Thr Arg Gln Asn Ala Leu
        120                 125                 130

gaa tcc gag tgg ttt ggc acc ctg acc gac atc gag cag gat tta ttg   547
Glu Ser Glu Trp Phe Gly Thr Leu Thr Asp Ile Glu Gln Asp Leu Leu
    135                 140                 145

gag tcg ttg ctc agg aaa ctg ctc gac tcc aac cgc gca tcc aag gtt   595
Glu Ser Leu Leu Arg Lys Leu Leu Asp Ser Asn Arg Ala Ser Lys Val
150                 155                 160                 165

cgt aaa aac cga tct aac tagcgtcgat ccttagggat gta                636
Arg Lys Asn Arg Ser Asn
                170
```

<210> 2658
<211> 171
<212> PRT
<213> Corynebacterium glutamicum

<400> 2658

```
Met Thr Gln Asp Glu His Pro Arg Gln Ala Asp Ser His Phe Asn Met
  1               5                  10                  15

Leu Leu Pro Asp Gly Asn Glu Asn Ala His Gln Leu Ser Val Ala Leu
             20                  25                  30

Asn Gln Val Ala His Leu Leu Ala Tyr Asp Ala Asp Ser Ser Ile His
         35                  40                  45

Arg Pro Asp Gly Leu Ser Leu Ala Ser Tyr Arg Ile Leu Phe Ser Leu
     50                  55                  60

Trp Thr Asp Gly Pro Met Ser Pro Leu Gln Val Thr Asp Lys Thr Gly
```

```
 65                  70                  75                  80

Met Lys Lys Ser Ala Ile Ser Asn Leu Leu Lys Pro Leu Leu Ala Glu
                 85                  90                  95

Ser Leu Ile Val Gln Val Thr Ala Glu Asn Asp Arg Arg Ser Lys Val
            100                 105                 110

Leu Ser Leu Ser Glu Lys Gly Thr Thr Tyr Ile Gln Lys Thr Ala Thr
        115                 120                 125

Arg Gln Asn Ala Leu Glu Ser Glu Trp Phe Gly Thr Leu Thr Asp Ile
    130                 135                 140

Glu Gln Asp Leu Leu Glu Ser Leu Leu Arg Lys Leu Leu Asp Ser Asn
145                 150                 155                 160

Arg Ala Ser Lys Val Arg Lys Asn Arg Ser Asn
                165                 170
```

<210> 2659
<211> 996
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(973)
<223> RXA02267

<400> 2659

```
tgcgctcggc aagtgttttg cttatcgacg tctccccaca taacaatccc aactcgaagc 60

accaacgatt caagccttat cagttttgta caggaaaata gtg caa aaa tgg ggt   115
                                            Val Gln Lys Trp Gly
                                              1               5

tta agc ttc gtg gag agg att gtc atc gtg aac aac gtg caa cag ttt   163
Leu Ser Phe Val Glu Arg Ile Val Ile Val Asn Asn Val Gln Gln Phe
                10                  15                  20

cat cga ttt ttt gat gat tcc gca gtc tat tat ccc tgc ttc gtc ccg   211
His Arg Phe Phe Asp Asp Ser Ala Val Tyr Tyr Pro Cys Phe Val Pro
            25                  30                  35

ctt gac cga gcc atc ggc gaa cac ttt gat cgt cag aac aaa ccg atg   259
Leu Asp Arg Ala Ile Gly Glu His Phe Asp Arg Gln Asn Lys Pro Met
        40                  45                  50

tcc aga ttc atc gga acg ctc att ctg ccg tta gcc aaa ctg gaa gaa   307
Ser Arg Phe Ile Gly Thr Leu Ile Leu Pro Leu Ala Lys Leu Glu Glu
    55                  60                  65

gcc gcc caa tac acc ggc gat gaa gtc ctt cgc gtg tcg gca gta atc   355
Ala Ala Gln Tyr Thr Gly Asp Glu Val Leu Arg Val Ser Ala Val Ile
70                  75                  80                  85

agt act gat ggg ctc gct gat ctg cga agg gat ttt tac gaa ctc ccc   403
Ser Thr Asp Gly Leu Ala Asp Leu Arg Arg Asp Phe Tyr Glu Leu Pro
                90                  95                 100
```

```
aac atc gac atc gcc tcg gtg gaa atc aag ctg gtc ggc gca gcc ctc   451
Asn Ile Asp Ile Ala Ser Val Glu Ile Lys Leu Val Gly Ala Ala Leu
            105                 110                 115

acc aac acc gct tgg ttg gga gat gtg gaa aaa ctc atc caa caa cat   499
Thr Asn Thr Ala Trp Leu Gly Asp Val Glu Lys Leu Ile Gln Gln His
        120                 125                 130

cgc aac act ttc gta tgg gtt gag att ccg aca gcc ctg gtc acc gca   547
Arg Asn Thr Phe Val Trp Val Glu Ile Pro Thr Ala Leu Val Thr Ala
    135                 140                 145

gat att gtc cga aaa ctc cgc cac atg gga gct ggc ctg aaa tac aga   595
Asp Ile Val Arg Lys Leu Arg His Met Gly Ala Gly Leu Lys Tyr Arg
150                 155                 160                 165

act gga ggt gat agg gaa gag ctc ttc ccc tca ccg cag gac ttg gtc   643
Thr Gly Gly Asp Arg Glu Glu Leu Phe Pro Ser Pro Gln Asp Leu Val
                170                 175                 180

act gtg ctg cgc acc gcc atc gat gct gca ttg ccg ttt aaa ctc act   691
Thr Val Leu Arg Thr Ala Ile Asp Ala Ala Leu Pro Phe Lys Leu Thr
            185                 190                 195

gca ggc ctg cat cgt gct ctc agg tat cgt gac gag aaa acc ggc cga   739
Ala Gly Leu His Arg Ala Leu Arg Tyr Arg Asp Glu Lys Thr Gly Arg
        200                 205                 210

ctt cac ttc gga ttc ctc aac att gca gcc gcc gtg gcg aca ctt cgt   787
Leu His Phe Gly Phe Leu Asn Ile Ala Ala Ala Val Ala Thr Leu Arg
    215                 220                 225

gct gga aaa ggc gag gca gag gca ctg aag atc ctt gaa ggc gat gat   835
Ala Gly Lys Gly Glu Ala Glu Ala Leu Lys Ile Leu Glu Gly Asp Asp
230                 235                 240                 245

gcc gct ccg ctt att cac gca cta caa agc ggc gaa aac tgg cgg gat   883
Ala Ala Pro Leu Ile His Ala Leu Gln Ser Gly Glu Asn Trp Arg Asp
                250                 255                 260

tcc ttc cgc agc ttc agt acc tgc aat gtt gtt gaa cca ctc aac act   931
Ser Phe Arg Ser Phe Ser Thr Cys Asn Val Val Glu Pro Leu Asn Thr
            265                 270                 275

ctg att gat ctt gat gtg ttg gcg gaa gga gac gta cat ccc           973
Leu Ile Asp Leu Asp Val Leu Ala Glu Gly Asp Val His Pro
        280                 285                 290

taaggatcga cgctagttag atc                                        996
```

<210> 2660
<211> 291
<212> PRT
<213> Corynebacterium glutamicum

<400> 2660

```
Val Gln Lys Trp Gly Leu Ser Phe Val Glu Arg Ile Val Ile Val Asn
  1               5                  10                  15
```

```
Asn Val Gln Gln Phe His Arg Phe Phe Asp Asp Ser Ala Val Tyr Tyr
            20                  25                  30

Pro Cys Phe Val Pro Leu Asp Arg Ala Ile Gly Glu His Phe Asp Arg
        35                  40                  45

Gln Asn Lys Pro Met Ser Arg Phe Ile Gly Thr Leu Ile Leu Pro Leu
    50                  55                  60

Ala Lys Leu Glu Glu Ala Ala Gln Tyr Thr Gly Asp Glu Val Leu Arg
65                  70                  75                  80

Val Ser Ala Val Ile Ser Thr Asp Gly Leu Ala Asp Leu Arg Arg Asp
                85                  90                  95

Phe Tyr Glu Leu Pro Asn Ile Asp Ile Ala Ser Val Glu Ile Lys Leu
            100                 105                 110

Val Gly Ala Ala Leu Thr Asn Thr Ala Trp Leu Gly Asp Val Glu Lys
        115                 120                 125

Leu Ile Gln Gln His Arg Asn Thr Phe Val Trp Val Glu Ile Pro Thr
    130                 135                 140

Ala Leu Val Thr Ala Asp Ile Val Arg Lys Leu Arg His Met Gly Ala
145                 150                 155                 160

Gly Leu Lys Tyr Arg Thr Gly Gly Asp Arg Glu Glu Leu Phe Pro Ser
                165                 170                 175

Pro Gln Asp Leu Val Thr Val Leu Arg Thr Ala Ile Asp Ala Ala Leu
            180                 185                 190

Pro Phe Lys Leu Thr Ala Gly Leu His Arg Ala Leu Arg Tyr Arg Asp
        195                 200                 205

Glu Lys Thr Gly Arg Leu His Phe Gly Phe Leu Asn Ile Ala Ala Ala
    210                 215                 220

Val Ala Thr Leu Arg Ala Gly Lys Gly Glu Ala Glu Ala Leu Lys Ile
225                 230                 235                 240

Leu Glu Gly Asp Asp Ala Ala Pro Leu Ile His Ala Leu Gln Ser Gly
                245                 250                 255

Glu Asn Trp Arg Asp Ser Phe Arg Ser Phe Ser Thr Cys Asn Val Val
            260                 265                 270

Glu Pro Leu Asn Thr Leu Ile Asp Leu Asp Val Leu Ala Glu Gly Asp
        275                 280                 285

Val His Pro
    290
```

<210> 2661
<211> 776
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (1)..(753)
<223> RXA02280

<400> 2661

```
gcg gac ctg gct gaa acc atg ttg ggt ctt ctc acc ttg gag acc tcc   48
Ala Asp Leu Ala Glu Thr Met Leu Gly Leu Leu Thr Leu Glu Thr Ser
  1               5                  10                  15

cgt ggt cgc atc tcg atc ggt gag atc acc acg ttg tcc atc acc gag   96
Arg Gly Arg Ile Ser Ile Gly Glu Ile Thr Thr Leu Ser Ile Thr Glu
            20                  25                  30

gat gtg tcg ctg cag ctg gct acc acg ttg gat gat ttc agg cag ctc   144
Asp Val Ser Leu Gln Leu Ala Thr Thr Leu Asp Asp Phe Arg Gln Leu
        35                  40                  45

aac acc att gcg cgc ccg gac acc ttg att att aat ggc ggc tac att   192
Asn Thr Ile Ala Arg Pro Asp Thr Leu Ile Ile Asn Gly Gly Tyr Ile
    50                  55                  60

cac gac agc gat ctg gct cgg ctc att ccc gtt cac tac cca ccg ctt   240
His Asp Ser Asp Leu Ala Arg Leu Ile Pro Val His Tyr Pro Pro Leu
65                  70                  75                  80

acg gta tct act gct gac ctg cgc gaa tcc atg gat ctg atg gag ctt   288
Thr Val Ser Thr Ala Asp Leu Arg Glu Ser Met Asp Leu Met Glu Leu
                85                  90                  95

ccg ccg ctg cag gac att gag aaa gcc aag gca ctg gat gcg cag gtc   336
Pro Pro Leu Gln Asp Ile Glu Lys Ala Lys Ala Leu Asp Ala Gln Val
            100                 105                 110

acg gaa tca ttg aag gat ttt cag atc aag ggc gca acg agg gtt ttt   384
Thr Glu Ser Leu Lys Asp Phe Gln Ile Lys Gly Ala Thr Arg Val Phe
        115                 120                 125

gaa ccc gca gat gtt cct gcc gtg gtg atc att gat tcc aag gcg cag   432
Glu Pro Ala Asp Val Pro Ala Val Val Ile Ile Asp Ser Lys Ala Gln
    130                 135                 140

gcc tca cgg gat cgc aat gaa aca caa agc gca acc act gat cgt tgg   480
Ala Ser Arg Asp Arg Asn Glu Thr Gln Ser Ala Thr Thr Asp Arg Trp
145                 150                 155                 160

gct gac att ttg gca acg gtg gat aac acg ttg agc cgt caa aca gcc   528
Ala Asp Ile Leu Ala Thr Val Asp Asn Thr Leu Ser Arg Gln Thr Ala
                165                 170                 175

aac att cca cag gat cag gga ctg tcg gcg ttg tgc ttg aat tgg aac   576
Asn Ile Pro Gln Asp Gln Gly Leu Ser Ala Leu Cys Leu Asn Trp Asn
            180                 185                 190

aat tcg ctg gtc agg aaa ttg gcg tcc act gat gac acc gcc gtg gtg   624
Asn Ser Leu Val Arg Lys Leu Ala Ser Thr Asp Asp Thr Ala Val Val
        195                 200                 205

tcg cgc acg gtg cgt ttg ctc tac gtt cag gca ttg ttg tcc agc aag   672
Ser Arg Thr Val Arg Leu Leu Tyr Val Gln Ala Leu Leu Ser Ser Lys
    210                 215                 220
```

```
agg cca ctg cgg gtg aag gaa cgc gcg ctg ctt aat gat tcg ctg gca   720
Arg Pro Leu Arg Val Lys Glu Arg Ala Leu Leu Asn Asp Ser Leu Ala
225                 230                 235                 240

gat ctg gtt tct ttg tct ttg tca tcc gat atc taagacaatc ctccgctaat 773
Asp Leu Val Ser Leu Ser Leu Ser Ser Asp Ile
                245                 250

ctt                                                               776
```

<210> 2662
<211> 251
<212> PRT
<213> Corynebacterium glutamicum

<400> 2662

```
Ala Asp Leu Ala Glu Thr Met Leu Gly Leu Leu Thr Leu Glu Thr Ser
  1               5                  10                  15

Arg Gly Arg Ile Ser Ile Gly Glu Ile Thr Thr Leu Ser Ile Thr Glu
             20                  25                  30

Asp Val Ser Leu Gln Leu Ala Thr Thr Leu Asp Asp Phe Arg Gln Leu
         35                  40                  45

Asn Thr Ile Ala Arg Pro Asp Thr Leu Ile Ile Asn Gly Gly Tyr Ile
     50                  55                  60

His Asp Ser Asp Leu Ala Arg Leu Ile Pro Val His Tyr Pro Pro Leu
 65                  70                  75                  80

Thr Val Ser Thr Ala Asp Leu Arg Glu Ser Met Asp Leu Met Glu Leu
                 85                  90                  95

Pro Pro Leu Gln Asp Ile Glu Lys Ala Lys Ala Leu Asp Ala Gln Val
            100                 105                 110

Thr Glu Ser Leu Lys Asp Phe Gln Ile Lys Gly Ala Thr Arg Val Phe
        115                 120                 125

Glu Pro Ala Asp Val Pro Ala Val Val Ile Ile Asp Ser Lys Ala Gln
    130                 135                 140

Ala Ser Arg Asp Arg Asn Glu Thr Gln Ser Ala Thr Thr Asp Arg Trp
145                 150                 155                 160

Ala Asp Ile Leu Ala Thr Val Asp Asn Thr Leu Ser Arg Gln Thr Ala
                165                 170                 175

Asn Ile Pro Gln Asp Gln Gly Leu Ser Ala Leu Cys Leu Asn Trp Asn
            180                 185                 190

Asn Ser Leu Val Arg Lys Leu Ala Ser Thr Asp Asp Thr Ala Val Val
        195                 200                 205

Ser Arg Thr Val Arg Leu Leu Tyr Val Gln Ala Leu Leu Ser Ser Lys
    210                 215                 220

Arg Pro Leu Arg Val Lys Glu Arg Ala Leu Leu Asn Asp Ser Leu Ala
225                 230                 235                 240
```

```
Asp Leu Val Ser Leu Ser Leu Ser Ser Asp Ile
                245                 250


<210> 2663
<211> 672
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(649)
<223> RXA02286

<400> 2663
gcagcgcaca cgctttcccc tcagcctgct gataccccg ttttgccacc taaaacaacc 60

tctcatcttc atttcatatt cacttcatag ggttgaatac atg aag aac gca aaa   115
                                            Met Lys Asn Ala Lys
                                              1               5

ctt ttc ctc gcg ctc ata tcc gct cct ctt atc ctc gct ggc tgc agc   163
Leu Phe Leu Ala Leu Ile Ser Ala Pro Leu Ile Leu Ala Gly Cys Ser
               10                  15                  20

tcc acc gat act gga aca gca gaa tcc acc att tcc agc gaa act gct   211
Ser Thr Asp Thr Gly Thr Ala Glu Ser Thr Ile Ser Ser Glu Thr Ala
           25                  30                  35

tct gca gta gat gcc acc act tct acc tcc tca agt acc gcc acc tct   259
Ser Ala Val Asp Ala Thr Thr Ser Thr Ser Ser Ser Thr Ala Thr Ser
       40                  45                  50

gcc gtg att gat gac gat ccg gta ttc gac atc atc gac atc gtc ctt   307
Ala Val Ile Asp Asp Asp Pro Val Phe Asp Ile Ile Asp Ile Val Leu
   55                  60                  65

gcc caa tac ccc gac agg atc atc acc gac att gac cgc gaa gac tcc   355
Ala Gln Tyr Pro Asp Arg Ile Ile Thr Asp Ile Asp Arg Glu Asp Ser
70                  75                  80                  85

tcc gat caa tac gaa gtc gat gtt gtg gtt ggc caa gaa gtc ctt gaa   403
Ser Asp Gln Tyr Glu Val Asp Val Val Val Gly Gln Glu Val Leu Glu
               90                  95                 100

ctt gat gtc acc acc agt ggc cag atc cat acc gac gac cgc gac aac   451
Leu Asp Val Thr Thr Ser Gly Gln Ile His Thr Asp Asp Arg Asp Asn
           105                 110                 115

gat gat gat gac gac atc cgc gaa gct cac gca gcc aca gtc acc gca   499
Asp Asp Asp Asp Asp Ile Arg Glu Ala His Ala Ala Thr Val Thr Ala
       120                 125                 130

gct caa gcc att ggc cta gcg ctg gat caa tac cca gac gga att att   547
Ala Gln Ala Ile Gly Leu Ala Leu Asp Gln Tyr Pro Asp Gly Ile Ile
   135                 140                 145

gat tct gtt gaa tta gac gaa gac gac ggc cag ctg aaa tgg aaa ata   595
Asp Ser Val Glu Leu Asp Glu Asp Asp Gly Gln Leu Lys Trp Lys Ile
150                 155                 160                 165
```

```
gac ctc gat gac act tcc ggc aat gat ctt gct gac gtt gaa atc gca   643
Asp Leu Asp Asp Thr Ser Gly Asn Asp Leu Ala Asp Val Glu Ile Ala
                170                 175                 180

gca gtt taagcacgcg cacggaaagc cac                                672
Ala Val
```

<210> 2664
<211> 183
<212> PRT
<213> Corynebacterium glutamicum

<400> 2664

```
Met Lys Asn Ala Lys Leu Phe Leu Ala Leu Ile Ser Ala Pro Leu Ile
  1               5                  10                  15

Leu Ala Gly Cys Ser Ser Thr Asp Thr Gly Thr Ala Glu Ser Thr Ile
             20                  25                  30

Ser Ser Glu Thr Ala Ser Ala Val Asp Ala Thr Thr Ser Thr Ser Ser
         35                  40                  45

Ser Thr Ala Thr Ser Ala Val Ile Asp Asp Asp Pro Val Phe Asp Ile
     50                  55                  60

Ile Asp Ile Val Leu Ala Gln Tyr Pro Asp Arg Ile Ile Thr Asp Ile
 65                  70                  75                  80

Asp Arg Glu Asp Ser Ser Asp Gln Tyr Glu Val Asp Val Val Val Gly
                 85                  90                  95

Gln Glu Val Leu Glu Leu Asp Val Thr Thr Ser Gly Gln Ile His Thr
            100                 105                 110

Asp Asp Arg Asp Asn Asp Asp Asp Asp Asp Ile Arg Glu Ala His Ala
        115                 120                 125

Ala Thr Val Thr Ala Ala Gln Ala Ile Gly Leu Ala Leu Asp Gln Tyr
    130                 135                 140

Pro Asp Gly Ile Ile Asp Ser Val Glu Leu Asp Glu Asp Asp Gly Gln
145                 150                 155                 160

Leu Lys Trp Lys Ile Asp Leu Asp Asp Thr Ser Gly Asn Asp Leu Ala
                165                 170                 175

Asp Val Glu Ile Ala Ala Val
            180
```

<210> 2665
<211> 675
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(652)

<223> RXA02287

<400> 2665

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ttgaaaaagg aacattagtg ccagtaacaa gagcccagtt gaattcaagc gggcagagac 60

acatctggcc ctcaaaattt tccttttact ggagaccact gtg tac tca att tca   115
                                            Val Tyr Ser Ile Ser
                                              1               5

gaa act atc gcc cga act ctt atg ccc cgc acc gat cac gtt ttc gac   163
Glu Thr Ile Ala Arg Thr Leu Met Pro Arg Thr Asp His Val Phe Asp
                 10                  15                  20

ctg atg ggc aac gga aac gcc tgg ttc gtc gat gcc cta gaa cgc ctc   211
Leu Met Gly Asn Gly Asn Ala Trp Phe Val Asp Ala Leu Glu Arg Leu
             25                  30                  35

ggg cga ggc atc atc acc gtc cgc ccc aca gtt gaa acc gtg gcc gcc   259
Gly Arg Gly Ile Ile Thr Val Arg Pro Thr Val Glu Thr Val Ala Ala
         40                  45                  50

gcg gac acc tac cac cgc gtc acc cgc cgc ccg gcg gtc gct acc acc   307
Ala Asp Thr Tyr His Arg Val Thr Arg Arg Pro Ala Val Ala Thr Thr
     55                  60                  65

acc tat ggt gct ggt ttc acc aac acc atg acc acg ctt gcc gac gtc   355
Thr Tyr Gly Ala Gly Phe Thr Asn Thr Met Thr Thr Leu Ala Asp Val
 70                  75                  80                  85

gcc ctc tcc cgt atc cca ctt ctt tta gtt gtg ggc act gcc ccg agc   403
Ala Leu Ser Arg Ile Pro Leu Leu Leu Val Val Gly Thr Ala Pro Ser
                 90                  95                 100

gcc ggg cct cgc tgt ttc gac att gac cgg caa gga ctc gca cgt gcc   451
Ala Gly Pro Arg Cys Phe Asp Ile Asp Arg Gln Gly Leu Ala Arg Ala
            105                 110                 115

gta ggt gtg gaa acc ttc acc gtg cat gca gat gac gtt gct gcg gta   499
Val Gly Val Glu Thr Phe Thr Val His Ala Asp Asp Val Ala Ala Val
        120                 125                 130

act ctt cag gct tgg aat aat acg ccg gaa aac aca cac gtg atc ctg   547
Thr Leu Gln Ala Trp Asn Asn Thr Pro Glu Asn Thr His Val Ile Leu
    135                 140                 145

gaa atc ccc tat gac cta gca gct gcc aca gcc acc gat cca aca gtg   595
Glu Ile Pro Tyr Asp Leu Ala Ala Ala Thr Ala Thr Asp Pro Thr Val
150                 155                 160                 165

act aca tac ctg ctg cgc ccc gga ttt cag aaa ctc ccg atg tca ccg   643
Thr Thr Tyr Leu Leu Arg Pro Gly Phe Gln Lys Leu Pro Met Ser Pro
                170                 175                 180

acc ttg tcc tagctctacg caatgcccaa aat                            675
Thr Leu Ser
```

<210> 2666
<211> 184
<212> PRT

<213> Corynebacterium glutamicum

<400> 2666

```
Val Tyr Ser Ile Ser Glu Thr Ile Ala Arg Thr Leu Met Pro Arg Thr
  1               5                  10                  15

Asp His Val Phe Asp Leu Met Gly Asn Gly Asn Ala Trp Phe Val Asp
             20                  25                  30

Ala Leu Glu Arg Leu Gly Arg Gly Ile Ile Thr Val Arg Pro Thr Val
         35                  40                  45

Glu Thr Val Ala Ala Ala Asp Thr Tyr His Arg Val Thr Arg Arg Pro
     50                  55                  60

Ala Val Ala Thr Thr Thr Tyr Gly Ala Gly Phe Thr Asn Thr Met Thr
 65                  70                  75                  80

Thr Leu Ala Asp Val Ala Leu Ser Arg Ile Pro Leu Leu Leu Val Val
                 85                  90                  95

Gly Thr Ala Pro Ser Ala Gly Pro Arg Cys Phe Asp Ile Asp Arg Gln
            100                 105                 110

Gly Leu Ala Arg Ala Val Gly Val Glu Thr Phe Thr Val His Ala Asp
        115                 120                 125

Asp Val Ala Ala Val Thr Leu Gln Ala Trp Asn Asn Thr Pro Glu Asn
    130                 135                 140

Thr His Val Ile Leu Glu Ile Pro Tyr Asp Leu Ala Ala Ala Thr Ala
145                 150                 155                 160

Thr Asp Pro Thr Val Thr Thr Tyr Leu Leu Arg Pro Gly Phe Gln Lys
                165                 170                 175

Leu Pro Met Ser Pro Thr Leu Ser
            180
```

<210> 2667
<211> 498
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(475)
<223> RXA02294

<400> 2667

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tacctcacct ggcaacaaat ccaaggaatg tagataagtc ggggcaaact ctaagaaatc 60

atcctggttt gtggcaggga acattcctag gatgggaggc atg gca aag aca aaa   115
                                              Met Ala Lys Thr Lys
                                                1               5

cta gaa agc atc tcc gag cgc aac tcg gat gat ccg ctt agt tac ccc   163
Leu Glu Ser Ile Ser Glu Arg Asn Ser Asp Asp Pro Leu Ser Tyr Pro
                10                  15                  20
```

```
gac ctg act ctt gca cca ata tcc aca aca gtc aca gtc gtg gtc gcc   211
Asp Leu Thr Leu Ala Pro Ile Ser Thr Thr Val Thr Val Val Val Ala
             25                  30                  35

gaa gac acc cca aac gat aac ttc tca gaa ctt ctc ctc ggc gca gca   259
Glu Asp Thr Pro Asn Asp Asn Phe Ser Glu Leu Leu Leu Gly Ala Ala
         40                  45                  50

gaa tca acc cgt ctt tta gga ctc gac gag ctc cac atc atc gct cca   307
Glu Ser Thr Arg Leu Leu Gly Leu Asp Glu Leu His Ile Ile Ala Pro
     55                  60                  65

tca gtc cac cta ccc gct ctc gca gta gca gcc gcc gac atc gca cac   355
Ser Val His Leu Pro Ala Leu Ala Val Ala Ala Ala Asp Ile Ala His
 70                  75                  80                  85

cat ctg cca gag aaa ttc caa ttc tgt gaa gcc gaa acc tgc act cat   403
His Leu Pro Glu Lys Phe Gln Phe Cys Glu Ala Glu Thr Cys Thr His
                 90                  95                 100

ctc cac ccc gac gat gac acc tat ctc acg gct gaa tcc gtt gct caa   451
Leu His Pro Asp Asp Asp Thr Tyr Leu Thr Ala Glu Ser Val Ala Gln
            105                 110                 115

ttg ggt acg aag ctg aag tct gcg tagttgttag gagccaccac aga         498
Leu Gly Thr Lys Leu Lys Ser Ala
        120                 125
```

<210> 2668
<211> 125
<212> PRT
<213> Corynebacterium glutamicum

<400> 2668

```
Met Ala Lys Thr Lys Leu Glu Ser Ile Ser Glu Arg Asn Ser Asp Asp
  1               5                  10                  15

Pro Leu Ser Tyr Pro Asp Leu Thr Leu Ala Pro Ile Ser Thr Thr Val
             20                  25                  30

Thr Val Val Val Ala Glu Asp Thr Pro Asn Asp Asn Phe Ser Glu Leu
         35                  40                  45

Leu Leu Gly Ala Ala Glu Ser Thr Arg Leu Leu Gly Leu Asp Glu Leu
     50                  55                  60

His Ile Ile Ala Pro Ser Val His Leu Pro Ala Leu Ala Val Ala Ala
 65                  70                  75                  80

Ala Asp Ile Ala His His Leu Pro Glu Lys Phe Gln Phe Cys Glu Ala
                 85                  90                  95

Glu Thr Cys Thr His Leu His Pro Asp Asp Asp Thr Tyr Leu Thr Ala
            100                 105                 110

Glu Ser Val Ala Gln Leu Gly Thr Lys Leu Lys Ser Ala
        115                 120                 125
```

<210> 2669

<211> 903
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(880)
<223> RXA02295

<400> 2669
ttcccatgct aatccgcgaa aatggcactt caacagccat atactttaaa caacacaaat 60

gatgcaagac tgataccggg atgtgatagg agcgcaccac atg ggg ttg gaa tta 115
Met Gly Leu Glu Leu
1 5

gca gct agc ggg tgg ggc atc ctc atc gca ggc gcc gcc gta gcc gga 163
Ala Ala Ser Gly Trp Gly Ile Leu Ile Ala Gly Ala Ala Val Ala Gly
10 15 20

tgg atc gac gca gta atc ggc ggt ggc gga ctc gtc ctc atc ccg ctg 211
Trp Ile Asp Ala Val Ile Gly Gly Gly Gly Leu Val Leu Ile Pro Leu
25 30 35

atc ctc gcg gtc atg ccg caa ctc gca cct gtg aca gcg ctg gcc tcc 259
Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val Thr Ala Leu Ala Ser
40 45 50

aac aaa ctg gca gcc gtc acc ggc acg gca tcg gcg gca ttc acc ctg 307
Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser Ala Ala Phe Thr Leu
55 60 65

gtc agg cgc gtc aaa ccc gac aaa aaa ctg ctt gcg ctc tac gtt ctg 355
Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu Ala Leu Tyr Val Leu
70 75 80 85

gtg gca gct gtg tgc tcc ggt gca ggc gcc ctg gct gcg agt ctc att 403
Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu Ala Ala Ser Leu Ile
90 95 100

gac aaa caa atc atg cga ccg ctg atc atc gtg ttg atg ctg gtc gtt 451
Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val Leu Met Leu Val Val
105 110 115

ggc ctg atc gtg gtg ttc aaa cca aac ttc gga acc ggc gaa agc aaa 499
Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly Thr Gly Glu Ser Lys
120 125 130

gcc ctg ccc acc gga tgg aaa cgc tgg gcc gcc atc gtt gca gtc gga 547
Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala Ile Val Ala Val Gly
135 140 145

ctc atc gca gcc tac gac ggc atc ttc gga ccc gga acc ggc atg ttc 595
Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro Gly Thr Gly Met Phe
150 155 160 165

ctc atc atg gcg ttc acc gca ctg ctc tcc caa aat ttc ctg tcc tcc 643
Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln Asn Phe Leu Ser Ser
170 175 180

gca gcc atg gcg aag gtc gta aac acc gca aca aac ctg ggt gcg cta 691

```
Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr Asn Leu Gly Ala Leu
            185                 190                 195

att gta ttc atc atc ggc ggc cac atg tgg tgg acc cta gga ctc gtg   739
Ile Val Phe Ile Ile Gly Gly His Met Trp Trp Thr Leu Gly Leu Val
        200                 205                 210

ctg gca gtc gcc aat gtc gca ggc gca caa ctc ggt gcc cga acg gtg   787
Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu Gly Ala Arg Thr Val
    215                 220                 225

ctt ggt ggc ggt acc agg cta att aga tac gca cta cta acc ctg gtt   835
Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala Leu Leu Thr Leu Val
230                 235                 240                 245

gtc gtc atg agc gtc tac ctc acc tgg caa caa atc caa gga atg       880
Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln Ile Gln Gly Met
                250                 255                 260

tagataagtc ggggcaaact cta                                        903
```

<210> 2670
<211> 260
<212> PRT
<213> Corynebacterium glutamicum

<400> 2670

```
Met Gly Leu Glu Leu Ala Ala Ser Gly Trp Gly Ile Leu Ile Ala Gly
  1               5                  10                  15

Ala Ala Val Ala Gly Trp Ile Asp Ala Val Ile Gly Gly Gly Gly Leu
             20                  25                  30

Val Leu Ile Pro Leu Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val
         35                  40                  45

Thr Ala Leu Ala Ser Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser
     50                  55                  60

Ala Ala Phe Thr Leu Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu
 65                  70                  75                  80

Ala Leu Tyr Val Leu Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu
                 85                  90                  95

Ala Ala Ser Leu Ile Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val
            100                 105                 110

Leu Met Leu Val Val Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly
        115                 120                 125

Thr Gly Glu Ser Lys Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala
    130                 135                 140

Ile Val Ala Val Gly Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro
145                 150                 155                 160

Gly Thr Gly Met Phe Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln
                165                 170                 175
```

```
Asn Phe Leu Ser Ser Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr
            180                 185                 190

Asn Leu Gly Ala Leu Ile Val Phe Ile Ile Gly Gly His Met Trp Trp
        195                 200                 205

Thr Leu Gly Leu Val Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu
    210                 215                 220

Gly Ala Arg Thr Val Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala
225                 230                 235                 240

Leu Leu Thr Leu Val Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln
                245                 250                 255

Ile Gln Gly Met
            260
```

<210> 2671
<211> 1260
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1237)
<223> RXA02297

<400> 2671

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tgctgatcac gcctgactcc tatgaagtgt tgaccgattc cgctgctaaa gtgaaagcga 60

cattatgaaa taaacgtgga tcaaggagtc cggtgcccaa ttg agc gat aaa gaa   115
                                              Leu Ser Asp Lys Glu
                                                1               5

cca gac ccc cac gaa caa att cca gag aag cca tcc cgc aag gtt att   163
Pro Asp Pro His Glu Gln Ile Pro Glu Lys Pro Ser Arg Lys Val Ile
                  10                  15                  20

gca ctt cgt tgg tgc atc gta gcg ccg ctg tcg cta gcc gtg ggg tgg   211
Ala Leu Arg Trp Cys Ile Val Ala Pro Leu Ser Leu Ala Val Gly Trp
              25                  30                  35

ctt ttt act atg tgg ggt gtg cca gcc gca tgg atc ctc ggg gcg atc   259
Leu Phe Thr Met Trp Gly Val Pro Ala Ala Trp Ile Leu Gly Ala Ile
          40                  45                  50

ctt gtt gcc ggt gta tgt gcg ctg acc aca ggg caa gat ctt ccg atg   307
Leu Val Ala Gly Val Cys Ala Leu Thr Thr Gly Gln Asp Leu Pro Met
      55                  60                  65

gcc aag ggg gtg cat gtt ttt ggt cgc tca atc gtg gcg atg ctg gcg   355
Ala Lys Gly Val His Val Phe Gly Arg Ser Ile Val Ala Met Leu Ala
  70                  75                  80                  85

gcg ctg cct ttg att agt tct tct ggt tcg gaa ctt gtt cgt ttc ctc   403
Ala Leu Pro Leu Ile Ser Ser Ser Gly Ser Glu Leu Val Arg Phe Leu
                  90                  95                 100

atc ccg ggt ctt gtg att tcc ttt ttc acc atc gcg gta ggc atc gtt   451
```

```
Ile Pro Gly Leu Val Ile Ser Phe Phe Thr Ile Ala Val Gly Ile Val
            105                 110                 115

ggt ggt ttg ttg ctg gca aga tcc agg ccg gag att ttg ccg gaa act   499
Gly Gly Leu Leu Leu Ala Arg Ser Arg Pro Glu Ile Leu Pro Glu Thr
        120                 125                 130

ggt gtg ctg tcc atg ctg gcg ggt ggc gcg tcg gtg atg ccg att ctg   547
Gly Val Leu Ser Met Leu Ala Gly Gly Ala Ser Val Met Pro Ile Leu
    135                 140                 145

gcc cga gag ttg ggc gct gat ttc cgc tat gtg gcg ctg acg cag tac   595
Ala Arg Glu Leu Gly Ala Asp Phe Arg Tyr Val Ala Leu Thr Gln Tyr
150                 155                 160                 165

ctc agg ttg ttg gtt gtg tcc atg acg ttg ccg ctg gtg acg cac ttt   643
Leu Arg Leu Leu Val Val Ser Met Thr Leu Pro Leu Val Thr His Phe
                170                 175                 180

ttc gtc cct ggc ggg gcg gat ttg gga tcg ccg cct gag aaa tgg ttg   691
Phe Val Pro Gly Gly Ala Asp Leu Gly Ser Pro Pro Glu Lys Trp Leu
            185                 190                 195

gac gtg ttg agt ttg gga gag ttc ggg acg tcg ata agc gtt tta tcg   739
Asp Val Leu Ser Leu Gly Glu Phe Gly Thr Ser Ile Ser Val Leu Ser
        200                 205                 210

ctg ctg gtg ctc ttc ggt att gtg ctg gcc ggc gaa cct ctc ggc agg   787
Leu Leu Val Leu Phe Gly Ile Val Leu Ala Gly Glu Pro Leu Gly Arg
    215                 220                 225

ttg ctg cgc ttg cct gcc cct gcg gtg atg ggg ccg ctg atc ctg acc   835
Leu Leu Arg Leu Pro Ala Pro Ala Val Met Gly Pro Leu Ile Leu Thr
230                 235                 240                 245

gtg ctg gtg agt ttt gtg att cca gat gat ctc agc ctg caa ccg cca   883
Val Leu Val Ser Phe Val Ile Pro Asp Asp Leu Ser Leu Gln Pro Pro
                250                 255                 260

acc gtg ttt aag att atc gcg ttc atg gcg atc ggt tgg atg tgt ggc   931
Thr Val Phe Lys Ile Ile Ala Phe Met Ala Ile Gly Trp Met Cys Gly
            265                 270                 275

ggt ccc ttg aat atg acc gcg ctg aag gtg ttt tct aag cag ctt ccg   979
Gly Pro Leu Asn Met Thr Ala Leu Lys Val Phe Ser Lys Gln Leu Pro
        280                 285                 290

gcc acg ttc ttg ttt att ttc gcg ctg ctt gcg gtg tgc gca ggt gcg   1027
Ala Thr Phe Leu Phe Ile Phe Ala Leu Leu Ala Val Cys Ala Gly Ala
    295                 300                 305

gcg ggg ctg ctc acc tgg tgg ttg gat atc agc ttc ttc gag gct tac   1075
Ala Gly Leu Leu Thr Trp Trp Leu Asp Ile Ser Phe Phe Glu Ala Tyr
310                 315                 320                 325

cta gca acc agc cct gga gct ctg gag acg gtg ttg gcg ctg tcc tcg   1123
Leu Ala Thr Ser Pro Gly Ala Leu Glu Thr Val Leu Ala Leu Ser Ser
                330                 335                 340

gaa gga tct gca ggc ccg gtg gtg gtc acg atc cag atc att cga cta   1171
Glu Gly Ser Ala Gly Pro Val Val Val Thr Ile Gln Ile Ile Arg Leu
```

```
            345                 350                 355

ctg gca atc ttg acc atc gcc ggt ttg atc ccc acg cta ctg cga cgc   1219
Leu Ala Ile Leu Thr Ile Ala Gly Leu Ile Pro Thr Leu Leu Arg Arg
        360                 365                 370

att ttg cgt agg gat cgt taaaggcctt ctagttcagc acc                1260
Ile Leu Arg Arg Asp Arg
    375
```

<210> 2672
<211> 379
<212> PRT
<213> Corynebacterium glutamicum

<400> 2672

```
Leu Ser Asp Lys Glu Pro Asp Pro His Glu Gln Ile Pro Glu Lys Pro
  1               5                  10                  15

Ser Arg Lys Val Ile Ala Leu Arg Trp Cys Ile Val Ala Pro Leu Ser
             20                  25                  30

Leu Ala Val Gly Trp Leu Phe Thr Met Trp Gly Val Pro Ala Ala Trp
         35                  40                  45

Ile Leu Gly Ala Ile Leu Val Ala Gly Val Cys Ala Leu Thr Thr Gly
     50                  55                  60

Gln Asp Leu Pro Met Ala Lys Gly Val His Val Phe Gly Arg Ser Ile
 65                  70                  75                  80

Val Ala Met Leu Ala Ala Leu Pro Leu Ile Ser Ser Ser Gly Ser Glu
                 85                  90                  95

Leu Val Arg Phe Leu Ile Pro Gly Leu Val Ile Ser Phe Phe Thr Ile
            100                 105                 110

Ala Val Gly Ile Val Gly Gly Leu Leu Leu Ala Arg Ser Arg Pro Glu
        115                 120                 125

Ile Leu Pro Glu Thr Gly Val Leu Ser Met Leu Ala Gly Gly Ala Ser
    130                 135                 140

Val Met Pro Ile Leu Ala Arg Glu Leu Gly Ala Asp Phe Arg Tyr Val
145                 150                 155                 160

Ala Leu Thr Gln Tyr Leu Arg Leu Leu Val Val Ser Met Thr Leu Pro
                165                 170                 175

Leu Val Thr His Phe Phe Val Pro Gly Gly Ala Asp Leu Gly Ser Pro
            180                 185                 190

Pro Glu Lys Trp Leu Asp Val Leu Ser Leu Gly Glu Phe Gly Thr Ser
        195                 200                 205

Ile Ser Val Leu Ser Leu Leu Val Leu Phe Gly Ile Val Leu Ala Gly
    210                 215                 220

Glu Pro Leu Gly Arg Leu Leu Arg Leu Pro Ala Pro Ala Val Met Gly
225                 230                 235                 240
```

```
Pro Leu Ile Leu Thr Val Leu Val Ser Phe Val Ile Pro Asp Asp Leu
               245                 250                 255

Ser Leu Gln Pro Pro Thr Val Phe Lys Ile Ile Ala Phe Met Ala Ile
            260                 265                 270

Gly Trp Met Cys Gly Gly Pro Leu Asn Met Thr Ala Leu Lys Val Phe
        275                 280                 285

Ser Lys Gln Leu Pro Ala Thr Phe Leu Phe Ile Phe Ala Leu Leu Ala
    290                 295                 300

Val Cys Ala Gly Ala Ala Gly Leu Leu Thr Trp Trp Leu Asp Ile Ser
305                 310                 315                 320

Phe Phe Glu Ala Tyr Leu Ala Thr Ser Pro Gly Ala Leu Glu Thr Val
               325                 330                 335

Leu Ala Leu Ser Ser Glu Gly Ser Ala Gly Pro Val Val Val Thr Ile
            340                 345                 350

Gln Ile Ile Arg Leu Leu Ala Ile Leu Thr Ile Ala Gly Leu Ile Pro
        355                 360                 365

Thr Leu Leu Arg Arg Ile Leu Arg Arg Asp Arg
    370                 375
```

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<210> 2673
<211> 1782
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1759)
<223> RXA02298

<400> 2673

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aaatcatagc gtgagatgac aaggaaagga atatttcgat ccggcaacaa cccccgcgtc 60

aggtgggatt atgccgaaaa aatcgctacg atagccactt atg act ctt cag agt   115
                                              Met Thr Leu Gln Ser
                                                1               5

tct gat aaa cgt tct cct tca ctg tta gac gcc tcc tcc gag gtc ttt   163
Ser Asp Lys Arg Ser Pro Ser Leu Leu Asp Ala Ser Ser Glu Val Phe
                10                  15                  20

gtc cat gat ttg gca gct ttg tct ccc act gat gcc act gca tgg ggt   211
Val His Asp Leu Ala Ala Leu Ser Pro Thr Asp Ala Thr Ala Trp Gly
            25                  30                  35

atc tca ggc ttc gaa ggt gat ctt cag gat ttc tct cct gac tat tgg   259
Ile Ser Gly Phe Glu Gly Asp Leu Gln Asp Phe Ser Pro Asp Tyr Trp
        40                  45                  50

aat gcc atc gcc gaa cgc aac cgc gac atg gtt gcc gat gtt gat gct   307
Asn Ala Ile Ala Glu Arg Asn Arg Asp Met Val Ala Asp Val Asp Ala
    55                  60                  65
```

```
ttt gat gac ggc act gat gac aac gat gac gaa gaa gat ttc gat gac   355
Phe Asp Asp Gly Thr Asp Asp Asn Asp Asp Glu Glu Asp Phe Asp Asp
 70                  75                  80                  85

gtt gac cgc gtc acc gct gat gtt ctc cgt gat cgc gta tgc ctg gat   403
Val Asp Arg Val Thr Ala Asp Val Leu Arg Asp Arg Val Cys Leu Asp
                90                  95                 100

ctg gcc ctg cac cac cag ggc gaa acc tta gcg aat ctc aac aac att   451
Leu Ala Leu His His Gln Gly Glu Thr Leu Ala Asn Leu Asn Asn Ile
            105                 110                 115

gat tcc cca gtc cag acc atc cgc gat acc ttc ctc atc atg ccc cgc   499
Asp Ser Pro Val Gln Thr Ile Arg Asp Thr Phe Leu Ile Met Pro Arg
        120                 125                 130

gag acg gac gat gat gtg gaa aat ctc cgc gaa cgt ctc tcc cgc gtc   547
Glu Thr Asp Asp Asp Val Glu Asn Leu Arg Glu Arg Leu Ser Arg Val
    135                 140                 145

ccc gac gct ctc cac gga tac tgt gaa tca ctc gct gag gct gcc agc   595
Pro Asp Ala Leu His Gly Tyr Cys Glu Ser Leu Ala Glu Ala Ala Ser
150                 155                 160                 165

caa ggc cat gtt gca gcg gtc cgc cag gtg gaa gaa gtg gtg tcg caa   643
Gln Gly His Val Ala Ala Val Arg Gln Val Glu Glu Val Val Ser Gln
                170                 175                 180

tgt gag gac ctc gct gat gag gac tcc gtt ttg cag cac ctt ggc ttg   691
Cys Glu Asp Leu Ala Asp Glu Asp Ser Val Leu Gln His Leu Gly Leu
            185                 190                 195

gat gaa aat gat cca gta gtt gta gag gcc cag gaa gct ttt gca cga   739
Asp Glu Asn Asp Pro Val Val Val Glu Ala Gln Glu Ala Phe Ala Arg
        200                 205                 210

gtt gcc ggt tgg tta gca gag caa ctg gct ccg cat gct cct cat gtg   787
Val Ala Gly Trp Leu Ala Glu Gln Leu Ala Pro His Ala Pro His Val
    215                 220                 225

gat gcg gtt ggc cgg gat cgc tat gaa atg ttc tcc cac ctg cac gtc   835
Asp Ala Val Gly Arg Asp Arg Tyr Glu Met Phe Ser His Leu His Val
230                 235                 240                 245

ggc gag ttt gta gat ctg gat gag gct tac caa tgg tcc ctg gaa cag   883
Gly Glu Phe Val Asp Leu Asp Glu Ala Tyr Gln Trp Ser Leu Glu Gln
                250                 255                 260

ctg cgt gac att gat gct cag cag ctt cag gta gcc cag cag ctg tac   931
Leu Arg Asp Ile Asp Ala Gln Gln Leu Gln Val Ala Gln Gln Leu Tyr
            265                 270                 275

ggc cct ggc acc acg atc cgt gag gcc atg aag aag ctc aat gct gat   979
Gly Pro Gly Thr Thr Ile Arg Glu Ala Met Lys Lys Leu Asn Ala Asp
        280                 285                 290

gag cgc tac ctc atc cga ggc act gat gct ctg cag gag tgg atg caa   1027
Glu Arg Tyr Leu Ile Arg Gly Thr Asp Ala Leu Gln Glu Trp Met Gln
    295                 300                 305
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aag acc gct gat cag gca atc gct gat cta gat ggc gtt tcc ttc aac   1075
Lys Thr Ala Asp Gln Ala Ile Ala Asp Leu Asp Gly Val Ser Phe Asn
310                 315                 320                 325

att cca gag cag gct cga cag gtt gag tgc ctc atc gat cct gct gga   1123
Ile Pro Glu Gln Ala Arg Gln Val Glu Cys Leu Ile Asp Pro Ala Gly
                330                 335                 340

act ggc ggc att ttc tac acc cca cca agc gat gat ttc tcc agg cct   1171
Thr Gly Gly Ile Phe Tyr Thr Pro Pro Ser Asp Asp Phe Ser Arg Pro
            345                 350                 355

ggc cgc atg tgg tgg tct gtg cct aaa acc cag gaa gtc ttc cac acc   1219
Gly Arg Met Trp Trp Ser Val Pro Lys Thr Gln Glu Val Phe His Thr
        360                 365                 370

tgg caa gag ctc acc acc gtg ttc cac gag ggt gtt cct ggc cac cac   1267
Trp Gln Glu Leu Thr Thr Val Phe His Glu Gly Val Pro Gly His His
    375                 380                 385

ctg cag atc tcc caa act ttg gtg gaa aag gat ctg aac ctg tgg cgt   1315
Leu Gln Ile Ser Gln Thr Leu Val Glu Lys Asp Leu Asn Leu Trp Arg
390                 395                 400                 405

cga gtc gct tgc tgg aac tct ggc cac ggt gaa ggt tgg gcg ctg tac   1363
Arg Val Ala Cys Trp Asn Ser Gly His Gly Glu Gly Trp Ala Leu Tyr
                410                 415                 420

gca gaa tct ctc atg aag gaa ttg gga tac cac gaa gat cca ggc aac   1411
Ala Glu Ser Leu Met Lys Glu Leu Gly Tyr His Glu Asp Pro Gly Asn
            425                 430                 435

ctc atg ggc tac ctt gat gct cag cga ctc cgt gca gcc cgc gtg gcc   1459
Leu Met Gly Tyr Leu Asp Ala Gln Arg Leu Arg Ala Ala Arg Val Ala
        440                 445                 450

att gac atc gga att cac ctg aac aag agg aac cca gag tgc acc ggc   1507
Ile Asp Ile Gly Ile His Leu Asn Lys Arg Asn Pro Glu Cys Thr Gly
    455                 460                 465

ctg tgg gat gcg tct tat gcg cgc agc ttc ctg cgt gaa aat acg tcc   1555
Leu Trp Asp Ala Ser Tyr Ala Arg Ser Phe Leu Arg Glu Asn Thr Ser
470                 475                 480                 485

atg aat gaa gat gcg ctg tac ttt gag ctc aac cgt tac ctt ggt tgg   1603
Met Asn Glu Asp Ala Leu Tyr Phe Glu Leu Asn Arg Tyr Leu Gly Trp
                490                 495                 500

cca ggt cag gcc gca tcg tat gcc att ggt cag cga ctc tgg ttg aac   1651
Pro Gly Gln Ala Ala Ser Tyr Ala Ile Gly Gln Arg Leu Trp Leu Asn
            505                 510                 515

ctg cgc gat gag gcc att agc cag ggg caa acc ttg gcg caa ttc cac   1699
Leu Arg Asp Glu Ala Ile Ser Gln Gly Gln Thr Leu Ala Gln Phe His
        520                 525                 530

agc aag gca ttg tcc tat ggc agc atc ccg atg ggc att ttg cgc gat   1747
Ser Lys Ala Leu Ser Tyr Gly Ser Ile Pro Met Gly Ile Leu Arg Asp
    535                 540                 545

cag gtg ctg aac tagaaggcct ttaacgatcc cta                         1782
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Gln Val Leu Asn
550

<210> 2674
<211> 553
<212> PRT
<213> Corynebacterium glutamicum

<400> 2674
Met Thr Leu Gln Ser Ser Asp Lys Arg Ser Pro Ser Leu Leu Asp Ala
1 5 10 15

Ser Ser Glu Val Phe Val His Asp Leu Ala Ala Leu Ser Pro Thr Asp
20 25 30

Ala Thr Ala Trp Gly Ile Ser Gly Phe Glu Gly Asp Leu Gln Asp Phe
35 40 45

Ser Pro Asp Tyr Trp Asn Ala Ile Ala Glu Arg Asn Arg Asp Met Val
50 55 60

Ala Asp Val Asp Ala Phe Asp Asp Gly Thr Asp Asp Asn Asp Asp Glu
65 70 75 80

Glu Asp Phe Asp Asp Val Asp Arg Val Thr Ala Asp Val Leu Arg Asp
85 90 95

Arg Val Cys Leu Asp Leu Ala Leu His His Gln Gly Glu Thr Leu Ala
100 105 110

Asn Leu Asn Asn Ile Asp Ser Pro Val Gln Thr Ile Arg Asp Thr Phe
115 120 125

Leu Ile Met Pro Arg Glu Thr Asp Asp Asp Val Glu Asn Leu Arg Glu
130 135 140

Arg Leu Ser Arg Val Pro Asp Ala Leu His Gly Tyr Cys Glu Ser Leu
145 150 155 160

Ala Glu Ala Ala Ser Gln Gly His Val Ala Ala Val Arg Gln Val Glu
165 170 175

Glu Val Val Ser Gln Cys Glu Asp Leu Ala Asp Glu Asp Ser Val Leu
180 185 190

Gln His Leu Gly Leu Asp Glu Asn Asp Pro Val Val Val Glu Ala Gln
195 200 205

Glu Ala Phe Ala Arg Val Ala Gly Trp Leu Ala Glu Gln Leu Ala Pro
210 215 220

His Ala Pro His Val Asp Ala Val Gly Arg Asp Arg Tyr Glu Met Phe
225 230 235 240

Ser His Leu His Val Gly Glu Phe Val Asp Leu Asp Glu Ala Tyr Gln
245 250 255

Trp Ser Leu Glu Gln Leu Arg Asp Ile Asp Ala Gln Gln Leu Gln Val
260 265 270

```
Ala Gln Gln Leu Tyr Gly Pro Gly Thr Thr Ile Arg Glu Ala Met Lys
        275                 280                 285

Lys Leu Asn Ala Asp Glu Arg Tyr Leu Ile Arg Gly Thr Asp Ala Leu
    290                 295                 300

Gln Glu Trp Met Gln Lys Thr Ala Asp Gln Ala Ile Ala Asp Leu Asp
305                 310                 315                 320

Gly Val Ser Phe Asn Ile Pro Glu Gln Ala Arg Gln Val Glu Cys Leu
                325                 330                 335

Ile Asp Pro Ala Gly Thr Gly Gly Ile Phe Tyr Thr Pro Pro Ser Asp
            340                 345                 350

Asp Phe Ser Arg Pro Gly Arg Met Trp Trp Ser Val Pro Lys Thr Gln
        355                 360                 365

Glu Val Phe His Thr Trp Gln Glu Leu Thr Thr Val Phe His Glu Gly
    370                 375                 380

Val Pro Gly His His Leu Gln Ile Ser Gln Thr Leu Val Glu Lys Asp
385                 390                 395                 400

Leu Asn Leu Trp Arg Arg Val Ala Cys Trp Asn Ser Gly His Gly Glu
                405                 410                 415

Gly Trp Ala Leu Tyr Ala Glu Ser Leu Met Lys Glu Leu Gly Tyr His
            420                 425                 430

Glu Asp Pro Gly Asn Leu Met Gly Tyr Leu Asp Ala Gln Arg Leu Arg
        435                 440                 445

Ala Ala Arg Val Ala Ile Asp Ile Gly Ile His Leu Asn Lys Arg Asn
    450                 455                 460

Pro Glu Cys Thr Gly Leu Trp Asp Ala Ser Tyr Ala Arg Ser Phe Leu
465                 470                 475                 480

Arg Glu Asn Thr Ser Met Asn Glu Asp Ala Leu Tyr Phe Glu Leu Asn
                485                 490                 495

Arg Tyr Leu Gly Trp Pro Gly Gln Ala Ala Ser Tyr Ala Ile Gly Gln
            500                 505                 510

Arg Leu Trp Leu Asn Leu Arg Asp Glu Ala Ile Ser Gln Gly Gln Thr
        515                 520                 525

Leu Ala Gln Phe His Ser Lys Ala Leu Ser Tyr Gly Ser Ile Pro Met
    530                 535                 540

Gly Ile Leu Arg Asp Gln Val Leu Asn
545                 550
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<210> 2675
<211> 1014
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(991)
<223> RXA02304

<400> 2675
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agtgcaagtt ttttataaca gggcagtaac gtttactggt atg aaa act ccc cgt   115
                                            Met Lys Thr Pro Arg
                                              1               5

ctg ctg aag atc ctc agc gcg atg gtg gct gtc act gga ctt ctc att   163
Leu Leu Lys Ile Leu Ser Ala Met Val Ala Val Thr Gly Leu Leu Ile
                 10                  15                  20

cca acg gtg gtc ccc atg gcc gcc gct gat gct gct gaa ctg tcc gac   211
Pro Thr Val Val Pro Met Ala Ala Ala Asp Ala Ala Glu Leu Ser Asp
             25                  30                  35

aac gtt ccc gat cgc acc caa att gcc atc atc aac cct gat ggc agc   259
Asn Val Pro Asp Arg Thr Gln Ile Ala Ile Ile Asn Pro Asp Gly Ser
         40                  45                  50

gtg caa gaa tct gac aac gcc gaa gaa tcc cgc ccg gca tta tcc ctg   307
Val Gln Glu Ser Asp Asn Ala Glu Glu Ser Arg Pro Ala Leu Ser Leu
     55                  60                  65

gcc aag ctg tat ttg ggt tat tat gtg ttg gct caa ggc gcg gaa gaa   355
Ala Lys Leu Tyr Leu Gly Tyr Tyr Val Leu Ala Gln Gly Ala Glu Glu
 70                  75                  80                  85

gat att gaa cta gtc cca gat atg atc cgc tac tct gat gat ttc acc   403
Asp Ile Glu Leu Val Pro Asp Met Ile Arg Tyr Ser Asp Asp Phe Thr
                 90                  95                 100

gcg gat tat ttg gag agc gaa tac ccg gaa gca att cct gag gtt att   451
Ala Asp Tyr Leu Glu Ser Glu Tyr Pro Glu Ala Ile Pro Glu Val Ile
            105                 110                 115

gat gcc ttc gat ttg gaa gac acc gaa tgg gct ggt ttc tgg ggc aat   499
Asp Ala Phe Asp Leu Glu Asp Thr Glu Trp Ala Gly Phe Trp Gly Asn
        120                 125                 130

gca act acc agt gcg gtg gat att gcg acg ttt gta gca gca ctc atc   547
Ala Thr Thr Ser Ala Val Asp Ile Ala Thr Phe Val Ala Ala Leu Ile
    135                 140                 145

gac gat ccc acg gcg cag ccc ttg ctt gac gca atg tct gac acc gct   595
Asp Asp Pro Thr Ala Gln Pro Leu Leu Asp Ala Met Ser Asp Thr Ala
150                 155                 160                 165

gag tat gcg gcg gat ggc tac gcc cag aac ttt ggc act ttt aca ttg   643
Glu Tyr Ala Ala Asp Gly Tyr Ala Gln Asn Phe Gly Thr Phe Thr Leu
                170                 175                 180

tcc gat gtc acc ggt act aaa ttt ggt tgg tct gat tcc ctc gat gtg   691
Ser Asp Val Thr Gly Thr Lys Phe Gly Trp Ser Asp Ser Leu Asp Val
            185                 190                 195

cat tca tcg gtc agc ttt ggc cct ggt ttt gtg atc gct gcc aac acc   739
His Ser Ser Val Ser Phe Gly Pro Gly Phe Val Ile Ala Ala Asn Thr
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        200                 205                 210

tac ggt gac gcc gaa acg ctc acc gaa gat gtc caa gat tcc gtg tct   787
Tyr Gly Asp Ala Glu Thr Leu Thr Glu Asp Val Gln Asp Ser Val Ser
    215                 220                 225

tcg ctg tat ccg gag gaa gta acc acc gcg atc gag gag cag gtg gat   835
Ser Leu Tyr Pro Glu Glu Val Thr Thr Ala Ile Glu Glu Gln Val Asp
230                 235                 240                 245

cag ctg tgt gag tgc gct gca gag act acg cat ttg gga atg cac act   883
Gln Leu Cys Glu Cys Ala Ala Glu Thr Thr His Leu Gly Met His Thr
                250                 255                 260

ggc gcg gag ctg aaa gca cag ctt gag ggc act att tat gga aaa acc   931
Gly Ala Glu Leu Lys Ala Gln Leu Glu Gly Thr Ile Tyr Gly Lys Thr
            265                 270                 275

ctc agc ttt tta cct aat tca gcc cca gcg cca gcg ttt att tac aac   979
Leu Ser Phe Leu Pro Asn Ser Ala Pro Ala Pro Ala Phe Ile Tyr Asn
        280                 285                 290

ctg ctg gca cat tagcaaacag ttttaaggaa ctc                        1014
Leu Leu Ala His
    295


<210> 2676
<211> 297
<212> PRT
<213> Corynebacterium glutamicum

<400> 2676
Met Lys Thr Pro Arg Leu Leu Lys Ile Leu Ser Ala Met Val Ala Val
  1               5                  10                  15

Thr Gly Leu Leu Ile Pro Thr Val Val Pro Met Ala Ala Ala Asp Ala
             20                  25                  30

Ala Glu Leu Ser Asp Asn Val Pro Asp Arg Thr Gln Ile Ala Ile Ile
         35                  40                  45

Asn Pro Asp Gly Ser Val Gln Glu Ser Asp Asn Ala Glu Glu Ser Arg
     50                  55                  60

Pro Ala Leu Ser Leu Ala Lys Leu Tyr Leu Gly Tyr Tyr Val Leu Ala
 65                  70                  75                  80

Gln Gly Ala Glu Glu Asp Ile Glu Leu Val Pro Asp Met Ile Arg Tyr
                 85                  90                  95

Ser Asp Asp Phe Thr Ala Asp Tyr Leu Glu Ser Glu Tyr Pro Glu Ala
            100                 105                 110

Ile Pro Glu Val Ile Asp Ala Phe Asp Leu Glu Asp Thr Glu Trp Ala
        115                 120                 125

Gly Phe Trp Gly Asn Ala Thr Thr Ser Ala Val Asp Ile Ala Thr Phe
    130                 135                 140

Val Ala Ala Leu Ile Asp Asp Pro Thr Ala Gln Pro Leu Leu Asp Ala
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145                 150                 155                 160

Met Ser Asp Thr Ala Glu Tyr Ala Ala Asp Gly Tyr Ala Gln Asn Phe
                165                 170                 175

Gly Thr Phe Thr Leu Ser Asp Val Thr Gly Thr Lys Phe Gly Trp Ser
            180                 185                 190

Asp Ser Leu Asp Val His Ser Ser Val Ser Phe Gly Pro Gly Phe Val
        195                 200                 205

Ile Ala Ala Asn Thr Tyr Gly Asp Ala Glu Thr Leu Thr Glu Asp Val
    210                 215                 220

Gln Asp Ser Val Ser Ser Leu Tyr Pro Glu Glu Val Thr Thr Ala Ile
225                 230                 235                 240

Glu Glu Gln Val Asp Gln Leu Cys Glu Cys Ala Ala Glu Thr Thr His
                245                 250                 255

Leu Gly Met His Thr Gly Ala Glu Leu Lys Ala Gln Leu Glu Gly Thr
            260                 265                 270

Ile Tyr Gly Lys Thr Leu Ser Phe Leu Pro Asn Ser Ala Pro Ala Pro
        275                 280                 285

Ala Phe Ile Tyr Asn Leu Leu Ala His
    290                 295


<210> 2677
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(529)
<223> RXA02308

<400> 2677
gggtgagatt ggaatgattt cggcccgggc gctcgaaaac cgtgatagac acaatgaacc 60

gagcaaatcc gccaggaaat aaattaagta aggaatatcc atg agt gaa acc cag   115
                                              Met Ser Glu Thr Gln
                                                1               5

tcg aat tca gtg tca gcg gta atg cct gcg cag ctc cct cca ggg cct   163
Ser Asn Ser Val Ser Ala Val Met Pro Ala Gln Leu Pro Pro Gly Pro
                10                  15                  20

gcc gag cgt act gtg tac tcc tac ggt gtt cgc gca ggg gat cag gtg   211
Ala Glu Arg Thr Val Tyr Ser Tyr Gly Val Arg Ala Gly Asp Gln Val
            25                  30                  35

cac att tta aga atg gag gct ttt gat tct gac gcg aat att gtc ggc   259
His Ile Leu Arg Met Glu Ala Phe Asp Ser Asp Ala Asn Ile Val Gly
        40                  45                  50

gaa agg gac att gag gcg cat gct gaa caa gtc ttt aag aac ctg caa   307
Glu Arg Asp Ile Glu Ala His Ala Glu Gln Val Phe Lys Asn Leu Gln
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```
     55                  60                  65

gca gta atc cac gag gca gga gga acg atc aac aac att gtt tcc acc   355
Ala Val Ile His Glu Ala Gly Gly Thr Ile Asn Asn Ile Val Ser Thr
 70                  75                  80                  85

act act tat ctt gcc gat gtc acc gat gct ccc gtt gtt aac gct gct   403
Thr Thr Tyr Leu Ala Asp Val Thr Asp Ala Pro Val Val Asn Ala Ala
                90                  95                 100

cgc tcc cgc tat ttc acc gga gaa gta ttg ccc acc cac acc gta att   451
Arg Ser Arg Tyr Phe Thr Gly Glu Val Leu Pro Thr His Thr Val Ile
            105                 110                 115

gga gtt gct gct ctt gct cgg cca cag ttt cta gtc gag atc tca gcg   499
Gly Val Ala Ala Leu Ala Arg Pro Gln Phe Leu Val Glu Ile Ser Ala
        120                 125                 130

gtg gcc tat ttg ggg gac ctt tca aaa gac tagatacatg attatttttg     549
Val Ala Tyr Leu Gly Asp Leu Ser Lys Asp
    135                 140

cat                                                               552


<210> 2678
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 2678
Met Ser Glu Thr Gln Ser Asn Ser Val Ser Ala Val Met Pro Ala Gln
  1               5                  10                  15

Leu Pro Pro Gly Pro Ala Glu Arg Thr Val Tyr Ser Tyr Gly Val Arg
             20                  25                  30

Ala Gly Asp Gln Val His Ile Leu Arg Met Glu Ala Phe Asp Ser Asp
         35                  40                  45

Ala Asn Ile Val Gly Glu Arg Asp Ile Glu Ala His Ala Glu Gln Val
     50                  55                  60

Phe Lys Asn Leu Gln Ala Val Ile His Glu Ala Gly Gly Thr Ile Asn
 65                  70                  75                  80

Asn Ile Val Ser Thr Thr Thr Tyr Leu Ala Asp Val Thr Asp Ala Pro
                85                  90                  95

Val Val Asn Ala Ala Arg Ser Arg Tyr Phe Thr Gly Glu Val Leu Pro
            100                 105                 110

Thr His Thr Val Ile Gly Val Ala Ala Leu Ala Arg Pro Gln Phe Leu
        115                 120                 125

Val Glu Ile Ser Ala Val Ala Tyr Leu Gly Asp Leu Ser Lys Asp
    130                 135                 140


<210> 2679
<211> 1209
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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1186)
<223> RXA02324

<400> 2679
gaaggtcaaa aaacttgact ttattgaaaa caatttccat taagaagtgt acacttgcgt 60

cgactctatt gaaaatgatt cccaaaagga gggctttcac atg gcc aca acg acc 115
Met Ala Thr Thr Thr
1 5

cca gtc acc gtg cta tca gga ttt ctc ggc tcc gga aaa acc aca ttg 163
Pro Val Thr Val Leu Ser Gly Phe Leu Gly Ser Gly Lys Thr Thr Leu
10 15 20

ctc aac cag atc ctc cac cac cga gga tcc cgg aaa atc gca gtc att 211
Leu Asn Gln Ile Leu His His Arg Gly Ser Arg Lys Ile Ala Val Ile
25 30 35

gtc aac gat ttt tca gaa atc aac atc gac gca gcc ctc atc gca tcc 259
Val Asn Asp Phe Ser Glu Ile Asn Ile Asp Ala Ala Leu Ile Ala Ser
40 45 50

gaa ggc cac ctc acc cgc ggc gaa gac cgc ttc gtg gaa ctg acc aac 307
Glu Gly His Leu Thr Arg Gly Glu Asp Arg Phe Val Glu Leu Thr Asn
55 60 65

gga tgc atc tgc tgc acc ctg cgc gaa gac ctc gtg gat tcc gtc ggc 355
Gly Cys Ile Cys Cys Thr Leu Arg Glu Asp Leu Val Asp Ser Val Gly
70 75 80 85

gaa ctc gcc agc agc gac cgc ttc gac cac atc gtc atc gaa tcc acg 403
Glu Leu Ala Ser Ser Asp Arg Phe Asp His Ile Val Ile Glu Ser Thr
90 95 100

ggt atc tcc gaa cca atg ccg gta gcc gcc aca ttt gaa tgg cag tgg 451
Gly Ile Ser Glu Pro Met Pro Val Ala Ala Thr Phe Glu Trp Gln Trp
105 110 115

gat gac ggc acc cgc ctg gct gac aaa gca ccg atc gac acc atg gtc 499
Asp Asp Gly Thr Arg Leu Ala Asp Lys Ala Pro Ile Asp Thr Met Val
120 125 130

acc ctg gtc gat gcc acc caa ttc atc gac ctc atc cgc aaa aac acc 547
Thr Leu Val Asp Ala Thr Gln Phe Ile Asp Leu Ile Arg Lys Asn Thr
135 140 145

tcc ctc acc gag gct gac atg ggc gca acc gag gac gat gaa cgc acc 595
Ser Leu Thr Glu Ala Asp Met Gly Ala Thr Glu Asp Asp Glu Arg Thr
150 155 160 165

atc gcc gac cta ctc acc gat caa atc gag ttc gcc gac cgc atc tac 643
Ile Ala Asp Leu Leu Thr Asp Gln Ile Glu Phe Ala Asp Arg Ile Tyr
170 175 180

atc acc aaa tcc gac ctg gtg gac cgc act gtc ctc gag caa acc cgc 691
Ile Thr Lys Ser Asp Leu Val Asp Arg Thr Val Leu Glu Gln Thr Arg

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            185                 190                 195

gca cta atc gcc agc atg agt cca cgc gcc cgc att gac tta ctc atc   739
Ala Leu Ile Ala Ser Met Ser Pro Arg Ala Arg Ile Asp Leu Leu Ile
        200                 205                 210

gat ggc ctc aat gac ggc tcc ccc atc acc gac gac atc ctc gga gct   787
Asp Gly Leu Asn Asp Gly Ser Pro Ile Thr Asp Asp Ile Leu Gly Ala
    215                 220                 225

ttc ctc tac gac gaa gcc acc gcc cgc gcc tac gag ggc tac acg gaa   835
Phe Leu Tyr Asp Glu Ala Thr Ala Arg Ala Tyr Glu Gly Tyr Thr Glu
230                 235                 240                 245

gaa ctc gaa aac ccg cac act ccc gaa acc gag gaa tac ggc atc agt   883
Glu Leu Glu Asn Pro His Thr Pro Glu Thr Glu Glu Tyr Gly Ile Ser
                250                 255                 260

tcc gtg gta ttc cgc tct gac cgg ccg ttc aac aag gat cgc cta ctt   931
Ser Val Val Phe Arg Ser Asp Arg Pro Phe Asn Lys Asp Arg Leu Leu
            265                 270                 275

cag gta ctg cgt tcc acc act gga ctc gtt cgc tcc aaa ggc tat tgc   979
Gln Val Leu Arg Ser Thr Thr Gly Leu Val Arg Ser Lys Gly Tyr Cys
        280                 285                 290

tgg atc gct gat cac ctc aac atc gtc cag gtc tgg cac caa gcc ggc   1027
Trp Ile Ala Asp His Leu Asn Ile Val Gln Val Trp His Gln Ala Gly
    295                 300                 305

ccc aat ttg agc att cgc ccg gcc gcc tat tgg gcc aat tca gag atc   1075
Pro Asn Leu Ser Ile Arg Pro Ala Ala Tyr Trp Ala Asn Ser Glu Ile
310                 315                 320                 325

acc ccc ggc act gaa ttg gtc ctg atc ggc atc cac atc gac ggc ccc   1123
Thr Pro Gly Thr Glu Leu Val Leu Ile Gly Ile His Ile Asp Gly Pro
                330                 335                 340

acc ttg ctc gca ctg cta caa ggc gcg acg ctt acc gat gcg gaa gtg   1171
Thr Leu Leu Ala Leu Leu Gln Gly Ala Thr Leu Thr Asp Ala Glu Val
            345                 350                 355

gcg gca ctg gtt ttg tgagttcctc aagtccgtga att                    1209
Ala Ala Leu Val Leu
        360


<210> 2680
<211> 362
<212> PRT
<213> Corynebacterium glutamicum

<400> 2680
Met Ala Thr Thr Thr Pro Val Thr Val Leu Ser Gly Phe Leu Gly Ser
  1               5                  10                  15

Gly Lys Thr Thr Leu Leu Asn Gln Ile Leu His His Arg Gly Ser Arg
             20                  25                  30

Lys Ile Ala Val Ile Val Asn Asp Phe Ser Glu Ile Asn Ile Asp Ala
         35                  40                  45
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```
Ala Leu Ile Ala Ser Glu Gly His Leu Thr Arg Gly Glu Asp Arg Phe
     50                  55                  60

Val Glu Leu Thr Asn Gly Cys Ile Cys Cys Thr Leu Arg Glu Asp Leu
 65                  70                  75                  80

Val Asp Ser Val Gly Glu Leu Ala Ser Ser Asp Arg Phe Asp His Ile
                85                  90                  95

Val Ile Glu Ser Thr Gly Ile Ser Glu Pro Met Pro Val Ala Ala Thr
            100                 105                 110

Phe Glu Trp Gln Trp Asp Asp Gly Thr Arg Leu Ala Asp Lys Ala Pro
        115                 120                 125

Ile Asp Thr Met Val Thr Leu Val Asp Ala Thr Gln Phe Ile Asp Leu
    130                 135                 140

Ile Arg Lys Asn Thr Ser Leu Thr Glu Ala Asp Met Gly Ala Thr Glu
145                 150                 155                 160

Asp Asp Glu Arg Thr Ile Ala Asp Leu Leu Thr Asp Gln Ile Glu Phe
                165                 170                 175

Ala Asp Arg Ile Tyr Ile Thr Lys Ser Asp Leu Val Asp Arg Thr Val
            180                 185                 190

Leu Glu Gln Thr Arg Ala Leu Ile Ala Ser Met Ser Pro Arg Ala Arg
        195                 200                 205

Ile Asp Leu Leu Ile Asp Gly Leu Asn Asp Gly Ser Pro Ile Thr Asp
    210                 215                 220

Asp Ile Leu Gly Ala Phe Leu Tyr Asp Glu Ala Thr Ala Arg Ala Tyr
225                 230                 235                 240

Glu Gly Tyr Thr Glu Glu Leu Glu Asn Pro His Thr Pro Glu Thr Glu
                245                 250                 255

Glu Tyr Gly Ile Ser Ser Val Val Phe Arg Ser Asp Arg Pro Phe Asn
            260                 265                 270

Lys Asp Arg Leu Leu Gln Val Leu Arg Ser Thr Thr Gly Leu Val Arg
        275                 280                 285

Ser Lys Gly Tyr Cys Trp Ile Ala Asp His Leu Asn Ile Val Gln Val
    290                 295                 300

Trp His Gln Ala Gly Pro Asn Leu Ser Ile Arg Pro Ala Ala Tyr Trp
305                 310                 315                 320

Ala Asn Ser Glu Ile Thr Pro Gly Thr Glu Leu Val Leu Ile Gly Ile
                325                 330                 335

His Ile Asp Gly Pro Thr Leu Leu Ala Leu Leu Gln Gly Ala Thr Leu
            340                 345                 350

Thr Asp Ala Glu Val Ala Ala Leu Val Leu
        355                 360
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<210> 2681
<211> 993
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(970)
<223> RXA02325

<400> 2681
gggcagagat ttgaagatgg agaccaaggc tcaaagggaa tccatgccgt cttggtttaa 60

tactgcaccc gtctaatgaa aatcattact attaggtgtc atg atg gac cat gca 115
Met Met Asp His Ala
1 5

cac gat tcc tgc tca cca act ctg cgc cgt gat ttg gag gtc act ggc 163
His Asp Ser Cys Ser Pro Thr Leu Arg Arg Asp Leu Glu Val Thr Gly
10 15 20

cag ctc caa cct gag aaa gct gtc gat tta gca gcg ccg cac gaa ggg 211
Gln Leu Gln Pro Glu Lys Ala Val Asp Leu Ala Ala Pro His Glu Gly
25 30 35

aag gtt gcc aat ata acg aag gtg acc tcc tca aat atg gag cac acc 259
Lys Val Ala Asn Ile Thr Lys Val Thr Ser Ser Asn Met Glu His Thr
40 45 50

atc acg cag gcc tca aaa gct aag gag gtg gtg gtg ctc att ggt cac 307
Ile Thr Gln Ala Ser Lys Ala Lys Glu Val Val Val Leu Ile Gly His
55 60 65

tcc ctg ctg ccc aca ttt cag gat ttg gaa aaa gac att ctg cac ttt 355
Ser Leu Leu Pro Thr Phe Gln Asp Leu Glu Lys Asp Ile Leu His Phe
70 75 80 85

cag gca ggt aat aaa ggg cga ttt tct gta gcg att gtt gat cct gat 403
Gln Ala Gly Asn Lys Gly Arg Phe Ser Val Ala Ile Val Asp Pro Asp
90 95 100

cgc agt gca gat gtg gtt gcc aga ttt agg cca aaa cag att ccg gtg 451
Arg Ser Ala Asp Val Val Ala Arg Phe Arg Pro Lys Gln Ile Pro Val
105 110 115

gca tac gtg gtg aaa gat ggc gcc agc att gcg gag ttc aac tcg ctc 499
Ala Tyr Val Val Lys Asp Gly Ala Ser Ile Ala Glu Phe Asn Ser Leu
120 125 130

aac aag gag ccg gtt gca caa tgg ctt gat cat ttt gtg tcg cgg gaa 547
Asn Lys Glu Pro Val Ala Gln Trp Leu Asp His Phe Val Ser Arg Glu
135 140 145

acg atc ccc aat gaa aaa gag ggg gac gtc gat aag caa ata gac ccg 595
Thr Ile Pro Asn Glu Lys Glu Gly Asp Val Asp Lys Gln Ile Asp Pro
150 155 160 165

cgc ctg tgg cgg gca gcg gaa ttg gtg aac gcc ggt gat ttt cgc gcg 643
Arg Leu Trp Arg Ala Ala Glu Leu Val Asn Ala Gly Asp Phe Arg Ala
170 175 180

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gcg ttg gcg ttg tat gag cag ttg ccg cag gat gcg acg gtg aag cgg   691
Ala Leu Ala Leu Tyr Glu Gln Leu Pro Gln Asp Ala Thr Val Lys Arg
            185                 190                 195

gcg cac gcg gcg gtg tcg gta ttg gcg cgg atg tct gtg gcg gat cgg   739
Ala His Ala Ala Val Ser Val Leu Ala Arg Met Ser Val Ala Asp Arg
        200                 205                 210

gga gag gat ccg atc gag aag tcg cgc cgg gat cca gac gat gtg aac   787
Gly Glu Asp Pro Ile Glu Lys Ser Arg Arg Asp Pro Asp Asp Val Asn
    215                 220                 225

aag gcg ctg gcg gcg gcg gat atg tat gtg ttg atg aat cag ccg gac   835
Lys Ala Leu Ala Ala Ala Asp Met Tyr Val Leu Met Asn Gln Pro Asp
230                 235                 240                 245

aca gcg ctc gcg cac ctt gca gca cta ttg cca aaa ccg gag gct gcc   883
Thr Ala Leu Ala His Leu Ala Ala Leu Leu Pro Lys Pro Glu Ala Ala
                250                 255                 260

cgg cgg atc gtg gag ttg ctg aac ttg ttt gat ccg ctg gac ctg gtc   931
Arg Arg Ile Val Glu Leu Leu Asn Leu Phe Asp Pro Leu Asp Leu Val
            265                 270                 275

gca ttg gaa atc agg gcg cag gtg ggg aat gca atg agc taagaaaaca    980
Ala Leu Glu Ile Arg Ala Gln Val Gly Asn Ala Met Ser
        280                 285                 290

ctttaaatat tct                                                   993


<210> 2682
<211> 290
<212> PRT
<213> Corynebacterium glutamicum

<400> 2682
Met Met Asp His Ala His Asp Ser Cys Ser Pro Thr Leu Arg Arg Asp
  1               5                  10                  15

Leu Glu Val Thr Gly Gln Leu Gln Pro Glu Lys Ala Val Asp Leu Ala
             20                  25                  30

Ala Pro His Glu Gly Lys Val Ala Asn Ile Thr Lys Val Thr Ser Ser
         35                  40                  45

Asn Met Glu His Thr Ile Thr Gln Ala Ser Lys Ala Lys Glu Val Val
     50                  55                  60

Val Leu Ile Gly His Ser Leu Leu Pro Thr Phe Gln Asp Leu Glu Lys
 65                  70                  75                  80

Asp Ile Leu His Phe Gln Ala Gly Asn Lys Gly Arg Phe Ser Val Ala
                 85                  90                  95

Ile Val Asp Pro Asp Arg Ser Ala Asp Val Val Ala Arg Phe Arg Pro
            100                 105                 110

Lys Gln Ile Pro Val Ala Tyr Val Val Lys Asp Gly Ala Ser Ile Ala
        115                 120                 125
```

```
Glu Phe Asn Ser Leu Asn Lys Glu Pro Val Ala Gln Trp Leu Asp His
    130                 135                 140

Phe Val Ser Arg Glu Thr Ile Pro Asn Glu Lys Glu Gly Asp Val Asp
145                 150                 155                 160

Lys Gln Ile Asp Pro Arg Leu Trp Arg Ala Ala Glu Leu Val Asn Ala
                165                 170                 175

Gly Asp Phe Arg Ala Ala Leu Ala Leu Tyr Glu Gln Leu Pro Gln Asp
            180                 185                 190

Ala Thr Val Lys Arg Ala His Ala Ala Val Ser Val Leu Ala Arg Met
        195                 200                 205

Ser Val Ala Asp Arg Gly Glu Asp Pro Ile Glu Lys Ser Arg Arg Asp
    210                 215                 220

Pro Asp Asp Val Asn Lys Ala Leu Ala Ala Ala Asp Met Tyr Val Leu
225                 230                 235                 240

Met Asn Gln Pro Asp Thr Ala Leu Ala His Leu Ala Ala Leu Leu Pro
                245                 250                 255

Lys Pro Glu Ala Ala Arg Arg Ile Val Glu Leu Leu Asn Leu Phe Asp
            260                 265                 270

Pro Leu Asp Leu Val Ala Leu Glu Ile Arg Ala Gln Val Gly Asn Ala
        275                 280                 285

Met Ser
    290


<210> 2683
<211> 489
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(466)
<223> RXA02331

<400> 2683
tgcagcgtgc attcccacca tcgggtcaag aatctatccg cccagcccct gtccaactcc 60

tcaactaaaa aggcagcact taaaaaacac tatggaaccc atg gaa cta aac ggc   115
                                            Met Glu Leu Asn Gly
                                              1               5

ggt cgt ttc tac gcc cgc aag ctc acc tca gat aat cgg att gat gat   163
Gly Arg Phe Tyr Ala Arg Lys Leu Thr Ser Asp Asn Arg Ile Asp Asp
                  10                  15                  20

gtc ccg gcg ctc tca ctg atc ctt gcc gat gca gca cag ttc atc gcg   211
Val Pro Ala Leu Ser Leu Ile Leu Ala Asp Ala Ala Gln Phe Ile Ala
              25                  30                  35

gac gcc acc aca gcc tgg cac gag gac acc gaa tac acc tgg gct atc   259
```

```
Asp Ala Thr Thr Ala Trp His Glu Asp Thr Glu Tyr Thr Trp Ala Ile
         40                  45                  50

tgc gag cag acc agt gtt gaa cta ctg gca ctg gca cgc ctt gat ccc   307
Cys Glu Gln Thr Ser Val Glu Leu Leu Ala Leu Ala Arg Leu Asp Pro
     55                  60                  65

aag cag cgc aca ctc gag gtc gtg ccc gca ggt gat ccc gcc acc caa   355
Lys Gln Arg Thr Leu Glu Val Val Pro Ala Gly Asp Pro Ala Thr Gln
 70                  75                  80                  85

ttg ccc aat gat cca gtg ctc gct ccg aaa acc atc ggc gat gct gtg   403
Leu Pro Asn Asp Pro Val Leu Ala Pro Lys Thr Ile Gly Asp Ala Val
                 90                  95                 100

gcg gag ggc cgc gac acc atc acc aga tgg gca caa ggc tat tta gaa   451
Ala Glu Gly Arg Asp Thr Ile Thr Arg Trp Ala Gln Gly Tyr Leu Glu
            105                 110                 115

atc agc ctc act gat taggttctct ccgaaatggg cac                    489
Ile Ser Leu Thr Asp
        120
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Sequence Listing - 2009-12-22 - 15:00:00

<210> 2684
<211> 122
<212> PRT
<213> Corynebacterium glutamicum

<400> 2684

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Met Glu Leu Asn Gly Gly Arg Phe Tyr Ala Arg Lys Leu Thr Ser Asp
  1               5                  10                  15

Asn Arg Ile Asp Asp Val Pro Ala Leu Ser Leu Ile Leu Ala Asp Ala
             20                  25                  30

Ala Gln Phe Ile Ala Asp Ala Thr Thr Ala Trp His Glu Asp Thr Glu
         35                  40                  45

Tyr Thr Trp Ala Ile Cys Glu Gln Thr Ser Val Glu Leu Leu Ala Leu
     50                  55                  60

Ala Arg Leu Asp Pro Lys Gln Arg Thr Leu Glu Val Val Pro Ala Gly
 65                  70                  75                  80

Asp Pro Ala Thr Gln Leu Pro Asn Asp Pro Val Leu Ala Pro Lys Thr
                 85                  90                  95

Ile Gly Asp Ala Val Ala Glu Gly Arg Asp Thr Ile Thr Arg Trp Ala
            100                 105                 110

Gln Gly Tyr Leu Glu Ile Ser Leu Thr Asp
        115                 120
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<210> 2685
<211> 303
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(280)
<223> RXA02336

<400> 2685
caaatccaca cgacacaatt acacaaattt taccttgtgc attgaaagcc gtcagccgat 60

tagcgttaaa gaaaataaaa aaccacaagg ggagcacacc atg aaa gac acc acc 115
Met Lys Asp Thr Thr
1 5

gag atc aac tgg caa ggc tac gcc gat gga acc gca atc cgc gaa gca 163
Glu Ile Asn Trp Gln Gly Tyr Ala Asp Gly Thr Ala Ile Arg Glu Ala
10 15 20

gtc atc cac tcc att gaa cga gaa gta tca gcg ggc gag cag cca acc 211
Val Ile His Ser Ile Glu Arg Glu Val Ser Ala Gly Glu Gln Pro Thr
25 30 35

cca aac gat ctt aaa ttt ctc ggg ctg ttc cag cac cgc gcc ggg tat 259
Pro Asn Asp Leu Lys Phe Leu Gly Leu Phe Gln His Arg Ala Gly Tyr
40 45 50

gtg ggc tcg ttg atc acc ggt taagtgtggg gagcaggctg gct 303
Val Gly Ser Leu Ile Thr Gly
55 60

<210> 2686
<211> 60
<212> PRT
<213> Corynebacterium glutamicum

<400> 2686
Met Lys Asp Thr Thr Glu Ile Asn Trp Gln Gly Tyr Ala Asp Gly Thr
1 5 10 15

Ala Ile Arg Glu Ala Val Ile His Ser Ile Glu Arg Glu Val Ser Ala
20 25 30

Gly Glu Gln Pro Thr Pro Asn Asp Leu Lys Phe Leu Gly Leu Phe Gln
35 40 45

His Arg Ala Gly Tyr Val Gly Ser Leu Ile Thr Gly
50 55 60

<210> 2687
<211> 444
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(421)
<223> RXA02347

<400> 2687
acggttggaa cagagctgca cctttaatca ggcagttgct ggccaactga gttagcctaa 60

aacgatgaag aaaaatcctt tggttgaatg ggtctgggtt atg gat gaa ctc ggg 115

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                                                  Met Asp Glu Leu Gly
                                                    1               5

gtt ggc tgg tgc caa tgc gag aaa gat tcc atc acc gga aaa gca cca   163
Val Gly Trp Cys Gln Cys Glu Lys Asp Ser Ile Thr Gly Lys Ala Pro
                10                  15                  20

cat ccc gtg aac aag cca ctg gtc acc aaa tcc att atc agg gct cta   211
His Pro Val Asn Lys Pro Leu Val Thr Lys Ser Ile Ile Arg Ala Leu
            25                  30                  35

ggc gat gtc ccc gat gtc atg agc aac cag gac atc agc ctt gtg gtg   259
Gly Asp Val Pro Asp Val Met Ser Asn Gln Asp Ile Ser Leu Val Val
        40                  45                  50

gtg gat ttg tgg aaa ttc gat acc att act cct cca atc gca gaa tcc   307
Val Asp Leu Trp Lys Phe Asp Thr Ile Thr Pro Pro Ile Ala Glu Ser
    55                  60                  65

ctc atg cgt tcc gtc aaa gct gtt aac ggt gag atg cac ccg cag tat   355
Leu Met Arg Ser Val Lys Ala Val Asn Gly Glu Met His Pro Gln Tyr
70                  75                  80                  85

ccc acc gcg aca gca atg gct gcg atc aag cat ttc tcc aac act ttt   403
Pro Thr Ala Thr Ala Met Ala Ala Ile Lys His Phe Ser Asn Thr Phe
                90                  95                  100

gat gga cag att aac gct taaaaggcct gttatagact gat                444
Asp Gly Gln Ile Asn Ala
            105
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<210> 2688
<211> 107
<212> PRT
<213> Corynebacterium glutamicum

<400> 2688

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Met Asp Glu Leu Gly Val Gly Trp Cys Gln Cys Glu Lys Asp Ser Ile
  1               5                  10                  15

Thr Gly Lys Ala Pro His Pro Val Asn Lys Pro Leu Val Thr Lys Ser
            20                  25                  30

Ile Ile Arg Ala Leu Gly Asp Val Pro Asp Val Met Ser Asn Gln Asp
        35                  40                  45

Ile Ser Leu Val Val Val Asp Leu Trp Lys Phe Asp Thr Ile Thr Pro
    50                  55                  60

Pro Ile Ala Glu Ser Leu Met Arg Ser Val Lys Ala Val Asn Gly Glu
65                  70                  75                  80

Met His Pro Gln Tyr Pro Thr Ala Thr Ala Met Ala Ala Ile Lys His
                85                  90                  95

Phe Ser Asn Thr Phe Asp Gly Gln Ile Asn Ala
            100                 105
```

<210> 2689

<211> 490
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(490)
<223> RXA02349

<400> 2689
cttcgagtgc tgtggcgaaa aatccgaact ccaaagaact agcctaagaa ctagccccat 60

gagctatccc tcaaaaaatt actgatagtg aggttttcgc atg tca act gca tat 115
Met Ser Thr Ala Tyr
1 5

ttt att gcg cac gga aac gat acg tac cgc cca acg gag cat tcc agc 163
Phe Ile Ala His Gly Asn Asp Thr Tyr Arg Pro Thr Glu His Ser Ser
10 15 20

ggt gcg tgg cgc gat gat gaa ctc cac ctt gca ccg gtt gcc ggt ttg 211
Gly Ala Trp Arg Asp Asp Glu Leu His Leu Ala Pro Val Ala Gly Leu
25 30 35

gtg att cac cat atg gaa cgt tgg cgc agg gaa gtg gtt ggc gat gct 259
Val Ile His His Met Glu Arg Trp Arg Arg Glu Val Val Gly Asp Ala
40 45 50

ttg gtg ttc agc cgt ttt agt ttg gag gtc ttg ggc cag atc gct cgg 307
Leu Val Phe Ser Arg Phe Ser Leu Glu Val Leu Gly Gln Ile Ala Arg
55 60 65

gat gat gtc acc ttg aga aca gag atc gtt cgt ccc ggg cgc acc att 355
Asp Asp Val Thr Leu Arg Thr Glu Ile Val Arg Pro Gly Arg Thr Ile
70 75 80 85

gaa ctt att gaa acc gtg gct gaa atc aac ggc aga gtg acg att cgt 403
Glu Leu Ile Glu Thr Val Ala Glu Ile Asn Gly Arg Val Thr Ile Arg
90 95 100

gca cgc gcc tgg ttg ctg aag acc tct gat ctt gcc cat att tct ggc 451
Ala Arg Ala Trp Leu Leu Lys Thr Ser Asp Leu Ala His Ile Ser Gly
105 110 115

gat act ttt gaa gcg ttg ccg tca atg act gaa ctg gca 490
Asp Thr Phe Glu Ala Leu Pro Ser Met Thr Glu Leu Ala
120 125 130

<210> 2690
<211> 130
<212> PRT
<213> Corynebacterium glutamicum

<400> 2690
Met Ser Thr Ala Tyr Phe Ile Ala His Gly Asn Asp Thr Tyr Arg Pro
1 5 10 15

Thr Glu His Ser Ser Gly Ala Trp Arg Asp Asp Glu Leu His Leu Ala
20 25 30

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Pro Val Ala Gly Leu Val Ile His His Met Glu Arg Trp Arg Arg Glu
         35                  40                  45

Val Val Gly Asp Ala Leu Val Phe Ser Arg Phe Ser Leu Glu Val Leu
     50                  55                  60

Gly Gln Ile Ala Arg Asp Asp Val Thr Leu Arg Thr Glu Ile Val Arg
 65                  70                  75                  80

Pro Gly Arg Thr Ile Glu Leu Ile Glu Thr Val Ala Glu Ile Asn Gly
                 85                  90                  95

Arg Val Thr Ile Arg Ala Arg Ala Trp Leu Leu Lys Thr Ser Asp Leu
            100                 105                 110

Ala His Ile Ser Gly Asp Thr Phe Glu Ala Leu Pro Ser Met Thr Glu
        115                 120                 125

Leu Ala
    130
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Application Ref: 2019-00-00 Input Set: 2019-00-00 Output Set: 2019-00-00

<210> 2691
<211> 578
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(555)
<223> RXA02352

<400> 2691

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atc tac aac aca tcg agc acg ctc aac ggc ttc atc gca gac aaa gac   48
Ile Tyr Asn Thr Ser Ser Thr Leu Asn Gly Phe Ile Ala Asp Lys Asp
  1               5                  10                  15

aac tcc ctg caa tgg ctt ttc gac gtc ccc ggc agc gac ggt gcc tct   96
Asn Ser Leu Gln Trp Leu Phe Asp Val Pro Gly Ser Asp Gly Ala Ser
             20                  25                  30

gaa gac ttc ggt aat ttc ctt tca aaa gcc ggc acc atc gta atg gga   144
Glu Asp Phe Gly Asn Phe Leu Ser Lys Ala Gly Thr Ile Val Met Gly
         35                  40                  45

tcc acc acc tat gaa tgg ctg ctc aag gac cta gat ttc atc agc gat   192
Ser Thr Thr Tyr Glu Trp Leu Leu Lys Asp Leu Asp Phe Ile Ser Asp
     50                  55                  60

ccc cac aag tgg acc gat gtg tat ggc gat cgc ccc acg tgg gtg ttc   240
Pro His Lys Trp Thr Asp Val Tyr Gly Asp Arg Pro Thr Trp Val Phe
 65                  70                  75                  80

agc agc agg aac ttg gaa acc ccg gaa gga aaa cct gtc aag gta gta   288
Ser Ser Arg Asn Leu Glu Thr Pro Glu Gly Lys Pro Val Lys Val Val
                 85                  90                  95

aat gga gat gtc gcc gat gtt ctc ccc gcc ata ctg gaa gag agt cca   336
Asn Gly Asp Val Ala Asp Val Leu Pro Ala Ile Leu Glu Glu Ser Pro
            100                 105                 110
```

```
gag aac act gat att tgg atc gtc ggt ggt ggc gat ctg gcg ggt caa   384
Glu Asn Thr Asp Ile Trp Ile Val Gly Gly Gly Asp Leu Ala Gly Gln
        115                 120                 125

ttc ttt gat gcg ggt gca ctc gat cgg atc atc ttg acc atg gcg cca   432
Phe Phe Asp Ala Gly Ala Leu Asp Arg Ile Ile Leu Thr Met Ala Pro
    130                 135                 140

gtg ttt ctc gat gaa ggg cag cca gcg atg ccc cgc cgg atc gaa agt   480
Val Phe Leu Asp Glu Gly Gln Pro Ala Met Pro Arg Arg Ile Glu Ser
145                 150                 155                 160

aat cgt ctc cgc acc gta aat gtc cgc gag gtt gga caa ttc acc gag   528
Asn Arg Leu Arg Thr Val Asn Val Arg Glu Val Gly Gln Phe Thr Glu
                165                 170                 175

atc acc ctg gag acg att aaa ggg gct taatttgtag agttttgggc         575
Ile Thr Leu Glu Thr Ile Lys Gly Ala
            180                 185

aga                                                               578
```

<210> 2692
<211> 185
<212> PRT
<213> Corynebacterium glutamicum

<400> 2692

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Ile Tyr Asn Thr Ser Ser Thr Leu Asn Gly Phe Ile Ala Asp Lys Asp
  1               5                  10                  15

Asn Ser Leu Gln Trp Leu Phe Asp Val Pro Gly Ser Asp Gly Ala Ser
             20                  25                  30

Glu Asp Phe Gly Asn Phe Leu Ser Lys Ala Gly Thr Ile Val Met Gly
         35                  40                  45

Ser Thr Thr Tyr Glu Trp Leu Leu Lys Asp Leu Asp Phe Ile Ser Asp
     50                  55                  60

Pro His Lys Trp Thr Asp Val Tyr Gly Asp Arg Pro Thr Trp Val Phe
 65                  70                  75                  80

Ser Ser Arg Asn Leu Glu Thr Pro Glu Gly Lys Pro Val Lys Val Val
                 85                  90                  95

Asn Gly Asp Val Ala Asp Val Leu Pro Ala Ile Leu Glu Glu Ser Pro
            100                 105                 110

Glu Asn Thr Asp Ile Trp Ile Val Gly Gly Gly Asp Leu Ala Gly Gln
        115                 120                 125

Phe Phe Asp Ala Gly Ala Leu Asp Arg Ile Ile Leu Thr Met Ala Pro
    130                 135                 140

Val Phe Leu Asp Glu Gly Gln Pro Ala Met Pro Arg Arg Ile Glu Ser
145                 150                 155                 160

Asn Arg Leu Arg Thr Val Asn Val Arg Glu Val Gly Gln Phe Thr Glu
                165                 170                 175
```

```
Ile Thr Leu Glu Thr Ile Lys Gly Ala
            180                 185


<210> 2693
<211> 1119
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1096)
<223> RXA02356

<400> 2693
ttggcagtag ccatgcgttc tgctcctgac cttgaacagc ggtcccaatt tagacccgct 60

aaacccacaa tgtgtactgg tgctggtaat ttagtagaac atg gca acg gtc aca   115
                                            Met Ala Thr Val Thr
                                              1               5

ttc gac aag gtc aca atc cgg tac ccc ggc gcg gag cgc gca aca gtt   163
Phe Asp Lys Val Thr Ile Arg Tyr Pro Gly Ala Glu Arg Ala Thr Val
                 10                  15                  20

cat gag ctt gat tta gat atc gct gat ggc gag ttt ttg gtg ctc gtc   211
His Glu Leu Asp Leu Asp Ile Ala Asp Gly Glu Phe Leu Val Leu Val
             25                  30                  35

ggc cct tcg ggt tgt ggt aaa tcc act acg ctg cgt gct ttg gcg ggg   259
Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu Arg Ala Leu Ala Gly
         40                  45                  50

ctt gag ggc gtg gag tcg ggt gtg atc aaa att gat ggc aag gat gtc   307
Leu Glu Gly Val Glu Ser Gly Val Ile Lys Ile Asp Gly Lys Asp Val
     55                  60                  65

act ggt cag gag ccg gcg gat cgc gat atc gcg atg gtg ttc cag aat   355
Thr Gly Gln Glu Pro Ala Asp Arg Asp Ile Ala Met Val Phe Gln Asn
 70                  75                  80                  85

tat gct ctg tac cct cac atg acg gtg gcg aag aat atg ggt ttt gcg   403
Tyr Ala Leu Tyr Pro His Met Thr Val Ala Lys Asn Met Gly Phe Ala
                 90                  95                 100

ctg aag ttg gct aag ctg ccg cag gcg cag atc gat gcg aag gtc aat   451
Leu Lys Leu Ala Lys Leu Pro Gln Ala Gln Ile Asp Ala Lys Val Asn
             105                 110                 115

gag gct gcg gaa att ctt ggg ttg acg gag ttt ttg gat cgc aag cct   499
Glu Ala Ala Glu Ile Leu Gly Leu Thr Glu Phe Leu Asp Arg Lys Pro
         120                 125                 130

aag gat tta tcg ggt ggt cag cgt cag cgt gtg gcg atg ggt cgc gcg   547
Lys Asp Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala
     135                 140                 145

ttg gtg cgt gat ccg aag gtg ttc ctc atg gat gag ccg ctg tcc aac   595
Leu Val Arg Asp Pro Lys Val Phe Leu Met Asp Glu Pro Leu Ser Asn
150                 155                 160                 165
```

```
ctg gat gcg aaa ttg cgc gtg caa acc cgc gcg gag gtc gct gct ttg   643
Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Ala Glu Val Ala Ala Leu
                170                 175                 180

cag cgt cgc ctg ggc acc acc acg gtg tat gtc acc cac gat cag gtt   691
Gln Arg Arg Leu Gly Thr Thr Thr Val Tyr Val Thr His Asp Gln Val
            185                 190                 195

gag gca atg acg atg ggc gat cgg gtt gcg gtg ctc aag gac ggg ttg   739
Glu Ala Met Thr Met Gly Asp Arg Val Ala Val Leu Lys Asp Gly Leu
        200                 205                 210

ctg cag cag gtc gca ccg ccc agg gag ctt tac gac gcc ccg gtc aac   787
Leu Gln Gln Val Ala Pro Pro Arg Glu Leu Tyr Asp Ala Pro Val Asn
    215                 220                 225

gaa ttc gtt gcg ggc ttc atc ggc tcg ccg tcc atg aac ctc ttc cct   835
Glu Phe Val Ala Gly Phe Ile Gly Ser Pro Ser Met Asn Leu Phe Pro
230                 235                 240                 245

gcc aac ggg cac aag atg ggt gtg cgc ccg gag aag atg ctg gtc aat   883
Ala Asn Gly His Lys Met Gly Val Arg Pro Glu Lys Met Leu Val Asn
                250                 255                 260

gag acc cct gag ggt ttc aca agc att gat gct gtg gtg gat atc gtc   931
Glu Thr Pro Glu Gly Phe Thr Ser Ile Asp Ala Val Val Asp Ile Val
            265                 270                 275

gag gag ctt ggc tcc gaa tcg tat gtt tat gcc act tgg gag ggc cac   979
Glu Glu Leu Gly Ser Glu Ser Tyr Val Tyr Ala Thr Trp Glu Gly His
        280                 285                 290

cgc ctg gtg gcc cgt tgg gtg gaa ggc ccc gtg cca gcc cct ggc acg   1027
Arg Leu Val Ala Arg Trp Val Glu Gly Pro Val Pro Ala Pro Gly Thr
    295                 300                 305

cct gtg act ttt tcc tat gat gcg gcg cag gcg cat cat ttc gat ctg   1075
Pro Val Thr Phe Ser Tyr Asp Ala Ala Gln Ala His His Phe Asp Leu
310                 315                 320                 325

gag tcg ggc gag cgt atc gct tagtttcgga cgtggggagg cgt             1119
Glu Ser Gly Glu Arg Ile Ala
                330
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<210> 2694
<211> 332
<212> PRT
<213> Corynebacterium glutamicum

<400> 2694

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Met Ala Thr Val Thr Phe Asp Lys Val Thr Ile Arg Tyr Pro Gly Ala
  1               5                  10                  15

Glu Arg Ala Thr Val His Glu Leu Asp Leu Asp Ile Ala Asp Gly Glu
             20                  25                  30

Phe Leu Val Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu
         35                  40                  45
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Arg Ala Leu Ala Gly Leu Glu Gly Val Glu Ser Gly Val Ile Lys Ile
     50                  55                  60

Asp Gly Lys Asp Val Thr Gly Gln Glu Pro Ala Asp Arg Asp Ile Ala
 65                  70                  75                  80

Met Val Phe Gln Asn Tyr Ala Leu Tyr Pro His Met Thr Val Ala Lys
                85                  90                  95

Asn Met Gly Phe Ala Leu Lys Leu Ala Lys Leu Pro Gln Ala Gln Ile
            100                 105                 110

Asp Ala Lys Val Asn Glu Ala Ala Glu Ile Leu Gly Leu Thr Glu Phe
        115                 120                 125

Leu Asp Arg Lys Pro Lys Asp Leu Ser Gly Gly Gln Arg Gln Arg Val
    130                 135                 140

Ala Met Gly Arg Ala Leu Val Arg Asp Pro Lys Val Phe Leu Met Asp
145                 150                 155                 160

Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Ala
                165                 170                 175

Glu Val Ala Ala Leu Gln Arg Arg Leu Gly Thr Thr Thr Val Tyr Val
            180                 185                 190

Thr His Asp Gln Val Glu Ala Met Thr Met Gly Asp Arg Val Ala Val
        195                 200                 205

Leu Lys Asp Gly Leu Leu Gln Gln Val Ala Pro Pro Arg Glu Leu Tyr
    210                 215                 220

Asp Ala Pro Val Asn Glu Phe Val Ala Gly Phe Ile Gly Ser Pro Ser
225                 230                 235                 240

Met Asn Leu Phe Pro Ala Asn Gly His Lys Met Gly Val Arg Pro Glu
                245                 250                 255

Lys Met Leu Val Asn Glu Thr Pro Glu Gly Phe Thr Ser Ile Asp Ala
            260                 265                 270

Val Val Asp Ile Val Glu Glu Leu Gly Ser Glu Ser Tyr Val Tyr Ala
        275                 280                 285

Thr Trp Glu Gly His Arg Leu Val Ala Arg Trp Val Glu Gly Pro Val
    290                 295                 300

Pro Ala Pro Gly Thr Pro Val Thr Phe Ser Tyr Asp Ala Ala Gln Ala
305                 310                 315                 320

His His Phe Asp Leu Glu Ser Gly Glu Arg Ile Ala
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Met Val Ser Tyr Ser
1 5

gtg cac ggc gca cta gat atc gac ggc agc ctc aaa aaa ctc acc ctc 163
Val His Gly Ala Leu Asp Ile Asp Gly Ser Leu Lys Lys Leu Thr Leu
10 15 20

gat ttc ctc aat aaa cta gcc acc aat cca gct tcc ccg ggg ctt cat 211
Asp Phe Leu Asn Lys Leu Ala Thr Asn Pro Ala Ser Pro Gly Leu His
25 30 35

att gag ccc atc aaa aac agc atc gac tcc cgc gtc cgc aca ggt cgg 259
Ile Glu Pro Ile Lys Asn Ser Ile Asp Ser Arg Val Arg Thr Gly Arg
40 45 50

gtc aat gat caa ttc cgc gca gtg ctt ttt gag ctt cac gac gaa ttt 307
Val Asn Asp Gln Phe Arg Ala Val Leu Phe Glu Leu His Asp Glu Phe
55 60 65

gat cat cac ttt gta gtg ggt ggg ttt atc ccc atg atg atg cca tca 355
Asp His His Phe Val Val Gly Gly Phe Ile Pro Met Met Met Pro Ser
70 75 80 85

cca agg cag gaa aaa tcc gcc ttg aag tca act ctg taacggcatt 401
Pro Arg Gln Glu Lys Ser Ala Leu Lys Ser Thr Leu
90 95

actcgactca tcg 414

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Ser Pro Gly Leu His Ile Glu Pro Ile Lys Asn Ser Ile Asp Ser Arg
35 40 45

Val Arg Thr Gly Arg Val Asn Asp Gln Phe Arg Ala Val Leu Phe Glu
50 55 60

Leu His Asp Glu Phe Asp His His Phe Val Val Gly Gly Phe Ile Pro
65 70 75 80

Met Met Met Pro Ser Pro Arg Gln Glu Lys Ser Ala Leu Lys Ser Thr
85 90 95

Leu

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Val Thr Ile Ser Arg
1 5

cga ctc aaa caa gag cgc agt ttc gct gac gat ctt caa gat ctc aaa 163
Arg Leu Lys Gln Glu Arg Ser Phe Ala Asp Asp Leu Gln Asp Leu Lys
10 15 20

act ctc aat gat caa ctg cgg ttt aca aac gcc aaa ttg caa gct cgc 211
Thr Leu Asn Asp Gln Leu Arg Phe Thr Asn Ala Lys Leu Gln Ala Arg
25 30 35

atc agt ggt att ggc aat gat gga aag aaa atc acg cgc cct acc cca 259
Ile Ser Gly Ile Gly Asn Asp Gly Lys Lys Ile Thr Arg Pro Thr Pro
40 45 50

ctc ctt gcg ctg gat ttt cag ctg acc gtt gaa gaa tac gaa acg atc 307
Leu Leu Ala Leu Asp Phe Gln Leu Thr Val Glu Glu Tyr Glu Thr Ile
55 60 65

att gca atc ttg gtg gaa gca gtt ggc gga aat caa tcc aag cca gcg 355
Ile Ala Ile Leu Val Glu Ala Val Gly Gly Asn Gln Ser Lys Pro Ala
70 75 80 85

att ctt aaa gat ctg ttt ata gaa tat cca ctc gtc ttc ctg gca gcg 403
Ile Leu Lys Asp Leu Phe Ile Glu Tyr Pro Leu Val Phe Leu Ala Ala
90 95 100

ctt tct gga acc gcc atg ctc gat gct caa gaa ggt ttc tgg cct gcg 451
Leu Ser Gly Thr Ala Met Leu Asp Ala Gln Glu Gly Phe Trp Pro Ala
105 110 115

ttc tgg aaa cgc act cag gtg tca gtt cca gag cat gta tac gac gcg 499
Phe Trp Lys Arg Thr Gln Val Ser Val Pro Glu His Val Tyr Asp Ala
120 125 130

atc cgt aaa gaa cta gtt aat agc atc cgc aaa aat ggc cta gaa act 547
Ile Arg Lys Glu Leu Val Asn Ser Ile Arg Lys Asn Gly Leu Glu Thr
135 140 145

ttt tct ctc gct gac ctc aat cga cgc gaa tat gtc gga ctc atc caa 595
Phe Ser Leu Ala Asp Leu Asn Arg Arg Glu Tyr Val Gly Leu Ile Gln
150 155 160 165

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ctt cac agt ggc ctt tct gca aaa gac atg ctc gcc ttg gtc aaa ttt   643
Leu His Ser Gly Leu Ser Ala Lys Asp Met Leu Ala Leu Val Lys Phe
                170                 175                 180

atc gat cac act cga gca gaa aac caa gga tgg gat tct ggt gag gac   691
Ile Asp His Thr Arg Ala Glu Asn Gln Gly Trp Asp Ser Gly Glu Asp
            185                 190                 195

ttt gca tca tat gcg aag agt gtc ttc tcc tcc ggg gac aac cta tta   739
Phe Ala Ser Tyr Ala Lys Ser Val Phe Ser Ser Gly Asp Asn Leu Leu
        200                 205                 210

acc acg gag tcg ctc aag caa tta gtc acc cac atc cct gcg cgt tcc   787
Thr Thr Glu Ser Leu Lys Gln Leu Val Thr His Ile Pro Ala Arg Ser
    215                 220                 225

gtc gac ttc atc gcc aga gtc tat gaa cta acc aat tgg tac cgc gac   835
Val Asp Phe Ile Ala Arg Val Tyr Glu Leu Thr Asn Trp Tyr Arg Asp
230                 235                 240                 245

ctc aaa gac ctc aat gaa gta gaa gcc ttc gta ggt act cat ggg ctg   883
Leu Lys Asp Leu Asn Glu Val Glu Ala Phe Val Gly Thr His Gly Leu
                250                 255                 260

ccg gaa ttg tct ttc aaa ttt ctt ctg gag tgt ctg agc ggc gaa gct   931
Pro Glu Leu Ser Phe Lys Phe Leu Leu Glu Cys Leu Ser Gly Glu Ala
            265                 270                 275

gaa caa att gcc gaa aag acg aaa gca gca cca gca agc ctg gaa aac   979
Glu Gln Ile Ala Glu Lys Thr Lys Ala Ala Pro Ala Ser Leu Glu Asn
        280                 285                 290

ctg gaa cct ccg cat ctc tat ctg gat cca cag agt ttt gaa ctc agt   1027
Leu Glu Pro Pro His Leu Tyr Leu Asp Pro Gln Ser Phe Glu Leu Ser
    295                 300                 305

ctt gtt ttc cca gcg atc tct aaa act gca gca ctt cag att cca gca   1075
Leu Val Phe Pro Ala Ile Ser Lys Thr Ala Ala Leu Gln Ile Pro Ala
310                 315                 320                 325

cca gaa tgg aca gtg att tat gac gga aac tcc att aaa gtt cgt ccc   1123
Pro Glu Trp Thr Val Ile Tyr Asp Gly Asn Ser Ile Lys Val Arg Pro
                330                 335                 340

gaa cag gac tgg tcc tac gga ggt ttc gcc gaa tac cgt ttg cct tta   1171
Glu Gln Asp Trp Ser Tyr Gly Gly Phe Ala Glu Tyr Arg Leu Pro Leu
            345                 350                 355

gac aaa ccg ctc tcc agc ttg aga gtc atc act cca aca gag aaa tcc   1219
Asp Lys Pro Leu Ser Ser Leu Arg Val Ile Thr Pro Thr Glu Lys Ser
        360                 365                 370

cta att ctg att gaa gga ttt ggc cac aag aat ccc att atg ttc ttt   1267
Leu Ile Leu Ile Glu Gly Phe Gly His Lys Asn Pro Ile Met Phe Phe
    375                 380                 385

aag aac aac ggt cag cca tat gca aac caa gaa atg ctc agt ggc aac   1315
Lys Asn Asn Gly Gln Pro Tyr Ala Asn Gln Glu Met Leu Ser Gly Asn
390                 395                 400                 405
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